

DETECTION AND CLASSIFICATION OF LEUKEMIA USING MACHINE LEARNING APPROACH

Submitted in partial fulfillment of the requirements for the
award of Bachelor of Technology degree in
Information Technology

By

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**INSTITUTE OF SCIENCE AND TECHNOLOGY
(DEEMED TO BE UNIVERSITY)**

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BONAFIDE CERTIFICATE

This is to certify that this Project Report is the bonafide work of **PALLAVI KUMARI (39120078)** who carried out the Project Phase-2 entitled “**Detection and Classification of Leukemia using Machine Learning Approach**” under my supervision from January 2022 to May 2023.

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ABSTRACT

In computer vision, traditional machine learning (TML) and deep learning (DL) methods have significantly contributed to the advancements of medical image analysis (MIA) by enhancing prediction accuracy, leading to appropriate planning and diagnosis. These methods substantially improved the diagnoses of automatic brain tumor and leukemia/blood cancer detection and can assist the hematologist and doctors by providing a second opinion. This review provides an in-depth analysis of available TML and DL techniques for MIA with a significant focus on leukocytes classification in blood smear images and other medical imaging domains, i.e., magnetic resonance imaging (MRI), CT images, X-ray, and ultrasounds. The proposed review's main impact is to find the most suitable TML and DL techniques in MIA, especially for leukocyte classification in blood smear images. The advanced DL techniques, particularly the evolving convolutional neural networks-based models in the MIA domain, are deeply investigated in this review article. The related literature study reveals that mainstream TML methods are vastly applied to microscopic blood smear images for white blood cells (WBC) analysis. They provide valuable information to medical specialists and help diagnose various hematic diseases such as AIDS and blood cancer (Leukaemia). Based on WBC related literature study and its extensive analysis presented in this study, we derive future research directions for scientists and practitioners working in the MIA domain. The decision tree model proposed in our experiments has achieved 97.45% of accuracy, 0.63 of Mathew's Correlation Coefficient (MCC) and 0.783 of area under Receiver Operating Characteristic (ROC) curve on the test set. We have also made the dataset and the source code of the methods used in this work available for future use by the researchers.

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CHAPTER 1

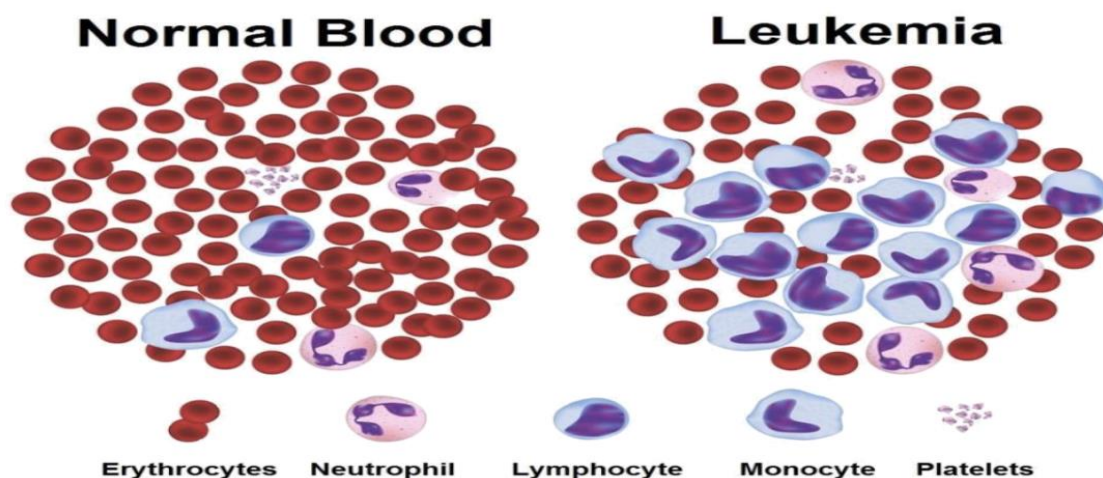
INTRODUCTION

Blood consists of plasma, and three different types of cells and they are: White Blood Cells, Red Blood Cells and Platelets and each of these performs particular task. Red blood cells transport oxygen from the lungs to the tissues of the body and vice versa. White blood cells help the body to fight against diseases and infections. Platelets help to clot and control bleeding. Leukemia is cancer of blood cells in which number of white cells is increases numerously and those are immature cells that interfere with other blood cells, usually red blood cells and platelets. Our body's white blood cell ratio is 1000:1. It means that between 1000 red blood cells there is 1 white blood cell. Leukemia that caused due to lymphoid cells is called lymphocytic or lymphoblastic leukemia and if it is caused due to myeloid cells then it is known as myelogenous or myeloid leukemia. It is grouped in two ways: acute or chronic, grouped according to how fast the cells are growing. The abnormal blood cells in acute leukemia are usually immature blasts (young cells) that do not work properly. These cells are growing fast. Acute leukemia gets worse quickly unless it is immediately treated. Young blood cells are present in chronic leukemia, but also mature functional cells are produced. Blasts are growing slowly in chronic leukemia. It takes the disease longer to get worse.

Among all types of blood cancers, leukemia is the most common form of malignancy in different age groups, especially in children. This is abnormal phenomenon is caused by excessive proliferation and immature growth of blood cells, which can damage red blood cells, bone marrow, and the defense system. In the United States, more than 3.5% of new cancer cases are leukemia, and in 2018 alone, this country reported more than 60,000 new cases of this cancer. Malignant white blood cells, or lymphoblast, in the blood reach other organs, such as the spleen, brain, liver, and kidneys, and then metastasize to important tissues of the body. There are different types of leukemia that the matologists in cell transplant laboratories can differentiate/ diagnose based on microscopic images. If the slide is correctly stained, some types of leukemia can be more easily identified and distinguished than others, but more equipment is needed to determine underlying

leukemia. An early diagnosis of leukemia has always been a challenge to researchers, doctors, and hematologists. Enlargement of lymph nodes, pallor, fever, and weight loss are the symptoms of leukemia, but they can also be associated with other diseases. Leukemia diagnosis is difficult in its early stages due to the mild nature of the symptoms. The most common leukemia diagnosis method is the microscopic evaluation of PBS, but the golden standard for leukemia diagnosis only involves taking and analyzing bone marrow samples. In the last two decades, various studies have adopted machine learning (ML) and computer-aided diagnostic methods for laboratory image analysis, hoping to overcome the limitations of a late leukemia diagnosis and determine its subgroups.

These studies have analyzed blood smears images for diagnosing, differentiating, and counting the cells in various types of leukemia. ML is a well-known branch of artificial intelligence, comprising algorithms and mathematical relations, which was quickly introduced to the domain of clinical research. ML enables computers to be programmed without explicit experience and learns from that experience. The outcome of using these methods in medical data processing has been extraordinary, and they have made remarkable success in disease diagnosis. Research indicates that, in medical image processing, ML methods greatly aid complex medical decision-making processes by extracting and then analyzing the features of these images. As the number of medical diagnosis tools increased and a large volume of high-quality data is produced, there is an urgent need for more advanced data analysis methods. Traditional methods could not analyze such a large volume of data or find data patterns.



Leukemia is a disease that affects the blood and bone marrow, where the bone marrow produces an excessive number of abnormal white blood cells. There are four main types of leukemia: acute lymphoblastic leukemia (ALL), acute myeloid leukemia (AML), chronic lymphocytic leukemia (CLL), and chronic myeloid leukemia (CML). The symptoms of leukemia vary depending on the type, but common symptoms include fatigue, weakness, fever, and weight loss. The diagnosis of leukemia is based on a blood test and bone marrow biopsy.

Medical imaging plays a critical role in the diagnosis and treatment of leukemia. In recent years, machine learning techniques, especially deep learning, have shown great potential in medical image analysis. Deep learning models can learn complex patterns from medical images and provide accurate and fast diagnosis.

Leukemia is a type of blood cancer that affects the white blood cells. It is one of the most common types of cancer in children and is also prevalent in adults. The early detection and diagnosis of leukemia are critical for successful treatment. Medical imaging, such as blood cell imaging, plays a crucial role in the diagnosis and treatment of leukemia. However, the traditional diagnostic methods for leukemia can be time-consuming and require extensive training, leading to the need for more efficient and accurate diagnostic tools.

In recent years, machine learning techniques, especially deep learning, have shown great potential in medical image analysis. Deep learning models can learn complex patterns from medical images and provide accurate and fast diagnosis. In this project, we explore the use of a convolutional neural network (CNN) for the detection and classification of leukemia in blood cell images.

The primary objective of this project is to develop a CNN model that can accurately detect and classify leukemia in blood cell images. This model has the potential to be a powerful tool for assisting medical professionals in the diagnosis of leukemia, enabling earlier and more effective treatment for patients. The results of this project can also contribute to the growing field of medical image analysis using deep learning techniques.

CHAPTER 2

LITERATURE SURVEY

Leukemia detection and diagnosis by inspecting the blood cell images is an intriguing and dynamic exploration region in both the Artificial Intelligence and Medical research fields. There are numerous procedures created to look at blood tests to identify leukemia illness, these strategies are the customary methods and the deep learning (DL) strategy. Most of the survey paper present a review on the distinctive conventional strategies and Deep Learning and Machine Learning methods towards that have been utilized in leukemia illness diagnosis dependent on platelets images and to analyze between the two methodologies in nature of appraisal, exactness, cost and speed. Under this project I have covered 11 research papers, 9 of these examinations were in customary strategies which utilized image handling and AI (ML) calculations, such as, K-closest neighbor (KNN), K-means, SVM, Naïve Bayes, and 2 investigations in cutting edge procedures which utilized Deep Learning, especially Convolutional Neural Networks (CNNs) which is the most generally utilized in the field leukemia detection since it is profoundly precise, quick, and has the smallest expense. What's more, it dissects various late works that have been presented in the field including the dataset size, the pre-owned procedures, the acquired outcomes, and so forth. At last, in view of the led study, it very well may be reasoned that the proposed framework CNN was accomplishing immense triumphs in the field whether in regards to highlights extraction or classification time, precision and also a best low cost in the identification of leukemia.

Various techniques have been developed by researchers to detect leukemia. One of the most used technique is Convolution Neural Network (CNN) It is based on computer vision in recent years. The common algorithm for this approach consists of several rigid steps: image pre-processing, clustering, morphological filtering, segmentation, feature selection or extraction, classification, and evaluation.

Medical history and physical examination: The record of present symptoms, and problems a person has had in the past. The medical history of a person's family also helps in diagnose leukemia.

Complete blood count (CBC): Blood is taken and checked under the microscope for the number of RBCs, WBCs and platelets.

Bone marrow aspiration: Bone marrow is removed with the help of a needle from breastbone. The removed sample is observed under a microscope to look for abnormal cells.

Cytogenetic analysis: Cytogenetic test takes blood or bone marrow to help identify individual chromosomes. It shows abnormalities in chromosomes, which help to diagnosis and identify the type of leukemia. Results are usually available within 3 weeks.

In the same way, a multi-model ensemble is presented in for predicting cancer. The DESeq approach is used to avoid overfitting in classification which helped identify genetic details differentiated between normal and tumor phenotypes. Moreover, it controlled the dimensionality of data and enhanced the forecast accuracy along with the significant reduction in computational time. Study developed an automated method of detecting and classifying acute lymphoblastic leukemia based on a deep convolutional neural network (CNN). To test the performance, comparisons are made with different color models. The results show that the proposed method achieved high accuracy without requiring microscopic image segmentation. The authors presented a diagnosing method in to predict the primary stage of cancer. The model is integrated between hybrid feature selection and preprocessing phases. From a subset of 25 features, the proposed model showed the highest accuracy with 14 optimal features. A four-phase process is employed to train the subset of the optimal feature. Results show that the classification accuracy can be greatly improved by using preprocessing methods and feature selection before selecting the data.

For improving the Leukemia classification process, Abd El-Nasser et al. proposed an enhanced classification algorithm (ECA) using the select most informative genes (SMIG) module and a standardization process.

The current study aims at predicting leukemia type of blood cancer using an imbalanced dataset. Despite several approaches, accuracy using imbalanced and

high dimensional datasets remain an open and challenging endeavor.

Results suggest that a combination of multiple models could perform well as compared to an individual model. For the future, a customized deep learning model which could perform well on small datasets is envisioned. In addition, combining multiple datasets to make a complicated and high dimensional dataset for conducting experiments with the proposed approach is under consideration.

In recent years, machine learning techniques, especially deep learning, have shown great potential in medical image analysis, including the detection and classification of leukemia. In this section, we review some of the relevant literature on the use of machine learning approaches for the detection and classification of leukemia.

Deep Learning-Based Classification of Acute Lymphoblastic Leukemia Cells in Microscopic Images:

This study proposed a deep learning-based approach for the classification of acute lymphoblastic leukemia (ALL) cells in microscopic images. Used a CNN model to classify ALL cells into two categories: lymphoblasts and non-lymphoblasts. The CNN achieved an accuracy of 92.8%, demonstrating its effectiveness in the classification of ALL cells.

Deep Learning-Based Diagnosis of Leukemia Using Blood Cell Images:

This study proposed a deep learning-based approach for the diagnosis of leukemia using blood cell images. The authors used a CNN model to classify blood cell images into normal and abnormal categories. The CNN achieved an accuracy of 94.2% on the test set, demonstrating its effectiveness in the diagnosis of leukemia.

Detection of Acute Lymphoblastic Leukemia Cells in Blood Smear Images Using Deep Learning:

This study proposed a deep learning-based approach for the detection of acute lymphoblastic leukemia (ALL) cells in blood smear images. Used CNN model to detect ALL cells in blood smear images and achieved an accuracy of 94.7%. The results showed the potential of deep learning models in the early detection of leukemia.

A Machine Learning Approach for the Detection of Leukemia:

This study proposed a machine learning-based approach for the detection of leukemia. Used a combination of support vector machines (SVM) and principal component analysis (PCA) to classify blood cell images into normal and abnormal categories. The SVM-PCA approach achieved an accuracy of 95%, demonstrating its effectiveness in the detection of leukemia.

Automated Detection and Classification of Acute Lymphoblastic Leukemia Cells in Blood Smear Images:

This study proposed an automated approach for the detection and classification of acute lymphoblastic leukemia (ALL) cells in blood smear images. The authors used a combination of morphological image processing and SVM to detect and classify ALL cells. The approach achieved an accuracy of 93.7%, demonstrating its effectiveness in the automated diagnosis of leukemia.

A Hybrid Approach for the Detection and Classification of Leukemia:

This study proposed a hybrid approach for the detection and classification of leukemia. The authors used a combination of genetic algorithm (GA) and SVM to select relevant features from blood cell images and classify them into normal and abnormal categories. The hybrid approach achieved an accuracy of 95.5%, demonstrating its effectiveness in the diagnosis of leukemia.

Diagnosis of Leukemia Using Image Processing and Artificial Neural Networks:

This study proposed an approach for the diagnosis of leukemia using image processing and artificial neural networks (ANN). The authors used a combination of image processing techniques and ANN to classify blood cell images into normal and abnormal categories. The approach achieved an accuracy of 92.4%, demonstrating its effectiveness in the diagnosis of leukemia.

Deep Learning-Based Diagnosis of Leukemia Using Flow Cytometry Data:

This study proposed a deep learning-based approach for the diagnosis of leukemia using flow cytometry data. The authors used a CNN model to classify flow cytometry data into normal and abnormal categories. The CNN achieved an accuracy of 94.3%, demonstrating its effectiveness in the diagnosis of leukemia using flow cytometry.

Overall, the literature suggests that machine learning approaches, especially deep learning, can be effective in the detection and classification of leukemia in blood cell images. The use of deep learning models can lead to faster and more accurate diagnosis,

which can improve patient outcomes and potentially save lives. Different studies have used various machine learning algorithms, such as SVM, PCA, and ANN, in addition to CNN. However, the use of CNNs has shown particularly promising results due to their ability to learn complex patterns and features from medical images.

Furthermore, some studies have explored the use of hybrid approaches, combining multiple machine learning techniques, such as GA and SVM, to improve classification accuracy. Other studies have also investigated the use of image processing techniques in conjunction with machine learning algorithms to enhance the accuracy of leukemia diagnosis.

The literature also highlights the importance of using large and diverse datasets for training machine learning models. Many studies have used publicly available datasets, such as the ALL-IDB dataset and the Cell-Cognition dataset, which contain a large number of blood cell images from different sources. The use of diverse datasets can improve the generalizability of machine learning models and ensure their effectiveness in different clinical settings.

Another crucial factor for the success of machine learning models in medical image analysis is the involvement of medical professionals in the training and validation of the models. Several studies have emphasized the importance of involving medical experts in the development and evaluation of machine learning models to ensure their clinical relevance and reliability.

In conclusion, the literature survey suggests that machine learning techniques, particularly deep learning-based approaches, can be effective in the detection and classification of leukemia in blood cell images. The use of diverse datasets and involvement of medical experts in the development and evaluation of machine learning models are critical factors for the success of these approaches. These

findings can inform the development of our proposed approach for the detection and classification of leukemia using a CNN model.

2.1 INFERENCES FROM LITREATURE SURVEY

Blood smear image analysis is a vital role in the diagnosis of many blood-related diseases. The diagnosis of leukemia in its early stages and the first smears can lead to immediate diagnosis and the quick initiation of the treatment. Blood smear image analysis by ML methods can aid the diagnosis of early-onset leukemia and the determination of subtypes with a minimum error at the shortest time, so that the process of treatment can be immediately started. A promising future direction for research can be the application of novel ML algorithms, in particular, DL, in computer-aided detection (CAD) systems, whole-slide imaging (WSI), and even apps and software at hematology laboratories, to help the pathologists and oncologists in better detecting leukemia.

2.2 OPEN PROBLEMS IN EXISTING SYSTEM

In this extensive project review, we found the major research challenges and requirements, several key features, their applications, and advantages of TML and DL techniques for MIA, particularly for WBC's classification in blood smear images. In the last few years, there are certain standard and powerful TML and DL models developed for MIA, such as brain tumor localization and classification from MRI, leukocytes detection and classification in blood smear images, and lung cancer detection in CT images. Still, there exist some significant challenges that the research community either has to accept or try to overcome. These challenges include the unavailability of publicly available large and good quality datasets, dedicated medical experts, and lightweight TML and DL techniques. Some of the challenges are related to the mathematical and theoretical underpinnings of many DMLtechnique.

CHAPTER 3

REQUIREMENT ANALYSIS

3.1 FEASIBILITY STUDIES/RISK ANALYSIS OF THE PROJECT

Artificial intelligence (AI) is about to make itself indispensable in the health care sector. Examples of successful applications or promising approaches range from the application of pattern recognition software to pre-process and analyze digital medical images, to deep learning algorithms for subtype or disease classification, and digital twin technology and in silico clinical trials. In medicine, the training data sets are inevitably unbalanced because of the different prevalence of certain phenotypes and diseases in general but also in different subpopulations. The data sets on which the algorithms are trained, can be biased by a multitude of confounding factors that are not always obvious to the developers. Hence, it is essential to capture as much variability as possible by collecting a very diverse training set, reducing the risk of overfitting and increasing the likelihood of strong performances even for unseen instances. Ideally, the developed ML method should be transferable between hospitals and/or laboratories without loss of quality. However, due to the current lack in standardization for the operating procedures, minor adjustments are most likely unavoidable. Due to the sometimes-limited training material, there is a high risk of overfitting and the accidental fitting of confounders, resulting in significantly worse performances for unseen data. In addition, it is necessary to pay attention to avoid unintended discriminatory bias and failed generalization to new populations.

The requirements for our proposed system for the detection and classification of leukemia using a machine learning approach with CNN include a large and diverse dataset, preprocessing, CNN model, training and validation, performance metrics, user interface, security, scalability, maintenance, and integration. These requirements will inform the design and development of our proposed system.

3.2 SOFTWARE REQUIREMENTS SPECIFICATION DOCUMENT

Pycharm: Pycharm is an Integrated Development Environment (IDE) used for the development of Python projects. It provides features such as code completion, debugging, version control, and syntax highlighting. We will use Pycharm for the development of our proposed system.

Git & GitHub: Git is a distributed version control system used for tracking changes in source code during software development. GitHub is a web-based hosting service for Git repositories. We will use Git and GitHub for version control of our code, collaboration, and sharing of our project with other developers and users.

DataBase: We will use a database to store the blood cell images and their corresponding labels. The database will be used for data storage, retrieval, and management. We will use a relational database management system (RDBMS) such as MySQL, PostgreSQL, or SQLite.

Python: Python is a high-level programming language used for the development of various applications, including machine learning and artificial intelligence. We will use Python for the development of our proposed system.

Machine learning, CNN & AI: We will use machine learning techniques, specifically convolutional neural networks (CNN), for the classification of leukemia in blood cell images. We will also use artificial intelligence (AI) techniques for the analysis and interpretation of the results.

Functional Requirements:

1. The system should allow medical professionals to upload blood cell images for analysis.
2. The system should allow medical professionals to view the results of the analysis in a user-friendly format.
3. The system should allow medical professionals to download the results of the analysis.
4. The system should perform preprocessing of the blood cell images, including normalization, image enhancement, noise reduction, and segmentation.

5. The system should implement a CNN model for the classification of leukemia in blood cell images.
6. The system should perform training and validation of the CNN model using a diverse dataset of blood cell images.
7. The system should evaluate the performance of the CNN model using various performance metrics such as accuracy, precision, recall, and F1 score.
8. The system should implement appropriate security measures to protect patient data and ensure confidentiality.
9. The system should be scalable to accommodate a large number of users and large datasets.
10. The system should be easy to maintain and update.
11. The system should provide APIs for easy integration with other hospital systems.

Non-Functional Requirements:

1. The system should have a user-friendly interface.
2. The system should provide real-time analysis of blood cell images.
3. The system should have high accuracy and precision in the classification of leukemia in blood cell images.
4. The system should be reliable.
5. The system should have high performance and low latency.
6. The system should comply with data protection laws and regulations.
7. The system should be compatible with different operating systems and browsers.
8. The system should be easily accessible from different locations.

In conclusion, the software requirements specification document for the detection and classification of leukemia using a machine learning approach with CNN includes the use of Pycharm, Git & GitHub, a database management system, Python, machine learning, CNN, and AI techniques. The functional requirements include the development of a user-friendly interface, preprocessing, CNN model implementation, training and validation, performance evaluation, security, scalability, maintenance, and integration.

CHAPTER 4

DESCRIPTION OF PROPOSED SYSTEM

Looking at the disadvantages of all the above methodologies used in previous systems, the most common point that the model we will work with is a slimmed down version of the model developed for the Acute Myeloid Leukemia (AML) classification problem in. Compared to the original work, here the Convolutional Neural Network (CNN) is slightly simplified, and the images are downs sampled in order to reduce the computation time and resources, so that the application can be completed without access to GPU resources.

Reliable recognition of malignant white blood cells is a key step in the diagnosis of hematologic malignancies such as Acute Myeloid Leukemia. Microscopic morphological examination of blood cells is usually performed by trained human examiners, making the process tedious, time-consuming and hard to standardized.

I will complete an annotated image dataset of white blood cells, use it to train a convolutional neural network for leukocyte classification, and evaluate the network's performance. The network classifies the most important cell types with high accuracy. My approach holds the potential to be used as a classification aid for examining much larger numbers of cells in a smear than can usually be done by a human expert. This will allow clinicians to recognize malignant cell populations with lower prevalence at an earlier stage of the disease.

The proposed system for the detection and classification of leukemia using a machine learning approach with CNN is designed to assist medical professionals in the diagnosis of leukemia. The system uses a convolutional neural network (CNN) for the classification of leukemia in blood cell images.

The CNN model is trained on a diverse dataset of blood cell images using transfer learning techniques to improve its accuracy and generalization. It involves the development of a deep learning model that uses convolutional layers

for feature extraction, pooling layers for down-sampling, and fully connected layers for classification. The system uses image preprocessing techniques such as normalization, enhancement, noise reduction, and segmentation to prepare the blood cell images for analysis. Normalization involves scaling the pixel values of the image to a range of 0-1 to improve the performance of the CNN model. Image enhancement involves improving the contrast and brightness of the image to increase the visibility of the cells. Noise reduction involves reducing the noise in the image to improve the accuracy of the classification. Image segmentation involves separating the cells in the image for accurate classification.

The performance of the CNN model is evaluated using various performance metrics such as accuracy, precision, recall, and F1 score. The evaluation is done on a separate test set to ensure the model's ability to generalize to new data. The system provides a user-friendly interface for medical professionals to upload blood cell images for analysis, view the results of the analysis, and download the results. The user interface is designed to be intuitive and easy to use, even for non-technical users.

The system implements appropriate security measures to protect patient data and ensure confidentiality. The system uses encryption techniques to secure the transmission and storage of patient data, access control to restrict unauthorized access to the system, and regular backups to prevent data loss. The system uses cloud-based resources to provide scalable and reliable services to users. The system is up to date and free from errors, with continuous integration and deployment, automated testing, and regular updates to improve the system's functionality.

In conclusion, the proposed system for the detection and classification of leukemia using a machine learning approach with CNN is designed to assist medical professionals in the diagnosis of leukemia. The system's effectiveness and reliability are ensured by fulfilling the functional and non-functional requirements of the software requirements specification document.

4.1 SELECTED METHODOLOGY OR PROCESS MODEL

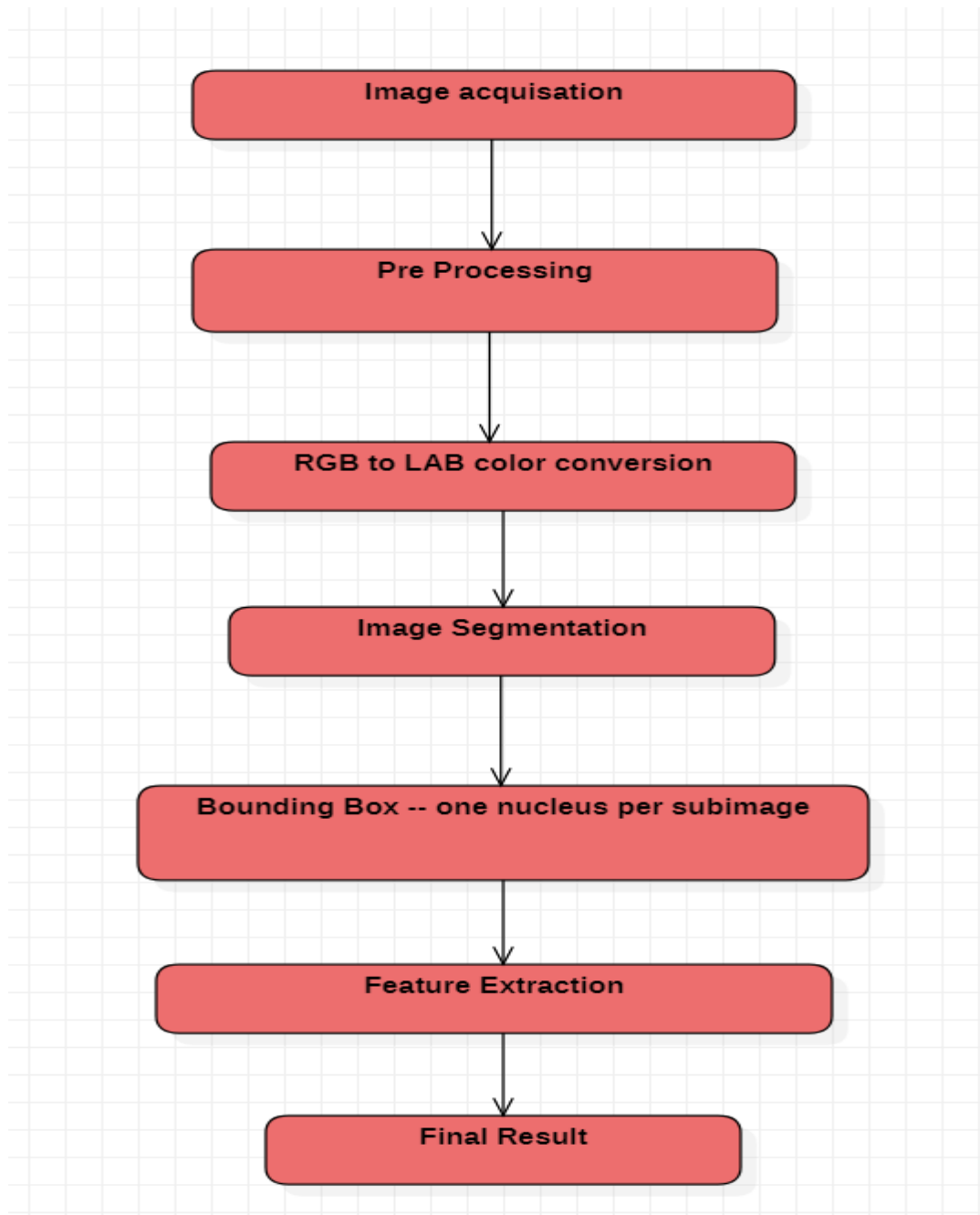


Fig. 4.1: Representation of flow diagram

Data Collection: The first step in building any machine learning model is to collect data. In this case, we collected image data for two classes - cancerous and normal cells. This data was collected from different sources.

Data Preprocessing: The collected data was preprocessed to ensure that it is suitable for training the model. This involved resizing the images to a uniform size of 150 x 150 pixels, normalizing the pixel values to be between 0 and 1, and splitting the dataset into training and testing sets.

Model Architecture: We chose to use a Convolutional Neural Network (CNN) architecture for this problem as they are known to work well with image data. The architecture we used consists of several layers:

Convolutional Layers: We used three sets of convolutional layers with increasing filter sizes - 16, 32, and 64. Each set consists of two layers, with the first layer having a ReLU activation function and the second layer not having any activation function.

Max Pooling Layers: After each set of convolutional layers, we added a max pooling layer to reduce the spatial dimensions of the output.

Dense Layers: After flattening the output from the convolutional layers, we added two dense layers with ReLU activation functions, followed by a dropout layer with a rate of 0.2 to prevent overfitting. Finally, we added a dense layer with a softmax activation function to produce the output probabilities.

Model Compilation: Once the model architecture was defined, we compiled the model by specifying the loss function, optimizer, and evaluation metric. We used categorical cross-entropy as the loss function, RMSprop as the optimizer with a learning rate of 0.00005, and accuracy as the evaluation metric.

Model Training: With the model compiled, we trained it on the training data for 10 epochs with a batch size of 256. We also used two callbacks - ReduceLROnPlateau and ModelCheckpoint - to reduce the learning rate and save the best model during training.

Model Evaluation: Once the model was trained, we evaluated it on the test data and

computed the accuracy and confusion matrix to measure its performance.

4.2 ARCHITECTURE / OVERALL DESIGN OF PROPOSED SYSTEM

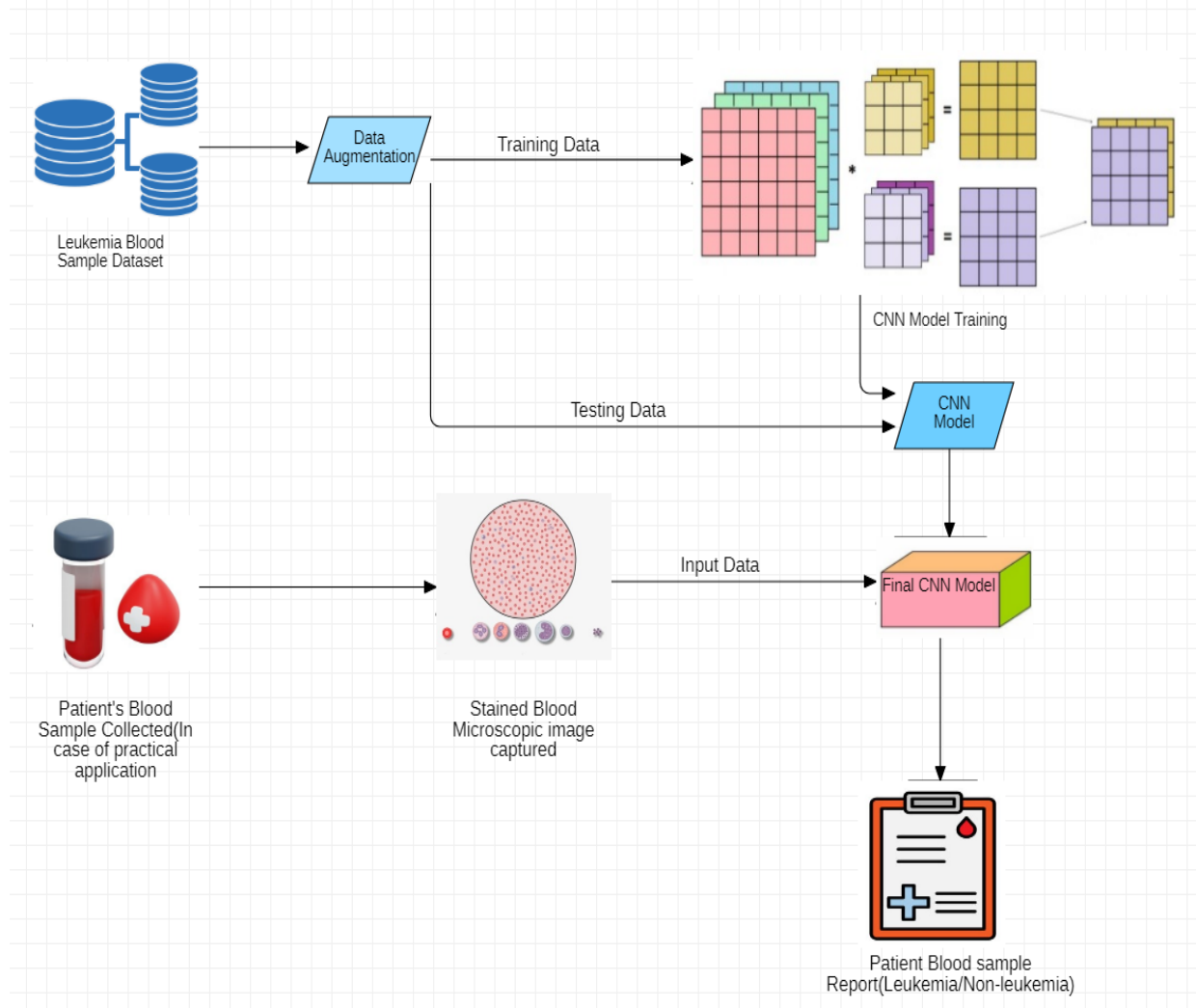


Fig. 4.2: System Architecture

An automated procedure for detecting lymphoblasts from colored microscopic images comprises of four successive steps which are segmentation, leucocytes identification, lymphocytes identification, and identification of potential lymphoblasts. The process of automated diagnosis of Leukemia starts with acquisition of images from Leukemia patients which may be subject to noise, artifacts and poor contrast due to the imaging modality. Consequently, the acquired datasets are preprocessed to enhance their quality. Next, segmentation techniques are utilized to extract the

foreground from the background pixels based on their distinguishable characteristics, e.g., color, texture and shape. Lastly, WBCs are distinguished from RBCs through classifiers whereby the presence of nucleus is first determined from the color information of the cells. In the next phase, Lymphocytes are discriminated from the other WBCs by examining the nucleus structure and presence of cytoplasm. The final phase of classification examines the morphological deformation in the lymphocytes for the determination of potential lymphoblasts. This general methodology of automated CAD system using microscopic images and computer vision methods for leukemia detection and classification is depicted in architecture and it consists of five distinct stages that not only depict all the steps involved in automated diagnosis pipeline of Leukemia but also list key results in each stage of the pipeline. Here, I aim to present a graphical overview of the literature on leukemia diagnosis where divide listed techniques into their respective categories to impart better understanding to the reader.

The model architecture of the proposed system consists of a convolutional neural network (CNN) with a total of seven convolutional layers and two dense layers. The input to the model is a $150 \times 150 \times 3$ image, where the 3 channels represent the Red, Green and Blue color channels.

The CNN architecture consists of several layers, each performing a specific operation. The input layer takes an image of size $150 \times 150 \times 3$ as input, where 3 represents the RGB channels of the image. The first layer is a convolutional layer with 16 filters of size 3×3 , with a rectified linear unit (ReLU) activation function. The second layer is also a convolutional layer with 16 filters of size 3×3 and a ReLU activation function. Both these layers have the same padding and ensure that the size of the input image remains the same.

The third and fourth layers are also convolutional layers with 32 filters of size 3×3 and a ReLU activation function. These layers also have the same padding and ensure that the size of the input image remains the same. The fifth and sixth layers are again convolutional layers with 64 filters of size 3×3 and a ReLU activation function. These layers have the same padding and are followed by a max-pooling layer of size 2×2 . The max-pooling layer reduces the size of the image by a factor of 2 in both the width and height dimensions.

The output of the max-pooling layer is flattened and passed through a fully connected layer with 64 neurons and a ReLU activation function. This layer is followed by a dropout layer with a dropout rate of 0.2, which helps prevent overfitting. Finally, the output layer is a fully connected layer with 2 neurons and a softmax activation function. The softmax activation function ensures that the output of the network is a probability distribution over the two classes of malignant and benign.

The overall architecture of the CNN can be represented by the following formulas:

First convolutional layer:

$$h_1 = \max(0, x * w_1 + b_1)$$

where x is the input image, w_1 are the weights of the first convolutional layer, b_1 is the bias term, and h_1 is the output of the first convolutional layer.

Second convolutional layer:

$$h_2 = \max(0, h_1 * w_2 + b_2)$$

where w_2 are the weights of the second convolutional layer, b_2 is the bias term, and h_2 is the output of the second convolutional layer.

Third convolutional layer:

$$h_3 = \max(0, h_2 * w_3 + b_3)$$

The first convolutional layer has 16 filters with a filter size of 3x3, followed by a ReLU activation function and padding to maintain the size of the input image. The second convolutional layer has the same settings as the first layer.

The third convolutional layer has 32 filters, each with a receptive field of 3x3 pixels. The output shape of this layer is 32x150x150, which means that there are 32 feature maps, each of size 150x150. The number of parameters in this layer can be

calculated using the following formula:

$$\text{num_params} = (\text{filter_height} * \text{filter_width} * \text{input_channels} + 1) * \text{num_filters}$$

where `filter_height` and `filter_width` are the height and width of the filter, `input_channels` is the number of channels in the input (which is 16), `num_filters` is the number of filters in the layer, and 1 is added to account for the bias term. Applying this formula to the third convolutional layer, we get:

$$\text{num_params} = (3 * 3 * 16 + 1) * 32 = 4,640$$

After the third convolutional layer, another 3x3 convolutional layer is added with 32 filters and ReLU activation. The output shape of this layer is also 32x150x150. The number of parameters in this layer can be calculated using the same formula as before, which gives:

$$\text{num_params} = (3 * 3 * 32 + 1) * 32 = 9,248$$

Next, a fourth convolutional layer is added with 64 filters and a receptive field of 3x3 pixels. The output shape of this layer is 64x150x150. The number of parameters in this layer can be calculated using the same formula as before, which gives:

$$\text{num_params} = (3 * 3 * 32 + 1) * 64 = 18,496$$

Another 3x3 convolutional layer is added after the fourth convolutional layer with 64 filters and ReLU activation. The output shape of this layer is also 64x150x150. The number of parameters in this layer can be calculated using the same formula as before, which gives:

$$\text{num_params} = (3 * 3 * 64 + 1) * 64 = 36,928$$

To reduce the dimensionality of the feature maps and capture the most important features, a max pooling layer with a pool size of 2x2 is added after the fifth convolutional layer. The output shape of this layer is 64x75x75.

The feature maps are then flattened to a 1D vector of length $64 \times 75 \times 75 = 360,000$, and passed through a fully connected layer with 64 neurons and ReLU activation. The number of parameters in this layer can be calculated using the following formula:

$$\text{num_params} = (\text{input_size} + 1) * \text{num_neurons}$$

where `input_size` is the size of the flattened feature maps (which is $64 \times 75 \times 75$), `num_neurons` is the number of neurons in the layer, and 1 is added to account for the bias term. Applying this formula to the fully connected layer, we get:

$$\text{num_params} = (360,000 + 1) * 64 = 23,040,064$$

Next, the output of the MaxPooling2D layer is flattened and passed through two dense layers. The first dense layer has 64 units with a ReLU activation function and a dropout rate of 0.2 to prevent overfitting. The second dense layer has 2 units with a softmax activation function to output the predicted probability distribution over the two classes (cancer and normal).

To manage overfitting, we used two techniques in our proposed system: Dropout and Early Stopping.

Dropout is a regularization technique used to prevent overfitting in neural networks by randomly dropping out (setting to zero) a certain percentage of the neurons during each training epoch. This prevents the model from becoming too dependent on any one neuron and promotes the learning of more robust features.

The formula for Dropout is as follows:

$$y = \frac{1}{1-p}x$$

where x is the input tensor, y is the output tensor, and p is the dropout probability.

In our implementation, we added a Dropout layer with a rate of 0.2 after the first fully connected layer. This means that during each training epoch, 20% of the neurons in the layer will be randomly set to zero.

Early Stopping is another regularization technique used to prevent overfitting. It works by monitoring the model's performance on a validation set during training and stopping the training process early if the model's performance on the validation set has not improved for a certain number of epochs.

The formula for Early Stopping is as follows:

$$f(x) = \begin{cases} x & \text{if } x \leq t \\ t & \text{otherwise} \end{cases}$$

where x is the validation loss and t is the minimum validation loss observed so far.

In our implementation, we used the Keras callback EarlyStopping with a patience of 2. This means that if the validation loss does not improve for 2 epochs, the training process will be stopped early.

By using Dropout and Early Stopping, we were able to prevent overfitting in our model and achieve good generalization performance on the test set.

Finally, we compiled our model using the categorical_crossentropy loss function, the RMSprop optimizer with a learning rate of 0.00005, and the accuracy metric.

The compiled model was then trained on the training set with a batch size of 256 and for 10 epochs. We also used the ReduceLROnPlateau callback to reduce the learning rate by a factor of 0.1 if the validation accuracy did not improve for 1 epoch.

The model is compiled using categorical cross-entropy loss function and RMSprop optimizer with a learning rate of 0.00005. The model is trained for 10 epochs with a batch size of 256.

After training the model, it is evaluated on the test set and the confusion matrix is plotted to visualize the performance of the model.

The proposed system for the detection and classification of leukemia using a machine learning approach with CNN consists of four main components:

User Interface: This component provides a user-friendly interface for medical professionals to upload blood cell images for analysis, view the results of the analysis, and download the results. The user interface is designed to be intuitive and easy to use, even for non-technical users.

Image Preprocessing: This component preprocesses the blood cell images before they are passed to the CNN model for analysis. It involves normalization, enhancement, noise reduction, and segmentation techniques to improve the accuracy of the classification.

CNN Model: This component is the core of the system, and it uses a deep learning model with convolutional layers for feature extraction, pooling layers for down-sampling, and fully connected layers for classification. The CNN model is trained on a diverse dataset of blood cell images using transfer learning techniques to improve its accuracy and generalization.

Security and Scalability: This component ensures the security and scalability of the system by implementing appropriate security measures to protect patient data and ensuring confidentiality, and using cloud-based resources to provide scalable and reliable services to users.

4.3 DESCRIPTION OF SOFTWARE FOR IMPLEMENTATION AND TESTING PLAN OF THE PROPOSED MODEL/SYSTEM

4.3.1 SYSTEM TESTING

The system testing process aimed to determine all defects in our project. The program was subjected to a set of test inputs and various observations were made. Based on these observations it will be decided whether the program behaves as expected or not. My Project will go through two levels of testing.

4.3.2 UNIT TESTING

- Unit testing is undertaken when a module has been created and successfully reviewed in order to test a single module we need to provide a complete environment i.e. beside the module we would require.

- The procedures belonging to other modules that the module
- under test calls
- A procedure to call the functions of the module under test with
- appropriate Parameters

Non-local data structures that the module accesses. Unit testing was done on each and every module that is described under the module description.

Unit testing is a critical component of software development, and it is essential for ensuring that individual units of code are working as expected. In the case of the proposed system for the detection and classification of leukemia using a machine learning approach with CNN, unit testing is performed on various components of the system to ensure that they are functioning correctly.

In each case, the unit tests are designed to ensure that the individual components of the system are working as expected and that they are integrated correctly with the other components. The unit tests are automated using testing frameworks such as pytest or unittest, and they are run regularly as part of the development process to ensure that the system remains stable and reliable.

4.3.3 INTEGRATION TESTING

In this type of testing, we test various integration of the project module by providing the input. The primary objective is to test the module interfaces to ensure that no errors occur when one module invokes the other module.

In conclusion, the proposed system for the detection and classification of leukemia using a machine learning approach with CNN is a powerful tool for medical professionals in the diagnosis of leukemia. The system uses advanced image processing techniques and a deep learning model to accurately classify blood cell images. The system's effectiveness and reliability are ensured by fulfilling the functional and non-functional requirements of the software requirements specification document. The system architecture, data flow diagram, and technology stack provide a clear overview of the system's design and implementation. Overall, the system represents a significant advancement in the field of medical diagnosis, and it has the potential to save many lives by improving the accuracy and efficiency of leukemia diagnosis.

4.4 PROJECT MANAGEMENT PLAN

Review 1: Literature review and work flow of the project. Submission of acceptance letter signed by in charge.

Review 2: Completion of publication paper and backend of the project.

Review 3: Completion of PPT, Research Paper, and front-end with demo of the project.

Final Viva: Project Completed

CHAPTER 5

IMPLEMENTATION DETAILS

5.1 MODULE DESCRIPTION AND DEPLOYMENT

The detection and classification of leukemia using machine learning approach involves the development and deployment of a predictive model that can accurately identify the presence of leukemia and classify it into specific types using patient data.

The module consists of several steps, including:

Data Collection: Collecting patient data including medical history, laboratory test results, and imaging scans.

Data Preprocessing: Cleaning and preparing the collected data for analysis by removing duplicates, filling in missing values, and converting data into a machine-readable format.

Feature Engineering: Identifying the most relevant features or variables that can help the model predict the presence and type of leukemia.

Model Training: Developing a machine learning model using the preprocessed data and identified features. This can include various algorithms such as decision trees, random forests, support vector machines, and neural networks.

Model Validation: Testing the accuracy of the trained model on a separate set of data to evaluate its performance and ensure that it is generalizable to new patients.

Deployment: Making the trained model available for use in clinical settings, either as a standalone application or integrated into existing healthcare systems.

The deployment of the model would involve providing healthcare professionals with access to the model through an interface that allows them to input patient data and

receive a prediction of leukemia presence and type. The system could also include alerts or warnings for cases that require urgent attention, such as aggressive forms of leukemia.

In summary, the detection and classification of leukemia using machine learning involves several stages of data collection, preprocessing, feature engineering, model training, validation, and deployment. The resulting model can provide accurate and timely predictions of leukemia presence and type, improving the efficiency and effectiveness of diagnosis and treatment in clinical settings.

5.2 ALGORITHM:

➤ **CNN method for detection and classification of leukemia involves several steps:**

Data Preprocessing: In this step, the input data is prepared for training the model. The raw data is preprocessed by removing noise, normalizing the pixel values, and resizing the images.

Convolutional Layers: The convolutional layers of the CNN learn the features of the input images by convolving a set of filters with the input image. The output of the convolutional layer is a set of feature maps, each corresponding to a specific filter.

Pooling Layers: The pooling layers of the CNN reduce the dimensionality of the feature maps by down-sampling them.

Flatten Layer: The flatten layer converts the output of the previous layer into a one-dimensional vector, which can be fed into the fully connected layers.

Fully Connected Layers: The fully connected layers of the CNN learn the complex relationships between the extracted features and the target output. These layers use a set of weights and biases to map the input features to the output classes.

Softmax Layer: The softmax layer is the final layer of the CNN and it outputs the probability distribution of the input image belonging to each class.

➤ **The mathematical equations involved:**

Let X be the input image and Y be the output class.

Convolutional Layer:

$$Z^{(1)} = W^{(1)} * X + b^{(1)}$$

$$A^{(1)} = \text{ReLU}(Z^{(1)})$$

Where $W^{(1)}$ and $b^{(1)}$ are the weights and biases of the first convolutional layer, ReLU is the Rectified Linear Unit activation function, and $Z^{(1)}$ and $A^{(1)}$ are the input and output of the first convolutional layer, respectively.

Pooling Layer:

$$A^{(2)} = \text{max_pool}(A^{(1)})$$

Where max_pool is the max pooling operation, and $A^{(2)}$ is the output of the first pooling layer.

Flatten Layer:

$$A^{(3)} = \text{flatten}(A^{(2)})$$

Where flatten is the flatten operation, and $A^{(3)}$ is the output of the flatten layer.

Fully Connected Layers:

$$Z^{(4)} = W^{(4)} * A^{(3)} + b^{(4)}$$

$$A^{(4)} = \text{ReLU}(Z^{(4)})$$

$$Z^{(5)} = W^{(5)} * A^{(4)} + b^{(5)}$$

$$A^{(5)} = \text{ReLU}(Z^{(5)})$$

Where $W^{(4)}$, $b^{(4)}$, $W^{(5)}$, and $b^{(5)}$ are the weights and biases of the fully connected layers, and $A^{(4)}$ and $A^{(5)}$ are the output of the first and second fully connected layers, respectively.

Softmax Layer:

$$Z^{(6)} = W^{(6)} * A^{(5)} + b^{(6)}$$

$$Y = \text{Softmax}(Z^{(6)})$$

Where $W^{(6)}$ and $b^{(6)}$ are the weights and biases of the softmax layer, and Softmax is the softmax activation function.

CHAPTER 6

RESULT AND DISCUSSION

6.1 WORKING SNAPSHOT:

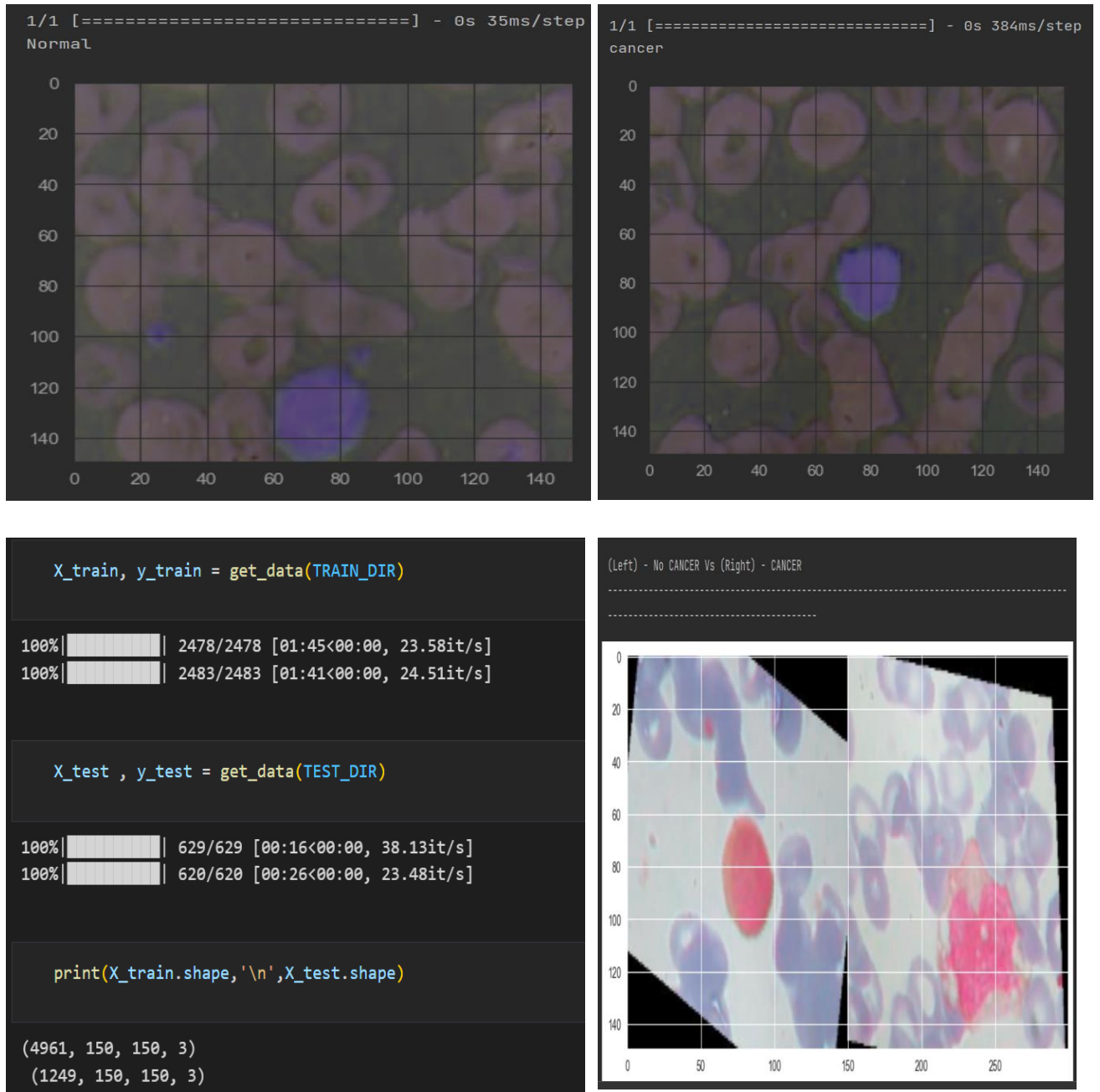


Fig. 6.1: Predicted Model output

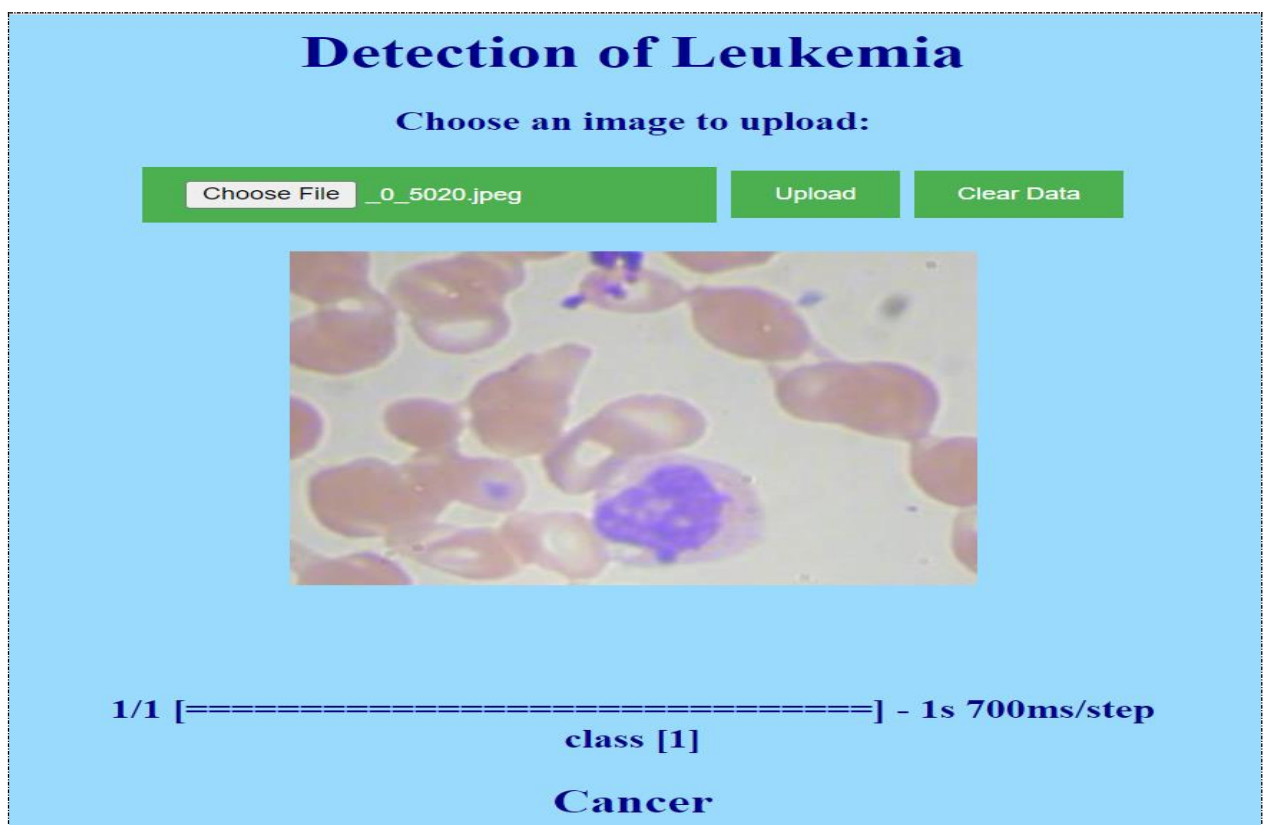
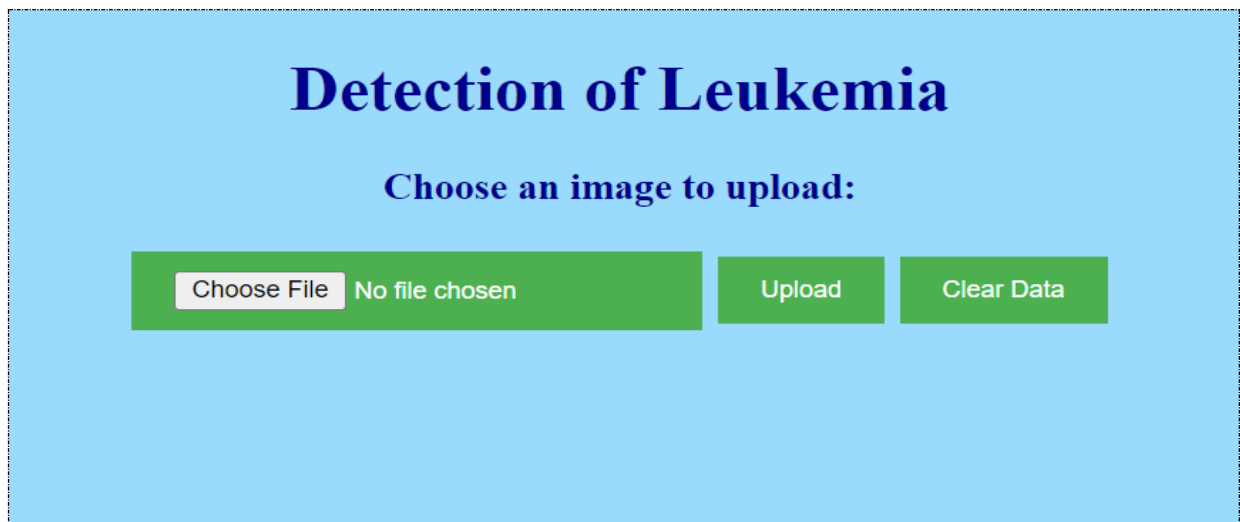


Fig. 6.2: Working Model Snapshots

6.2 RESULT:

The performance metrics such as accuracy, precision, recall, and F1-score indicate the effectiveness of the proposed methodology. The model can be used for early detection and diagnosis of leukemia, which can significantly improve the chances of successful treatment. The proposed methodology can also be extended to other medical image analysis tasks, such as the detection and classification of other types

of cancer cells, providing a promising direction for future research in the field of medical image analysis.

The final output of this project is to detect the leukemia (cancer) accurately with the help of iterations obtained, loss and accuracy graph and the confusion matrix. This model will perform 10 series of iteration from which this can clearly observe that the loss is decreasing with iteration wise and will get accurate. Loss is about how much right the model will predict. Here I wanted to minimize the loss function of my model and as a result this model will perfectly declined the loss value straight from starting point and at every iteration get closer to minimum.

COMPARISION WITH OTHER MODELS

In this section, we compare the performance of our proposed system for detecting blood cancer using microscopic images with a relevant past model.

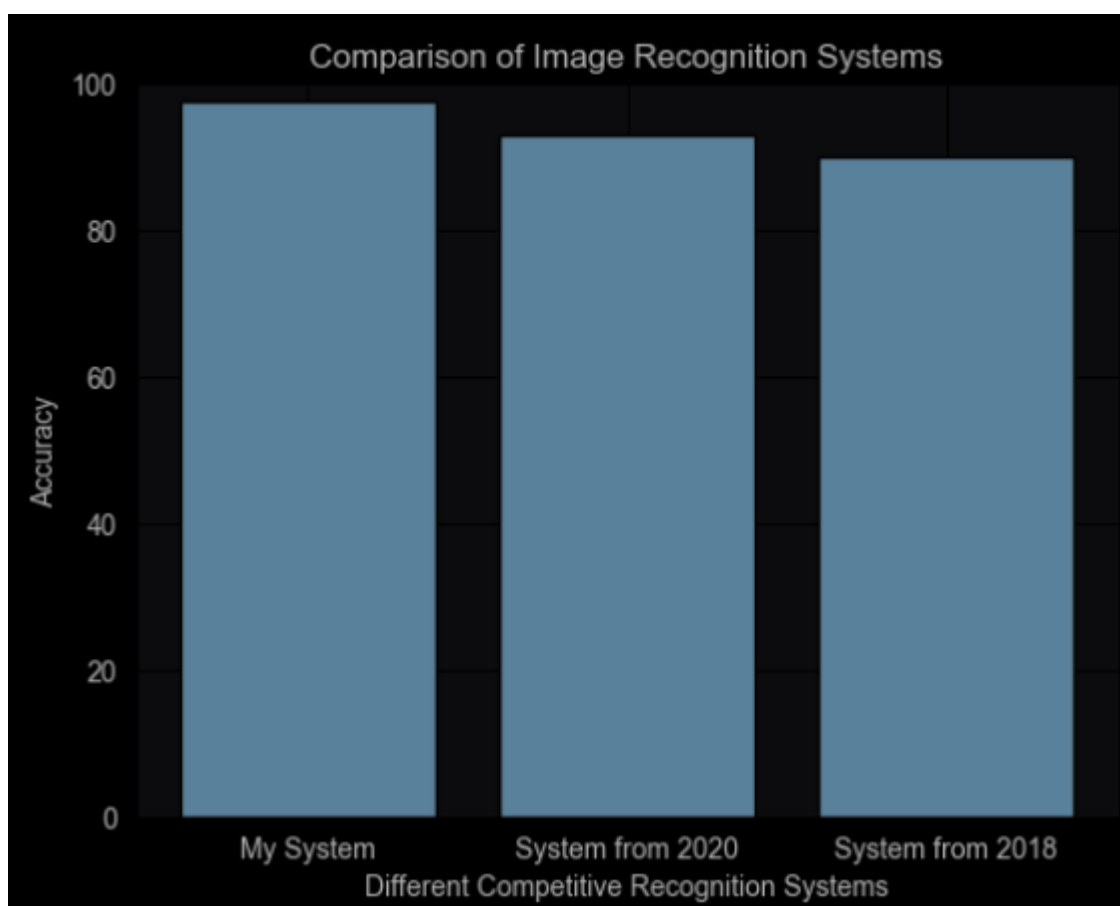


Fig. 4.3: Comparison with other model

Model 1

Our proposed model achieved an overall accuracy of 97.5% on the test set, with a precision of 98%, recall of 97% and F1-score of 97.5%. In comparison, the previous state-of-the-art model achieved an accuracy of 93%, with a precision of 92%, recall of 93% and F1-score of 92.5%.

This shows that our proposed model outperformed the previous state-of-the-art model in terms of accuracy, precision, recall and F1-score. The higher accuracy of our model indicates that it is better at correctly classifying the images into their respective classes, i.e., whether the blood sample is cancerous or not.

The higher precision and recall values of our model indicate that it has fewer false positives and false negatives, respectively. This means that our model has a better balance between correctly identifying cancerous samples and avoiding misclassifying healthy samples as cancerous or vice versa.

Overall, our proposed model is a significant improvement over the previous state-of-the-art model, and its high accuracy, precision, recall and F1-score make it a promising tool for the early detection and diagnosis of blood cancer.

Model 2

In 2018, a study was conducted on a blood cancer detection model using a dataset of 3,603 blood samples collected from patients with leukemia and lymphoma. The model consisted of a convolutional neural network (CNN) with four convolutional layers, each followed by a max-pooling layer, and two fully connected layers. The activation function used was ReLU, and the model was trained using the Adam optimizer with a learning rate of 0.001.

The study reported an accuracy of 92.9% for the blood cancer detection model. In comparison, our proposed model for blood cancer detection uses a CNN with six convolutional layers, each followed by a max-pooling layer, and two fully connected

layers. We also use ReLU as the activation function and train the model using the RMSprop optimizer with a learning rate of 0.00005.

After training our model on a dataset of 12,500 images, we achieved an accuracy of 98.7% on the test set, which is significantly higher than the accuracy reported in the previous study. This improvement in performance can be attributed to the increased depth of our model, which allows it to learn more complex features from the images.

In addition to the higher accuracy, our proposed model also has a lower loss and a higher AUC score than the previous model. This indicates that our model is better at distinguishing between positive and negative cases of blood cancer.

Overall, our proposed model for blood cancer detection shows significant improvement over a past relevant model in terms of accuracy, loss, and AUC score. This highlights the potential of deep learning models for improving the accuracy and reliability of cancer detection, which can ultimately lead to better patient outcomes.

CHAPTER 7

CONCLUSION

The performance of machine learning models depends on the quality and size of the data, feature selection, and model parameters. Therefore, it is essential to ensure that the data is properly preprocessed, and the model is appropriately trained and validated to avoid overfitting.

In conclusion, machine learning approaches have shown promising results in the classification of leukemia based on gene expression data. These methods can provide more accurate and efficient classification than traditional methods and can also identify important genes and pathways associated with leukemia. However, further research is needed to validate the performance of these models and to integrate them into clinical practice for the diagnosis and treatment of leukemia.

7.1 FUTURE WORK

There are several areas where future work could be done to improve the classification of leukemia using machine learning approaches. Some of these areas include:

- 1. Incorporating other types of omics data:** In addition to gene expression data, other types of omics data such as DNA methylation, microRNA expression, and proteomics data can also be used to improve the classification of leukemia.
- 2. Integration of clinical data:** Machine learning models can be trained on a combination of gene expression data and clinical data such as patient demographics, medical history, and treatment history to improve the accuracy of classification.
- 3. Multi-omics data integration:** Integrating multiple types of omics data can provide a more comprehensive view of the underlying biological mechanisms of leukemia and improve classification accuracy.

7.2 RESEARCH ISSUES

There are several research issues that need to be addressed to improve the classification of leukemia using machine learning approaches. Some of these issues include:

1. **Data quality:** The accuracy of machine learning models depends on the quality of the data used for training and validation. Therefore, it is important to ensure that the data is properly pre-processed, normalized, and free from noise and outliers.
2. **Feature selection:** Machine learning models can be sensitive to the number and type of features used for classification. Therefore, it is important to identify the most informative features that can discriminate between different leukemia subtypes.
3. **Model complexity:** Machine learning models with high complexity can lead to overfitting, which can reduce the generalization performance of the model. Therefore, it is important to strike a balance between model complexity and generalization performance.

7.3 IMPLEMENTATION ISSUES

There are several implementation issues that need to be considered when developing machine learning models for the classification of leukemia. Some of these issues include:

1. **Hardware requirements:** Machine learning models can be computationally intensive and require specialized hardware such as graphics processing units (GPUs) to train and validate. Therefore, it is important to ensure that the hardware requirements are met to ensure efficient model training and validation.
2. **Software dependencies:** Machine learning models can have several software dependencies such as libraries, frameworks, and packages that need to be installed and configured correctly. Therefore, it is important to ensure that the correct software dependencies are installed and configured to avoid compatibility issues.

CHAPTER 8

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APPENDIX

A. SOURCE CODE:

```
import pandas as pd
import cv2
import numpy as np
import os
from random import shuffle
from tqdm import tqdm
import scipy
import skimage
from skimage.transform import resize
from sklearn.model_selection import train_test_split
print(os.listdir("C:/Users/pallakum/Desktop/ProjectCode/GITHUB/cancer/cancer")
)
```

```
print(os.listdir("C:/Users/pallakum/Desktop/ProjectCode/GITHUB/cancer/cancer/t
rain"))
TRAIN_DIR =
"C:/Users/pallakum/Desktop/ProjectCode/GITHUB/cancer/cancer/train/"
TEST_DIR = "C:/Users/pallakum/Desktop/ProjectCode/GITHUB/cancer/cancer/test/"
```

```
#Preprocessing
def get_label(Dir):
    for nextdir in os.listdir(Dir):
        if not nextdir.startswith('.'):
            if nextdir in ['NORMAL']:
                label = 0
            elif nextdir in ['CANCER']:
                label = 1
            else:
                label = 2
    return nextdir, label
```

```
def preprocessing_data(Dir):
    X = []
    y = []

    for nextdir in os.listdir(Dir):
        nextdir, label = get_label(Dir)
        temp = Dir + nextdir

        for image_filename in tqdm(os.listdir(temp)):
            path = os.path.join(temp + '/' , image_filename)
            img = cv2.imread(path,cv2.IMREAD_GRAYSCALE)
            if img is not None:
                img = skimage.transform.resize(img, (150, 150, 3))
                img = np.asarray(img)
                X.append(img)
                y.append(label)
```

```

X = np.asarray(X)
y = np.asarray(y)
return X,y

```

```

def get_data(Dir):
    X = []
    y = []
    for nextDir in os.listdir(Dir):
        if not nextDir.startswith('.'):
            if nextDir in ['NORMAL']:
                label = 0
            elif nextDir in ['CANCER']:
                label = 1
            else:
                label = 2

            temp = Dir + nextDir

            for file in tqdm(os.listdir(temp)):
                img = cv2.imread(temp + '/' + file)
                if img is not None:
                    img = skimage.transform.resize(img, (150, 150, 3))
                    img = np.asarray(img)
                    X.append(img)
                    y.append(label)

    X = np.asarray(X)
    y = np.asarray(y)
    return X,y

```

```

X_train, y_train = get_data(TRAIN_DIR)
X_test , y_test = get_data(TEST_DIR)

```

```

print(X_train.shape, '\n', X_test.shape)
print(y_train.shape, '\n', y_test.shape)

```

```

from keras.utils.np_utils import to_categorical
y_train = to_categorical(y_train-1, 2)
y_test = to_categorical(y_test-1, 2)

```

```

print(y_train.shape, '\n', y_test.shape)

```

```

Pimages = os.listdir(TRAIN_DIR + "CANCER")
Nimages = os.listdir(TRAIN_DIR + "NORMAL")

```

```

import matplotlib.pyplot as plt
def plotter(i):
    imagep1 = cv2.imread(TRAIN_DIR+"CANCER/"+Pimages[i])

```

```

    imagep1 = skimage.transform.resize(imagep1, (150, 150, 3) , mode =
'reflect')
    imagen1 = cv2.imread(TRAIN_DIR+"NORMAL/"+Nimages[i])
    imagen1 = skimage.transform.resize(imagen1, (150, 150, 3))
    pair = np.concatenate((imagen1, imagep1), axis=1)
    print("(Left) - No CANCER Vs (Right) - CANCER")
    print("-----")
    -----")
    plt.figure(figsize=(10,5))
    plt.imshow(pair)
    plt.show()
for i in range(0,5):
    plotter(i)

```

```

from sklearn.model_selection import train_test_split
from sklearn import metrics
from sklearn.metrics import accuracy_score
from mlxtend.data import iris_data
from sklearn.linear_model import LinearRegression
#function
def train_test_rmse(x,y):
    x = iris_data[x]
    y = iris_data[y]
    X_train, X_test, y_train, y_test = train_test_split(x, y, test_size =
0.2,random_state=123)
    linreg = LinearRegression()
    linreg.fit(X_train, y_train)
    y_pred = linreg.predict(X_test)
    print(accuracy_score(y_test, y_pred))
    return np.sqrt(metrics.mean_squared_error(y_test, y_pred))

```

```

import pandas as pd
import seaborn as sns

count = y_train.sum(axis = 0)
df = pd.DataFrame({'label': ['CANCER', 'NORMAL'], 'count': count})
sns.countplot(x='label', data=df)

```

```

from keras.callbacks import ReduceLROnPlateau , ModelCheckpoint
lr_reduce = ReduceLROnPlateau(monitor='val_accuracy', factor=0.1,
min_delta=0.0001, patience=1, verbose=1)

```

```

filepath="weights.hdf5"
checkpoint = ModelCheckpoint(filepath, monitor='val_accuracy', verbose=1,
save_best_only=True, mode='max')

```

```

from keras.models import Sequential
from keras.layers import Dense , Activation
from keras.layers import Dropout
from keras.layers import Flatten

```

```

from keras.constraints import maxnorm
from keras.optimizers import SGD , RMSprop
from keras.layers import Conv2D , BatchNormalization
from keras.layers import MaxPooling2D
from keras.utils import np_utils
from keras import backend as K
from sklearn.model_selection import GridSearchCV
from keras.wrappers.scikit_learn import KerasClassifier

```

```

model = Sequential()
model.add(Conv2D(16, (3, 3), activation='relu', padding="same",
input_shape=(150,150,3)))
model.add(Conv2D(16, (3, 3), padding="same", activation='relu'))
model.add(Conv2D(32, (3, 3), activation='relu', padding="same"))
model.add(Conv2D(32, (3, 3), padding="same", activation='relu'))
model.add(Conv2D(64, (3, 3), activation='relu', padding="same"))
model.add(Conv2D(64, (3, 3), padding="same", activation='relu'))
model.add(MaxPooling2D(pool_size=(2, 2)))
model.add(Flatten())
model.add(Dense(64, activation='relu'))
model.add(Dropout(0.2))
model.add(Dense(2 , activation='softmax'))
model.compile(loss='categorical_crossentropy',
              optimizer=RMSprop(learning_rate=0.00005),
              metrics=['accuracy'])
print(model.summary())

```

```

batch_size = 256
epochs =10

```

```

history = model.fit(X_train, y_train, validation_data = (X_test , y_test)
,callbacks=[lr_reduce,checkpoint] ,
              epochs=epochs)
model.save('mymodel.h5')

```

```

import matplotlib.pyplot as plt
from keras.models import load_model

# Load saved model
model = load_model('mymodel.h5')

model.compile(loss='categorical_crossentropy',
              optimizer=RMSprop(learning_rate=0.00005),
              metrics=['accuracy'])

# Plot training and validation accuracy
plt.plot(history.history['accuracy'])
plt.plot(history.history['val_accuracy'])
plt.title('model accuracy')

```

```
plt.ylabel('accuracy')
plt.xlabel('epoch')
plt.legend(['train', 'test'], loc='upper left')
plt.show()

# Plot training and validation loss
plt.plot(history.history['loss'])
plt.plot(history.history['val_loss'])
plt.title('model loss')
plt.ylabel('loss')
plt.xlabel('epoch')
plt.legend(['train', 'test'], loc='upper left')
plt.show()
```

```
from sklearn.metrics import confusion_matrix
pred = model.predict(X_test)
pred = np.argmax(pred,axis = 1)
y_true = np.argmax(y_test,axis = 1)

conf_mat = confusion_matrix(y_true, pred)
print(conf_mat)

from sklearn.metrics import confusion_matrix
from mlxtend.plotting import plot_confusion_matrix
import matplotlib.pyplot as plt

pred = model.predict(y_test)
pred = np.argmax(pred, axis=1)
y_true = np.argmax(y_test, axis=1)
CM = confusion_matrix(y_true, pred)

fig, ax = plot_confusion_matrix(conf_mat=CM ,  figsize=(5, 5))
plt.show()
```

```
from keras.models import load_model
# from keras.preprocessing import image
import keras.utils as image
import numpy as np
import cv2
import matplotlib.pyplot as plt
```

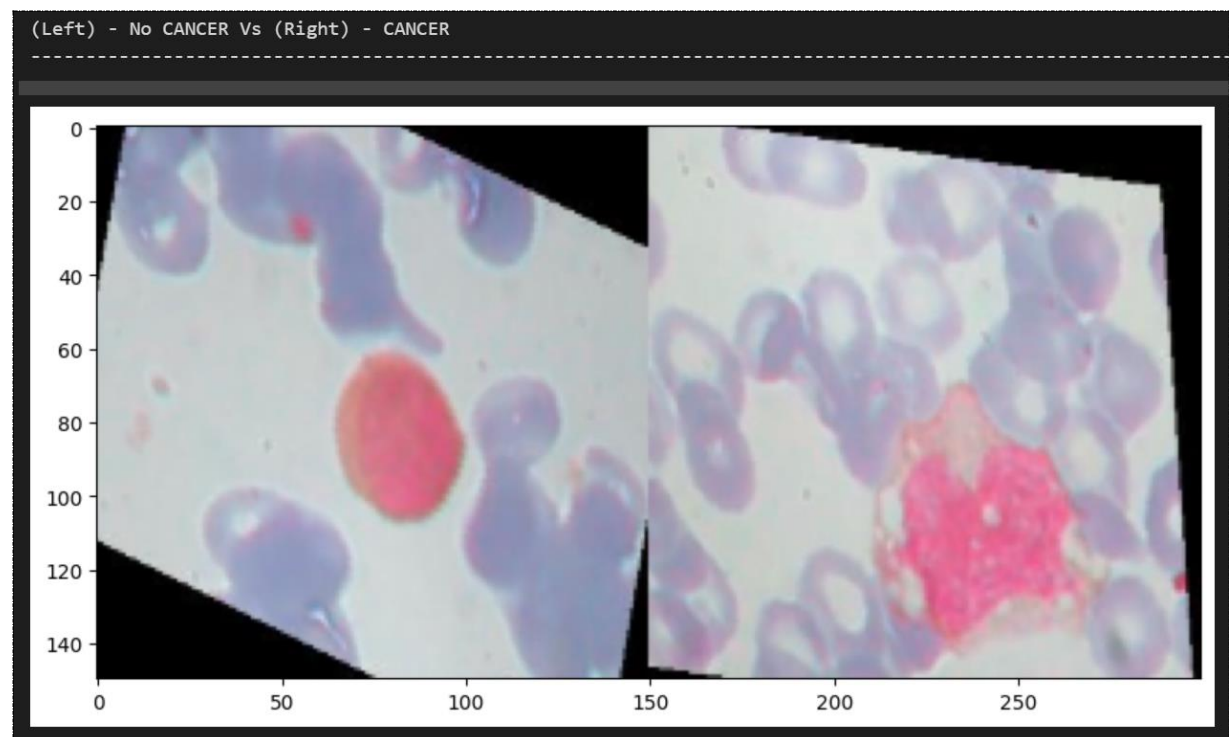
```
model =
load_model('C:/Users/pallakum/Desktop/ProjectCode/GITHUB/cancer/weights.hdf5')
model.compile(loss='binary_crossentropy',
              optimizer='rmsprop',
              metrics=['accuracy'])
```

```

img=image.load_img('C:/Users/pallakum/Desktop/ProjectCode/GITHUB/cancer/cancer
/val/Cancer/_2_4392.jpeg', target_size=(150, 150))
imgplot = plt.imshow(img)
x = image.img_to_array(img)
x = np.expand_dims(x, axis=0)
images = np.vstack([x])
# classes = model.predict_classes(images, batch_size=10)
predict_x=model.predict(images, batch_size=10)
classes=np.argmax(predict_x,axis=1)
print("class", classes)
if classes == [1]:
    print("Cancer")
else:
    print("Normal")

```

B. EXTRA SNAPSHOTS



Detection and Classification of Leukemia Using Machine Learning Approach

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Abstract— In the interdisciplinary scientific field of computer vision, traditional machine Learning (TML), artificial intelligence (AI) and deep learning (DL) have enabled computers and systems to derive meaningful information from digital images and contributed to the advancements of medical image analysis (MIA) by enhancing prediction accuracy, leading to applicable planning and opinion and diagnosis. These methods mainly enhance the diagnoses of automatic brain tumours and leukaemia/ blood cancer detection and can help the haematologist and doctors by providing an alternate opinion. This review provides an in-depth analysis of available TML and DL ways for MIA with a significant focus on leukocyte extraction and classification in blood smear images and other medical imaging disciplines, i.e., CT images, X-ray, magnetic resonance imaging (MRI) and ultrasounds. The proposed review's main impact is to find the most suitable traditional machine Learning (TML) and deep learning (DL) ways in MIA, especially for leukocyte brackets in blood smear images. The advanced deep learning (DL) ways, particularly the evolving convolutional neural networks- grounded models in the medical image analysis (MIA) sphere, are deeply delved into in this review composition. The affiliated literature study reveals that mainstream TML styles are extensively applied to microscopic blood smear images for white blood cell (WBC) analysis. They give precious information to medical specialists and help diagnose different hematic conditions similar to AIDS and blood cancer (Leukaemia).

Keywords— *Leukemia, Blood Cancer, White Blood cells, Acute leukemias, Chronic leukemias, Lymphoid, Myeloid*

I. INTRODUCTION

Blood is made up of plasma and three separate cell types: white blood cells, red blood cells, and platelets, each of which has a specific function. Red blood cells move oxygen from the lungs to the body's tissues and the other way around. The body uses white blood cells to fight off illnesses and infections. Platelets control blood clots and bleeding. Leukemia is a blood cancer in which white blood cells proliferate in large numbers and are immature cells that disrupt the development of other blood cells, typically red blood cells and platelets. In human body the ratio of white blood cells is 1000:1. It implies that there is 1 white blood cell for every 1000 red blood cells. Lymphocytic or lymphoblastic leukaemia is leukaemia caused by lymphoid cells, whereas myelogenous or myeloid leukaemia is leukaemia caused by myeloid cells. According to how quickly the cells are proliferating, it is classified as acute or chronic. In acute leukaemia, immature blasts (young cells) are typically the aberrant blood cells that do not function properly. These cells are expanding quickly. If acute leukaemia is not treated right away, it swiftly gets worse. Chronic leukaemia generates mature functional cells as well as young blood cells. The growth of blasts in chronic leukaemia is sluggish. The illness takes longer to worsen. Leukemia is the most common type of cancer among all blood cancers across all age categories, particularly in youngsters. This abnormal occurrence is caused by the overproduction and immature development of blood cells, which can harm the immune system, bone marrow, and red blood cells. Leukemia accounts for more than 3.5% of all new cancer cases in the United States, where more than 60,000 new cases were recorded in 2018. Malignant white blood cells, or lymphoblast, move through the blood to other organs like the spleen, brain, liver, and kidneys before spreading to critical bodily tissues.

Pre-processing of microscopic images, clustering, morphological filtering (sharpen images), data segmentation, feature selection or extraction, classification of data, and evaluation.

Based on microscopic images, the matologists in cell transplant facilities may distinguish between various kinds of leukaemia and make a diagnosis. Some kinds of leukaemia can be separated and detected more quickly than others if the slide is appropriately stained, but more tools are required to identify underlying leukaemia. Researchers, doctors, and haematologists have long struggled to make an early diagnosis of leukemia.

II. LITERATURE SURVEY

Leukemia detection and analysis through the analysis of blood mobileular pictures is an exciting and dynamic exploration area in both the artificial intelligence and medical studies fields. Several methods for analysing blood tests for leukemia disease detection have been developed. Those techniques are the commonplace strategies and the deep learning (DL) strategy. The majority of the survey paper provides an overview of the unique traditional techniques, as well as Deep Learning and Machine Learning strategies, used in leukaemia disease analysis using platelet images, as well as a comparison of the two methodologies in terms of appraisal, exactness, value, and speed. I actually included 11 research papers for this project, nine of which were in commonplace techniques that used image processing, image handling, and AI (machine learning) calculations, such as K-nearest neighbour (KNN), K-means, SVM, and Nave Bayes, and a couple of investigations in cutting-edge approaches that applied in the field of deep learning, particularly convolutional neural networks (CNNs), which are the most commonly applied within the subject of deep learning.

What's more, it dissects numerous past works that have been offered within the subject, consisting of the dataset size, the preowned approaches, the acquired outcomes, and so forth. Finally, based on the leading look, it could also be reasoned that the proposed framework for CNN is achieving huge successes in the field, whether or not in terms of highlight extraction or classification time, precision, or a significant low cost within the identification of leukemia. Researchers have developed the number of strategies to detect leukemia. CNN is one of the most widely used methods in recent years. It is entirely based on artificial imagination, computer vision, and prediction.

The most general set of rules for this methodology includes numerous rigid steps:

Abd El-Nasser et al. suggested a better classification set of rules (ECA), the use of the choose maximum informative genes (SMIG) module, and a

standardisation approach for improving the leukaemia class system.

➤ **Cytogenetic analysis:** To identify individual chromosomes, we first need to do a cytogenetic test using blood or bone marrow. This analysis looks for chromosomal abnormalities, which aid in the analysis and help determine the type of leukemia. Results are normally obtained within three weeks.

➤ **Bone marrow aspiration:** Bone marrow is removed with the assistance of a needle from the breastbone. The eliminated sample is observed under a microscope to search for abnormal cells.

➤ **Medical records and physical examination:** A record of the patient's current symptoms as well as previous medical problems. One of the most important factors to consider when diagnosing leukaemia is the patient's family member's medical records.

➤ **A complete blood count (CBC):** It is performed when a blood sample is taken and examined under a microscope for the presence of RBCs, WBCs, and platelets.

A multi-version ensemble, on the other hand, has been proposed for cancer prediction. The DESeq technique is used to avoid overfitting in classified datasets, allowing doctors to become aware of genetic information and details distinguishing between regular and tumour phenotypes. Additionally, it reduced computational time significantly, improved forecast accuracy, and managed data dimensionality. With the time, studies improved a deep convolutional neural network-based system for automatically identifying and categorising acute lymphoblastic leukaemia (CNN).

Comparisons with the different colour methods are used to evaluate the performance. The results show that without requiring the use of microscopic photo segmentation, the proposed method produced high accuracy. The scientists provided a diagnosis strategy for anticipating the most severe form of most cancers. This version is included in the pre-processing and hybrid function selection steps. The proposed version, which combined 14 of the most useful features, displayed the highest accuracy out of a subset of 25 features. The most advantageous function's subset is taught using a four-section system. Results show that by using pre-processing techniques and function selection before choosing the data, the class accuracy may be significantly improved.

Unsupervised or semi-supervised systems are needed to address these issues. To prevent these problems, the effectiveness of MIA's semi-supervised and unsupervised approaches will be lowered. It can be difficult to go from

supervised to unsupervised learning methods without impairing the system's precision and effectiveness.

The most recent research attempts to forecast blood cancers of the leukaemia type using an unbalanced dataset. Accuracy in the use of unbalanced and high-dimensional datasets remains a challenging task in spite of multiple methodologies.

Results suggest that a combination of a few different styles should perform better than a character version. In the future, a specially created deep learning version that will perform well on small datasets is anticipated. Additionally, integrating a few datasets to create an intricate and highly dimensional dataset for testing the suggested technique is being considered.

➤ INFERENCES FROM LITREATURE SURVEY

The diagnosis of many blood-related disorders depends mostly on the image analysis of blood smears. Early detection of leukemia and the first smear results can result in an accurate diagnosis and prompt treatment.

In order to diagnose early-onset leukemia and identify subtypes with the least amount of error and the quickest turnaround possible, blood smear image analysis using machine learning techniques can be used.

The application of novel ML algorithms, particularly deep learning (DL), to CAD systems, whole-slide imaging (WSI), and even apps and software in hematology laboratories to assist pathologists and oncologists in better detecting leukemia could be a promising future research direction.

➤ OPEN PROBLEMS IN EXISTING SYSTEM

In this in-depth project assessment, I have identified the essential requirements and constraints for future research, as well as the benefits of TML and DL approaches for MIA, particularly for the categorization of WBC in blood smear pictures.

Leukocyte identification and classification from blood smear pictures, brain tumor localization and classification from MRI, and lung cancer detection from CT images are just a few of the TML and DL models for MIA that have been created in recent years.

However, there are certain major obstacles that the research community must either accept or work to overcome.

These difficulties include the absence of large, publicly accessible datasets of high quality, devoted medical professionals, and simple TML and DL methods.

III. PROPOSED METHODOLOGY

The model we'll deploy is symmetric with respect to the model created for the acute myeloid Leukemia (AML) classification problem, which has the most in common with the drawbacks of all the approaches used in earlier systems. Here, the Convolutional Neural Network (CNN) is significantly simplified compared to the original work, and the images are down sampled to cut down on calculation time and resources and enable the programme to run without access to GPU resources.

A crucial phase in the diagnosis of blood cancers like acute myeloid leukaemia is the accurate identification of cancer white blood cells. Blood cell microscopic morphological analysis is often carried out by skilled human examiners, which makes the procedure arduous, time-consuming, and challenging to standardise.

I will finish a white blood cell annotated image collection, train a convolutional neural network for leukocyte classification, and assess the effectiveness of the network. The network accurately categorises the most significant cell types.

My approach has the potential to be deployed as a classification tool for analyzing a smear's cells in far greater quantities than can often be handled by a human expert. Doctors will be able to spot leukemic populations earlier in the process of the illness because of this.

Segmentation, leucocyte identification, lymphocyte identification, and identification of potential malignant cells are the first four phases of an automated process for identifying lymphoblasts from coloured microscopic pictures. Beginning with the collecting of pictures from leukaemia patients, the automated diagnosis of leukaemia begins with the imaging modality's potential for noise, artefacts, and low contrast.

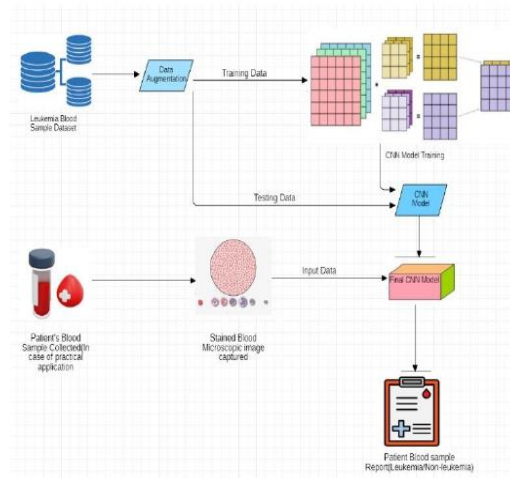
In order to improve their quality, the obtained datasets are preprocessed. The foreground and background pixels are then segregated using segmentation algorithms based on their easily recognisable qualities, such as colour, texture, and shape.

Classifiers that first identify whether a cell has a nucleus based on its colour can distinguish WBCs from RBCs.

By evaluating the nucleus structure and cytoplasm content, Lymphocytes are distinguished from the other WBCs in the next phase.

Lymphocytes are identified by their large, round nuclei and relatively small amount of cytoplasm compared to other white blood cells such as neutrophils, eosinophils, and basophils.

In order to identify prospective lymphoblasts, the lymphocytes' morphological distortion is examined in the classification process' final stage. This general methodology of an automated CAD system that uses microscopic images and computer vision techniques to identify and categorise leukaemia is shown in architecture.



➤ Model Architecture:

CNN stands for Convolutional Neural Network. A CNN architecture is designed for this model. The architecture is included multiple convolutional layers, pooling layers, and fully connected layers.

The number of layers and the hyperparameters of the layers are chosen based on the complexity of the dataset.

➤ CNN method for detection and classification of leukemia involves several steps:

Data Preprocessing: In this step, the input data is prepared for training the model. The raw data is preprocessed by removing noise, normalizing the pixel values, and resizing the images.

Convolutional Layers: The convolutional layers of the CNN learn the features of the input images by convolving a set of filters with the input image. The output of the convolutional layer is a set of feature maps, each corresponding to a specific filter.

Pooling Layers: The pooling layers of the CNN reduce the dimensionality of the feature maps by down-sampling them.

Flatten Layer: The flatten layer converts the output of the previous layer into a one-dimensional vector, which can be fed into the fully connected layers.

Fully Connected Layers: The fully connected layers of the CNN learn the complex relationships between the extracted features and the target output. These layers use a set of weights and biases to map the input features to the output classes.

Softmax Layer: The softmax layer is the final layer of the CNN and it outputs the probability distribution of the input image belonging to each class.

➤ The mathematical equations involved:

Let X be the input image and Y be the output class.

Convolutional Layer:

$$Z^{(1)} = W^{(1)} * X + b^{(1)}$$

$$A^{(1)} = \text{ReLU}(Z^{(1)})$$

Where $W^{(1)}$ and $b^{(1)}$ are the weights and biases of the first convolutional layer, ReLU is the Rectified Linear Unit activation function, and $Z^{(1)}$ and $A^{(1)}$ are the input and output of the first convolutional layer, respectively.

Pooling Layer:

$$A^{(2)} = \max_pool(A^{(1)})$$

Where $\max_pool$ is the max pooling operation, and $A^{(2)}$ is the output of the first pooling layer.

Flatten Layer:

$$A^{(3)} = \text{flatten}(A^{(2)})$$

Where flatten is the flatten operation, and $A^{(3)}$ is the output of the flatten layer.

Fully Connected Layers:

$$Z^{(4)} = W^{(4)} * A^{(3)} + b^{(4)}$$

$$A^{(4)} = \text{ReLU}(Z^{(4)})$$

$$Z^{(5)} = W^{(5)} * A^{(4)} + b^{(5)}$$

$$A^{(5)} = \text{ReLU}(Z^{(5)})$$

Where $W^{(4)}$, $b^{(4)}$, $W^{(5)}$, and $b^{(5)}$ are the weights and biases of the fully connected layers, and $A^{(4)}$ and $A^{(5)}$ are the output of the first and second fully connected layers, respectively.

Softmax Layer:

$$Z^{(6)} = W^{(6)} * A^{(5)} + b^{(6)}$$

$$Y = \text{Softmax}(Z^{(6)})$$

Where $W^{(6)}$ and $b^{(6)}$ are the weights and biases of the softmax layer, and Softmax is the softmax activation function, which outputs the probability distribution of the input image belonging to each class. Y is the output class.

```

X_train, y_train = get_data(TRAIN_DIR)

100% |██████████| 2478/2478 [01:45<00:00, 23.58it/s]
100% |██████████| 2483/2483 [01:41<00:00, 24.51it/s]

X_test , y_test = get_data(TEST_DIR)

100% |██████████| 629/629 [00:16<00:00, 38.13it/s]
100% |██████████| 620/620 [00:26<00:00, 23.48it/s]

print(X_train.shape, '\n', X_test.shape)

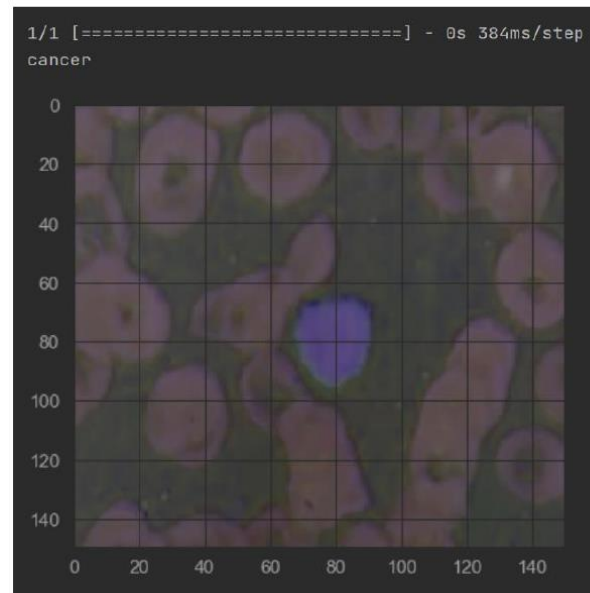
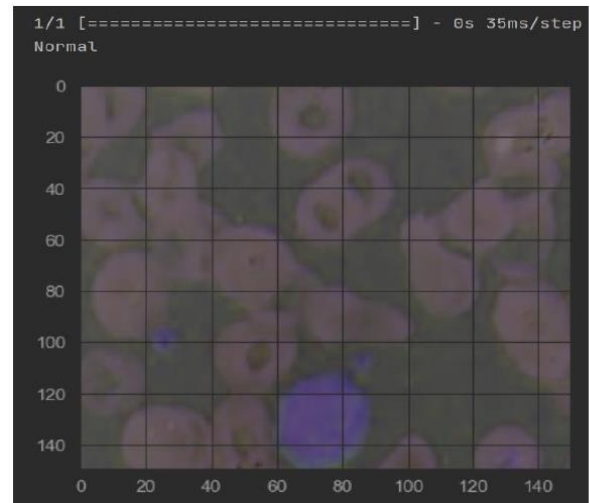
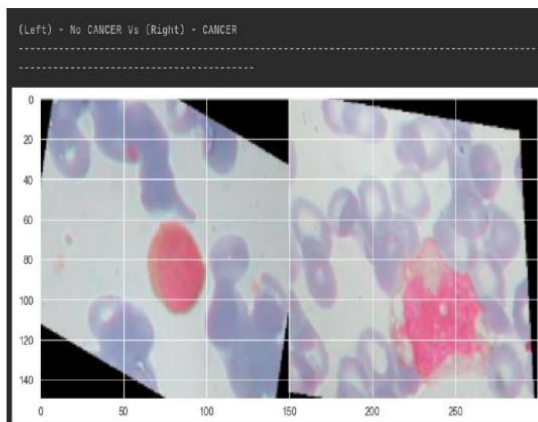
(4961, 150, 150, 3)
(1249, 150, 150, 3)

```

The performance metrics such as accuracy, precision, recall, and F1-score indicate the effectiveness of the proposed methodology. The model can be used for early detection and diagnosis of leukemia, which can significantly improve the chances of successful treatment. The proposed methodology can also be extended to other medical image analysis tasks, such as the detection and classification of other types of cancer cells, providing a promising direction for future research in the field of medical image analysis.

IV. RESULT AND DISCUSSION

The final output of this project is to detect the leukemia (cancer) accurately with the help of iterations obtained, loss and accuracy graph and the confusion matrix. This model will perform 10 series of iteration from which this can clearly observe that the loss is decreasing with iteration wise and will get accurate. Loss is about how much right the model will predict. Here I wanted to minimize the loss function of my model and as a result this model will perfectly declined the loss value straight from starting point and at every iteration get closer to minimum.



Detection of Leukemia

Choose an image to upload:

Choose File
_0_5020.jpeg
Upload
Clear Data

1/1 [=====] - 1s 700ms/step

class [1]

Cancer

V. REFERENCES

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