# University of Information Technology and Sciences (UITS)

Address: H-190, Rd-5, Block J, Baridhara Maddha Nayanagar, Vatara, 1212 Dhaka (Bangladesh)

## Department of Computer Science and Engineering

# A Transfer Learning Approach for Blood Cancer Detection

**A Research**
**Presented to**

Department of Computer Science and Engineering
University of Information Technology and Sciences (UITS)
Vatara, Dhaka-1212

**In partial Fulfilment of the requirements for the**
**Degree of Bachelor of Science**

Researcher
**Md. Golam Murtoza**
Student ID: 1944651079
Email: likhon.uits@gmail.com

Supervised By
**Al-Imtiaz**
Assistant Professor and Department Head
Department of Computer Science and Engineering
University of Information Technology and Sciences

Reviewed By
**Al-Imtiaz**
Assistant Professor and Department Head
Department of Computer Science and Engineering
University of Information Technology and Sciences
Email: al.imtiaz@uits.edu.bd

Approved By
**Dr. Md. Ashrafil Islam**
Professor and Dean
Faculty of Science and Engineering
University of Information Technology and Sciences
Email: ashraful47@uits.edu.bd

**July 2023**

# A Transfer Learning Approach for Blood Cancer Detection

Md. Golam Murtoza
*Department of CSE*
*University of Information Technology and Sciences*
Dhaka, Bangladesh
1944651079@uits.edu.bd

Md Imran Mir
*Department of CSE*
*University of Information Technology and Sciences*
Dhaka, Bangladesh
1944651035@uits.edu.bd

Olin Akon Chumky
*Department of CSE*
*University of Information Technology and Sciences*
Dhaka, Bangladesh
1944651032@uits.edu.bd

***Abstract*—Blood cancer, also known as hematological malignancy, is a complex and heterogeneous disease with various subtypes. Early detection and accurate diagnosis of blood cancer are crucial for effective treatment planning and improved patient outcomes. In recent years, deep learning techniques, particularly transfer learning, have shown promising results in medical image analysis tasks. This research presents a comprehensive study on the application of transfer learning for blood cancer detection using convolutional neural networks (CNNs). The proposed approach leverages pre-trained CNN models, fine-tuning techniques, and a diverse dataset to enhance the performance of blood cancer detection.**

**We evaluated different architectures and fine-tuning methods using 7 datasets containing approximately 3536 images with distinct characteristics of color, texture, contrast, and resolution. Additionally, data augmentation operations were applied to increase the training set by up to 20 times. The k-fold cross-validation (k = 5) results achieved 98.28% of accuracy. A cross-dataset validation technique, named Leave- One-Dataset-Out Cross-Validation (LODOCV), is also proposed to evaluate the developed model's generalization capability.**

***Keywords*—transfer learning, blood cancer detection, leukemia diagnosis, computer-aided diagnosis deep learning, convolutional neural networks, medical image analysis, feature extraction, classification.**

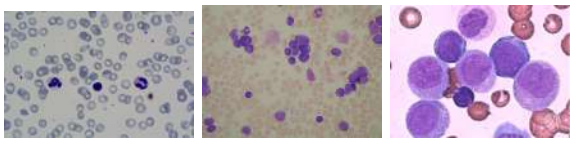
## 1. INTRODUCTION

Leukemia is one of the most dangerous diseases according to the American Cancer Society, with an estimated 61,780 new cases and 22,840 deaths in 2021. This disease has an unknown cause and affects the production of white blood cells in the bone marrow. Due to the disease, young cells or blasts are produced abnormally, replacing healthy blood cells, i.e., white blood cells, red blood cells, and platelets. Consequently, the affected individual suffers from oxygen transport problems and infections. Among the forms of diagnosis of leukemia, one can find the lumbar puncture, myelogram, blood count, and flow cytometry. Samples of blood smears with healthy and unhealthy leukocytes are shown in Figure 1.

The bone marrow produces a large proportion of blood cells, among them 100 million leucocytes (white blood cells) per day on average. Leukocytes act by combating and eliminating microorganisms and foreign chemical structures in the body by employing a catch (phagocytosis) or antibody production. One of the diseases affecting bone marrow function is leukemia.

Leukemia is a type of cancer that has a very high mortality rate [1 ]. It is accompanied by the malicious cloning of abnormal white blood cells (WBC) and is hence referred to as a malignant hematological tumor [2]. Usually, the human body comprises three cell types: red blood cells, white blood cells, and platelets, as shown in Figure 1. (e supply of oxygen from the heart to all tissues is often the responsibility of red blood cells [3]. (ey account for up to half of the total volume of blood. Likewise, the white blood cells play a pivotal role in the immune system of the human body and act as a defense wall from numerous infections and diseases[4]. As a result, the correct categorization of these white blood cells is critical to determine the nature of the disease. (ey are divided according to the composition of the cytoplasm. Lymphocytes are one of the categories of white blood cells and their disorders caused Acute Lymphoblastic

Leukemia (ALL) [5]. Generally, leukemia is categorized into two subtypes known as acute leukemia and chronic leukemia. Without any particular treatment, the overall recovery rate of acute leukemia is barely three months while the onset period of chronic leukemia is more than acute leukemia. Acute lymphocytic leukemia (ALL) is one of the widespread types of acute leukemia responsible for about 25% of all childhood cancers [6]. It originates in the lymphatic system, which generates the blood cells. At the beginning stage, it appears in the bone marrow and is subsequently disseminated throughout the human body. In a healthy individual, the growth of WBC is dependent on the requirements of the body, but in the context of leukemia, they are formed abnormally while becoming ineffective.



(a) (b) (c)

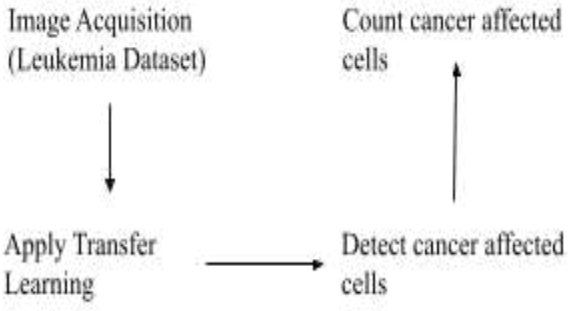
Figure 1. Examples of images used in this work: (a) ALL example [2], (b)
AML example [3], and (c) HBS example [4].

A technique that automatically detects and segments Acute Myeloid Leukemia (AML) in blood smears is presented. It uses the classification of complete blood smear images as opposed to sub-images and uses algorithms to segment and detect nucleated cells. The technique first separates leukocytes from the other blood cells and then lymphocytes are extracted. In this context, a novel Computer Aided Diagnostic system (CAD) is designed for the detection of hematological disorders like leukemia (blood cancer) based on Gray Level Co–Occurrence Matrices (GLCM) and shape-based features. A leukemoid reaction is a responsive elevation of WBC count, which can mimic leukemia. Elevated blast cells are not observed in leukemoid reaction in comparison with leukemia. The reaction is true because of an infection or inflammatory disease and cannot be a sign of cancer. WBC numbers generally recommence normally if the fundamental condition is medicated. The molecular interaction of irregular shapes has been discussed using the Geomco Positioning system. It combines an object-based method with an intensity-based method. The object-based method provides resilience against noise and the content of the fluorescence signal is estimated using the intensity-based method. Biological processing with “Digital Lensless holographic microscopy” states that the ImageJ plug-in has been used for interoperability for calculating numerical simulation. Hence this work used Image with JaCoP plug-ins for analysis. Semantic segmentation has been used initially after pre-processing the blood cell images the pixel-level features are extracted using a deep convolutional encoder and decoder. The accuracy in classifying the RBC, WBC, and platelets are better using the Intersection of Union and Boundary Score [7]. The use of computer systems can assist in fast leukemia diagnosis. Currently, Convolutional Neural Networks (CNNs) are one of the most effective techniques in diagnosing medical images. However, CNNs demand a high computational cost, and in systems with low processing and storage power, this technique becomes difficult to employ [8]. Therefore, in this work, we propose CNN architectures models with residual characteristics to classify blood slides into three classes: ALL, AML, and HBS. When building the model, we evaluated the tradeoff between accuracy and the number of parameters to attain a model that takes up less memory and has performance comparable to the state of the art. We evaluated the proposed model in 16 heterogeneous datasets with 2,415 images, combined with data augmentation techniques. Additionally, we compared the achieved results with the results obtained by the state-of-the-art methods, including those based on CCNs. This paper is organized as follows. Section II presents related works; In Section III, we present the proposed CNN models, the dataset used, the data augmentation technique employed, 978-1-7281-7539-3/20/$31.00 ©2467422020 IEEE, and the applied evaluation metrics. Sections IV and V present the achieved results and a discussion; and finally, we present the conclusion and possibilities of future work section.

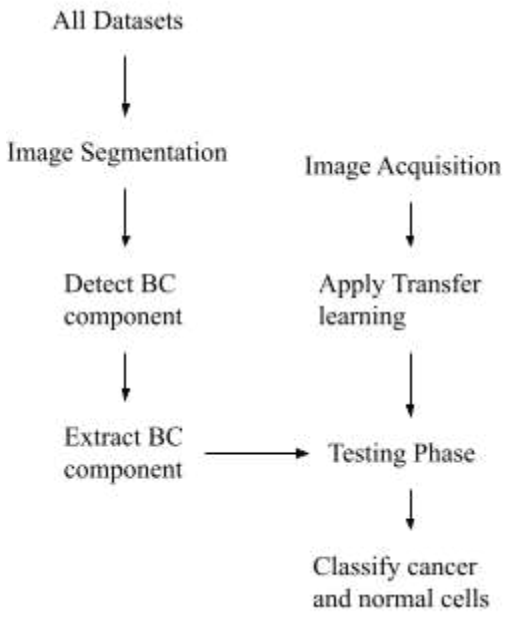
### 1.1 LEUKEMIA CLASSIFICATION

Leukemia classification systems evolved so far, certain works offer solutions in the classification of Acute Lymphoblastic Leukemia (ALL) and acute myeloid leukemia (AML), the two most common types from blood smear images. In [11], Madhukar et

al. proposed a method to detect ALL from multiple nuclei images. In preprocessing, they converted the images of the ALL-IDB1 database from RGB into L * a * b color space. In segmentation, the unsupervised K-means algorithm has been applied to the components to group them into three. A transfer learning of the pre-trained neural network using VGG-19 convolutional neural network (CNN) with an adapted connected classifier was used [12] and Gray Level Co-occurrence Matrix (GLCM) [13] as descriptors. The classification has been carried out with Support Vector Machine (SVM) and three methods for cross-validation such as k-fold, Hold-Out, and Leave-One-Out. Finally, they concluded that the best accuracy of 93.5% has been obtained from the Leave-One-Out method. In [14] started converting images from RGB to the L * a * b color space and applied a k-means clustering algorithm to separate the image based on their color information into 3 separate classes. For segmenting nuclei, contrast enhancement, auto-threshold, and morphological operations were used. Feature extraction and classification, they performed in two steps. As a first step, they applied Principle Component Analysis (PCA) algorithm over a feature vector set comprising 5 textural features, 4 GLCM features namely: entropy, energy, correlation and contrast, and 1 fractal feature from Hausdoff Dimension and gave
this as input to a neural network classifier which intended to classify the cells into normal and abnormal. As a second step, they applied the same PCA on different feature vector sets comprising 5 geometrical MCB, 2022, vol.19, no.1 31 features namely: cytoplasm area, nucleus area, cell area, nucleus-to-cell area ratio, and nucleus-to-cytoplasm area ratio and gave as input to the second form of neural network classifier to distinguish AML and Acute Lymphoblastic Leukemia (ALL). Levenberg-Marquardt's (LM) algorithm was utilized for both neural networks and obtained an accuracy of 97.70%. Reference [15] presented an automated method for finding leukemia from microscopic blood smears. They removed possible noises and applied K-means cluster and Zack algorithms on grayscale images and achieved an accuracy of 93.57% with Support Vector Machine (SVM). In [16], Agaian et al. proposed a method that converts the color space of RGB into L*a*b color space and applies K-means to extract features namely color, shape, GLCM, and Fractal dimension Haar wavelets. SVM was utilized as a classifier and obtained 94% accuracy. The survey presented in this section discussed several recent techniques that were used similarly to classify and count blood images for leukocytosis and classify malignant leukemia. Further, it was observed that there are no works yet involving the classification of malignant leukemia and non-malignant leukemoid reaction. Many researchers have been using deep learning techniques for classification with complex feature descriptors [17], which is assumed as a development work for powerful computational systems. Hence in this paper, for
finding leukocytosis, refer to Fig. 2a, a simple image segmentation process of HSV color-based watershed was applied on BBCD dataset images, and resulting segmented images were given as input to VGG16 CNN in the classification of WBC components. Experiments are carried out on the ALL-IDB1 dataset, and comparative analysis has been made with other existing schemes with sensitivity, specificity, and classification accuracy [18]. Further, to distinguish malignant leukemia and non-malignant leukemoid reaction, refer to Fig. 2b The morphological contour segmentation detects the edges of nuclei and eliminates the normal white blood cells from the microscopic blood image [19] VGG16 CNN network with ALL IDB2 dataset images were used to classify blast and normal cells. BCCD dataset of 349 images was used in the first part and ALL IDB 1 dataset of 108 images and the ALL IDB2 dataset of 110 images (blast cells and normal cells each).




(a)




(b)

Figure 2: (a) Proposed method to classify and count WBC components from BCCD image dataset to
determine leukocytosis (b) Segmentation and classification of blasts and normal cells from ALL
IDB1 dataset by training network with ALL IDB2 dataset

## 1.2 RELATED WORK

Related work is discussed in this section, in particular with respect to the image descriptor employed, the sample size, validation method and accuracy (A) results. Table I lists the works identified and their main characteristics. We identified two main approaches: handcrafted features, and deep learning models. From Table I, one can note that only Vogado et al. [5] used more than two datasets in the experiments. Still, in Table I, it is possible to verify that the used evaluation protocols are usually the holdout and k-fold within the same dataset. When using CNNs, holdout was the most used technique. Due to the availability of relatively small image datasets, one might question the convergence of the used classifiers and their ability to generalize since the relationship between the number of instances used for training and the complexity of the built model falls short in such scenarios. In this context, using more datasets would allow us to better evaluate the systems and their robustness in terms of considering different sources of images. Past research in the detection of deception can be broadly classified as Verbal and Non-verbal. In verbal deception detection, the features are based on the linguistic characteristics, such as n-grams and sentence count statistics [20], of the statement by the subject under consideration. The use of more complex features such as psycholinguistic features [21] based on the Linguistic Inquiry and Word Count (LIWC) lexicon, have also been explored by [22] and shown that they are helpful in detecting deceptive behavior. Yancheva and Rudzicz studied the re-relation between the syntactic complexity of the text and deceptive behavior [23]. 1 In non-verbal deception detection, physiological measures were the main source of signals for detecting deceptive behavior. Polygraph tests measure physiological features such as heart rate, respiration rate, and skin temperature of the subject under investigation. But these tests are not reliable and often misleading as indicated by [24] since judgments made by humans are often biased. Facial ex- pressions and hand gestures were found to be very helpful in detecting deceptive nature. Ekman [11] defined micro-expressions as short involuntary expressions, which could potentially indicate deceptive behavior. Caso et al. [12] identified particular hand gestures to be important to identify the act of deception. Co- hen et al. [13] found that fewer iconic hand gestures were a sign of a deceptive narration. Previous research was focused on detecting deceit behavior under constrained environments which may not be applicable in real-life surroundings. Recently, the focus has been on experiments in real-life scenarios. Towards this, Perez- Rosas et al. [14] introduced a new multi-modal deception dataset having real-life videos of courtroom trials. They demonstrated the use of features from different modalities and the importance of each modality in detecting deception. They also evaluated the performance of humans in deception detection and compared it with their machine-learning models. Wu et al. [25] have developed methods that leverage multi-modal features for detecting detection. Their method heavily emphasizes on feature engineering along with manual cropping and annotating videos for feature extraction. In this paper, we describe our attempt to use neural models that use features from multiple modalities for detecting deception. We believe our work is the first

attempt at using neural networks for deceit classification. We show that with the right features and simple models, we can detect the deceptive nature of real-life trial videos more accurately.

Summary of related work:
From the datasets used in our experiments, only three are class-balanced: UFG, ALL-IDB1, and ALL-IDB2 [14], as reported in Table II. Some of them have only one leukocyte per image and others have multiple leukocytes per image. Only UFG and Bloodline datasets have these two patterns.

TABLE II
SUMMARY OF THE IMAGE DATASETS USED IN THE EXPERIMENTS.

| Dataset | Non-pathological | Pathological | Total |
|---|---|---|---|
| ALL-IDB 1 | 59 | 49 | 108 |
| ALL-IDB 1 (Crop) | 0 | 510 | 510 |
| ALL-IDB 2 | 130 | 130 | 260 |
| Leukocytes | 149 | 0 | 149 |
| CellaVision | 109 | 0 | 109 |
| Atlas | 0 | 88 | 88 |
| Omid et al. 2014 | 154 | 0 | 154 |
| Omid et al. 2015 | 0 | 27 | 27 |
| ASH | 0 | 96 | 96 |
| Bloodline | 0 | 204 | 204 |
| ONKODIN | 0 | 78 | 78 |
| CellaVision 2 | 100 | 0 | 100 |
| JTSC | 300 | 0 | 300 |
| UFG | 57 | 64 | 121 |
| PN-ALL Dataset | 0 | 30 | 30 |
| leukemia-images | 0 | 140 | 140 |
| MDB Dataset | 0 | 673 | 673 |
| LISC Dataset | 376 | 0 | 376 |
| Total | 1434 | 2102 | 3536 |

## 1.3 PROBLEM STATEMENT

The accurate and timely detection of blood cancer from medical images is a challenging task that can benefit from advancements in deep learning techniques. Deep learning, specifically convolutional neural networks (CNNs), has shown remarkable success in various image recognition and classification tasks. However, training deep CNN models from scratch requires a large amount of annotated data, which may not be readily available in the context of blood cancer detection.

## 1.4 RESEARCH OBJECTIVE

The primary objective of this research is to develop a transfer learning approach using CNNs for blood cancer detection. The specific research objectives include:

1. Investigating the potential of transfer learning in improving the performance of blood cancer detection models.
2. Exploring the transferability of pre-trained CNN models from non-medical domains to blood cancer detection.
3. Designing and implementing a transfer learning framework for blood cancer detection, incorporating pre-processing techniques, feature extraction, and classification.
4. Evaluating the performance of the proposed transfer learning approach using appropriate metrics and comparing it with baseline models.
5. Investigating the robustness and generalizability of the transfer learning approach across different blood cancer subtypes and stages.
6. Assessing the practical implications and potential clinical applications of the proposed approach in assisting medical professionals.

## 1.5 SIGNIFICANCE OF THE STUDY

The successful development of a transfer learning approach for blood cancer detection can have significant implications for both clinical practice and research. By leveraging pre-trained CNN models and transfer learning techniques, the proposed approach has the potential to improve the accuracy and efficiency of a blood cancer diagnosis. Early detection of blood cancer can lead to timely interventions, personalized treatment plans, and ultimately, better patient outcomes. Furthermore, the research contributes to the broader field of medical image analysis and deep learning by exploring the transferability of pre-trained models to medical domains. The study also sheds light on the challenges and opportunities in adapting deep learning techniques for blood cancer detection, paving the way for future advancements in the field.

## 1.6 THESIS OUTLINE

The remainder of this thesis is organized as follows: Chapter 2 provides a comprehensive literature review, covering topics related to blood cancer, medical imaging, deep learning, transfer learning, and existing approaches for blood cancer detection. Chapter 3 presents the methodology employed in this research, including dataset description,

pre-processing techniques, transfer learning framework, model architecture, and training and evaluation procedures.

Chapter 4 presents the experimental results, including performance evaluation metrics, comparative analysis with baseline models, robustness analysis, and a discussion of the findings.

Chapter 5 provides a detailed discussion of the results, interpretation of findings, contributions of the study, limitations, and future research directions. Chapter 6 concludes the thesis, summarizing the study's key findings, practical implications, and recommendations for future research. References and appendices follow the main body of the thesis.

## 2. LITERATURE REVIEW

The literature review provides a comprehensive overview of the current state of research in blood cancer detection, highlighting the significance of medical imaging, the potential of deep learning and transfer learning techniques, and the existing approaches in the field. This review sets the foundation for the proposed transfer learning approach and identifies the research gap that this study aims to address.

An iterative thresholding algorithm is used for segmentation purposes especially from noisy images. This algorithm overcomes the problem of cell extraction and segmentation from heavy noisy images. This algorithm works over the adjusted threshold of images iteratively providing robustness to the image. It discusses the blood cell image processing system. This system detects and classifies malaria parasites in Giemsa stained blood slides images. Then after parasitaemia evaluation is done. A morphological approach to cell image segmentation is more precise than the classical watershed-based algorithm is shown in this paper. Grey scale granulometria are applied based on opening with disk-shaped elements, flat and non-flat. Non flat disk shaped structuring elements enhance the roundness and the red cells compactness.

### 2.1 OVERVIEW OF BLOOD CANCER

Blood cancer, also known as hematological malignancy, encompasses a group of malignant diseases that affect the blood, bone marrow, and lymphatic system. The main types of blood cancer include leukemia, lymphoma, and myeloma. These diseases arise from the uncontrolled growth and proliferation of abnormal blood cells, leading to disruptions in normal blood cell production and function. Blood cancer can manifest in various forms, such as acute or chronic, and can affect individuals of all ages.

### 2.2 MEDICAL IMAGING IN BLOOD CANCER DETECTION

Medical imaging techniques play a crucial role in the detection, diagnosis, and monitoring of blood cancer. Common imaging modalities used in blood cancer detection include blood smears, bone marrow aspirates, and histopathological slides. Blood smears provide detailed morphological information about blood cells, while bone marrow aspirates allow the examination of cellular composition within the bone marrow. Histopathological slides enable the assessment of tissue samples to identify cancerous cells and evaluate disease progression.

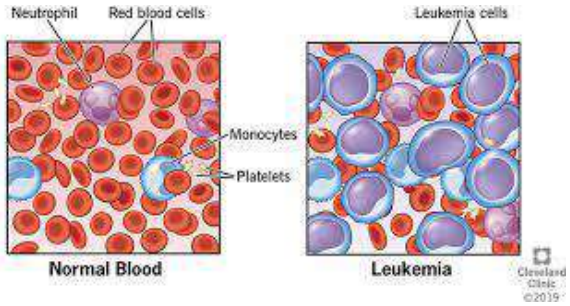



Figure 3. Medical Imaging

### 2.3 DEEP LEARNING AND CONVOLUTIONAL NEURAL NETWORKS

Deep learning has emerged as a powerful technique in the field of medical image analysis. Convolutional neural networks (CNNs) are a class of deep learning models that have demonstrated exceptional performance in various computer vision tasks, including image classification, object detection, and segmentation. CNNs are particularly effective in capturing hierarchical features from images, making them suitable for analyzing complex medical images.

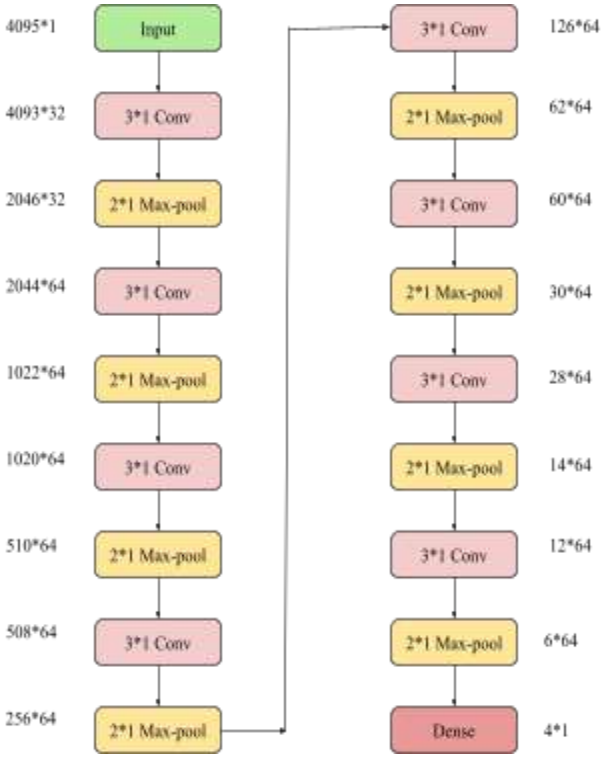



Figure 4. CNN

## 2.4 TRANSFER LEARNING IN MEDICAL IMAGE ANALYSIS

Transfer learning is a technique that leverages knowledge learned from one task to improve performance on a related but different task. In the context of medical image analysis, transfer learning offers several advantages, including the ability to train accurate models with limited labeled medical data. Pre-trained CNN models, such as VGG16, ResNet, or Inception, trained on large-scale datasets from non-medical domains, can be used as a starting point for medical image analysis tasks. By fine-tuning these pre-trained models on specific medical datasets, transfer learning enables the network to learn task-specific features and improve its performance.

## 2.5 EXISTING APPROACHES FOR BLOOD CANCER DETECTION

Several studies have explored the application of deep learning and transfer learning techniques for blood cancer detection. Researchers have employed CNN models to analyze blood smears, bone marrow aspirates, and histopathological slides to classify different blood cancer subtypes and detect abnormal cells. Transfer learning has been shown to improve the accuracy and efficiency of blood cancer detection models by leveraging pre-trained models and domain-specific fine-tuning.

About 15 research papers are revised and analysis of many methods and models.

List of analysis papers

a) "LeukNet" - A Model of Convolutional Neural Network for the Diagnosis of Leukemia.
b) Convolution Neural Network Models for Acute Leukemia Diagnosis.
c) A Deep Learning Framework for Leukemia Cancer Detection in Microscopic Blood Samples Using Squeeze and Excitation Learning.
d) Deep Transfer Learning in Diagnosing Leukemia in Blood Cells.
e) Detection and Classification of Blood Cancer from Microscopic Cell Images Using SVM KNN and NN Classifier.
f) Segmentation techniques for early cancer detection in red blood cells with deep learning-based classifiers—a comparative approach.
g) The accumulation of mercaptopurine metabolites in age fractionated red blood cells.
h) A Deep Learning Approach for Multimodal Deception Detection
i) Blood cancer prediction using leukemia microarray gene data and hybrid logistic vector trees model.
j) Classification of Leukemia and Leukemoid Using VGG-16 Convolutional Neural Network Architecture.

The above papers are already revised and find many issues in this paper. We resolve this error and implement a new paper on Leukemia.

Revised Model:

a) Xception
b) VGG16
c) VGG19
d) ResNet50
e) ResNet101
f) InceptionV3
g) MobileNet
h) DenseNet121
i) EfficientNetB0

We work on this above model and try to understand the accuracy and loss and also work on the model complexity of this model. We select some models from above to implement in our datasets.

## 2.6 RESEARCH GAP

While previous studies have demonstrated the potential of deep learning and transfer learning in blood cancer detection, there is still a need for further research to address some key challenges. These challenges include the availability of annotated medical image datasets, the transferability of pre-trained models to blood cancer-specific features, and the robustness of the proposed approaches across different blood cancer subtypes and stages. Additionally, there is a need to compare and evaluate the performance of different pre-trained CNN models and fine-tuning strategies in the context of blood cancer detection.pre-trained models to blood cancer-specific features, and the robustness of the proposed approaches across different blood cancer subtypes and stages. Additionally, there is a need to compare and evaluate the performance of different pre-trained CNN models and fine-tuning strategies in the context of blood cancer detection.

# 3. METHODOLOGY

This chapter outlines the methodology employed in this research to develop a transfer learning approach for blood cancer detection using convolutional neural networks (CNNs). The methodology includes dataset description, pre-processing techniques, transfer learning framework, model architecture, and training and evaluation procedures.

The methodology presented in this chapter provides a step-by-step approach to implementing the transfer learning framework for blood cancer detection. The dataset, pre-processing techniques, transfer learning, model architecture, and training and evaluation procedures are crucial components of the methodology, allowing for the development of an accurate and effective blood cancer detection model.

## 3.1 DATASETS DESCRIPTION

A diverse dataset of medical images is essential for training and evaluating the blood cancer detection model. The dataset consists of blood smears, bone marrow aspirates, or histopathological slides obtained from patients diagnosed with different types and stages of blood cancer. The dataset should include samples representing various blood cancer subtypes, as well as healthy control samples.

The images of this dataset were prepared in the bone marrow laboratory of Taleghani Hospital (Tehran, Iran). This dataset consisted of 3256 PBS images from 89 suspected ALL patients whose blood samples were prepared and stained by skillful laboratory staff. This dataset is divided into two classes benign and malignant. The former comprises hematogones; the latter is the ALL group with three subtypes of malignant lymphoblasts: Early Pre-B, Pre-B, and Pro-B ALL. All the images were taken using a Zeiss camera in a microscope with 100x magnification and saved as JPG files. A specialist using the flow cytometry tool made the definitive determination of the types and subtypes of these cells. After color thresholding-based segmentation in the HSV color space, we also provide segmented images.

## 3.2 DATA PRE-PROCESSING TECHNIQUES

Before feeding the images into the CNN model, pre-processing techniques are applied to enhance the quality and facilitate the learning process. Common pre-processing techniques include resizing the images to a standard size, normalizing pixel intensities, and applying data augmentation techniques such as rotation, flipping, and scaling. Pre-processing aims to reduce variations in image characteristics, improve robustness, and increase the model's ability to generalize. In this specific phase, the input image is compounded in a way such that even infinitesimal detail are ameliorated and unnoted noises are filtered. Commonly used noise filter methodologies are implemented which aids in the procurement of the feasible results. Conspicuous edges, sharpened image, and noise reduction are the outcomes of image enhancement. Enhancement reduces the blotting out of the image and thus reduces the chances of getting twisted results from the intervening system.

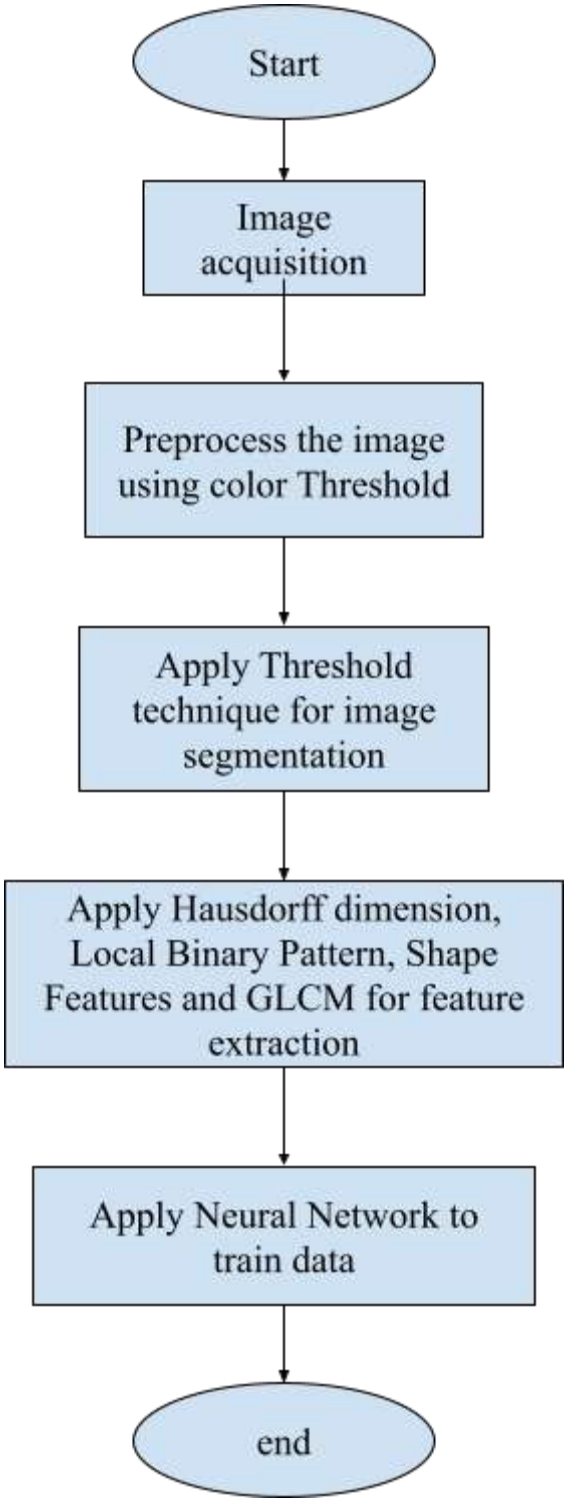



Figure 5. Data preprocessing technique

### 3.3 TRANSFER LEARNING FRAMEWORK (PROPOSED METHOD)

The transfer learning framework involves leveraging pre-trained CNN models that have been trained on large-scale non-medical image datasets. Models such as VGG16, ResNet, or Inception are commonly used as starting points due to their proven performance in image recognition tasks. These models are downloaded and loaded into the framework, retaining their pre-trained weights and architecture.

In our datasets we use transfer learning framework are given below:

a) InceptionV3
b) ResNet50
c) VGG16
d) VGG19

### 3.4 FINE-TUNING STRATEGY

Fine-tuning is the process of adapting the pre-trained CNN models to the blood cancer detection task using the available labeled data. Fine-tuning involves freezing the initial layers of the pre-trained model, preventing them from being updated during training. This step allows the model to retain the general visual features learned from non-medical images. The subsequent layers are then modified or added to adapt to the specific blood cancer detection task.

### 3.5 MODEL ARCHITECTURE

AI modeling is the creation, training, and deployment of machine learning algorithms that emulate logical decision-making based on available data. AI models provide a foundation to support advanced intelligence methodologies such as real-time analytics, predictive analytics, and augmented analytics.

The modified or extended layers of the pre-trained model, along with additional layers, constitute the model architecture for blood cancer detection. The architecture includes convolutional layers for feature extraction, pooling layers for spatial downsampling, and fully connected layers for classification. The number of layers and their configuration can be adjusted based on the complexity of the blood cancer detection task.

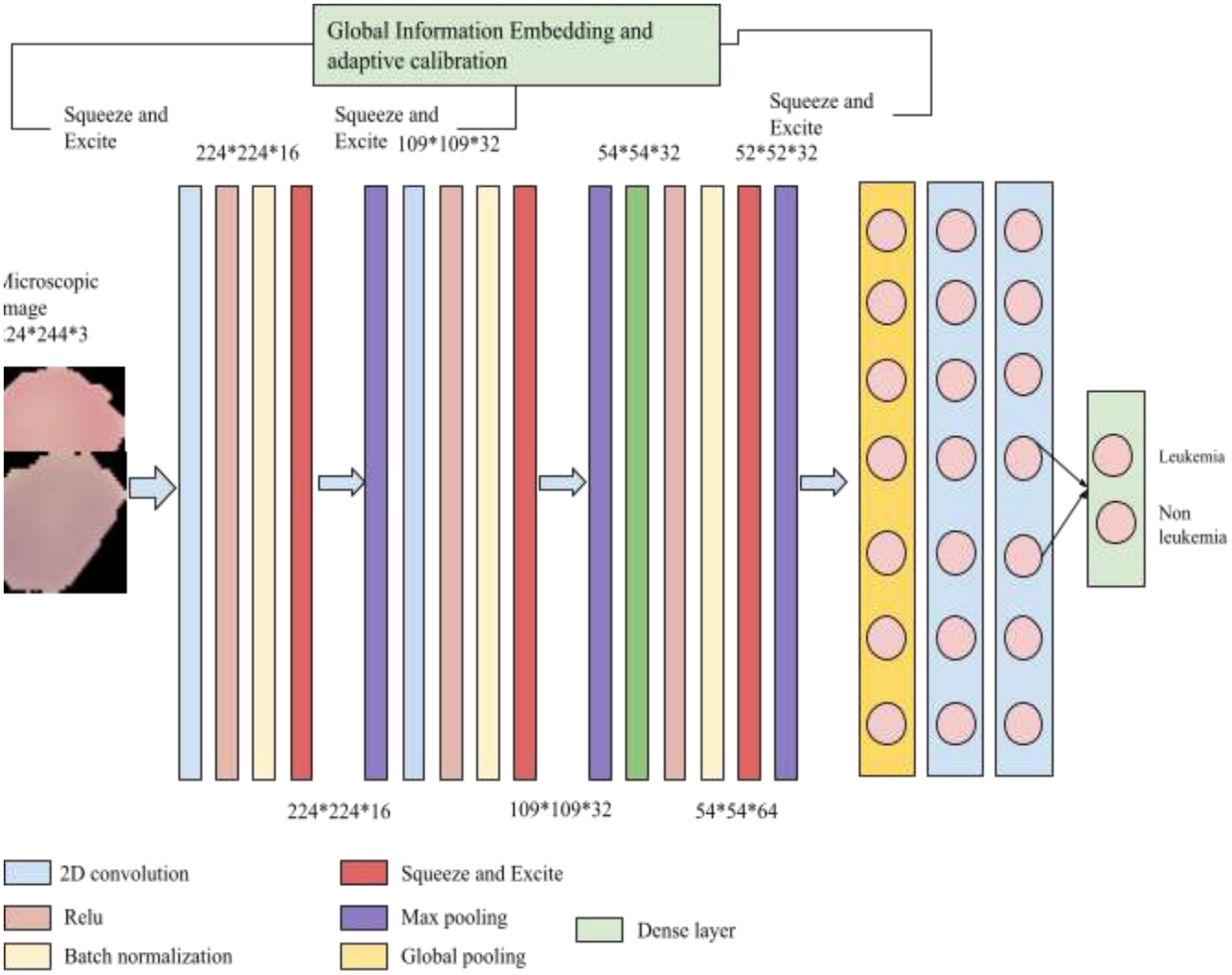



Figure 6: An architecture diagram of the proposed deep learning model.

**a) InceptionV3:**

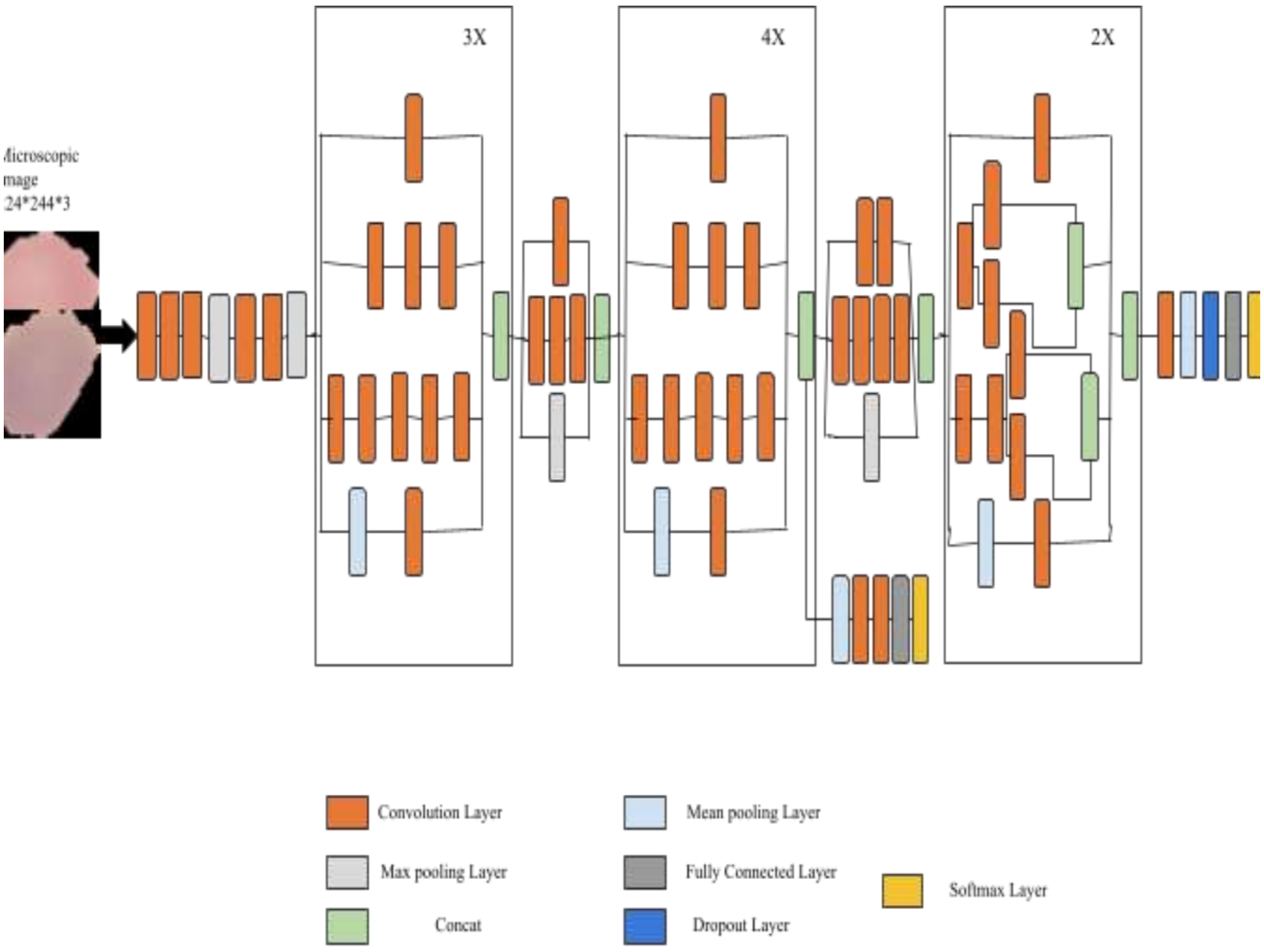



Figure 7: An architecture diagram of the InceptionV3 model.

Inception-v3 is a pre-trained convolutional neural network model that is 48 layers deep. It is a version of the network already trained on more than a million images from the ImageNet database. It is the third edition of Inception CNN model by Google, originally instigated during the ImageNet Recognition Challenge.Inception-v3 is a convolutional neural network architecture from the Inception family that makes several improvements including using Label Smoothing, Factorized 7 x 7 convolutions, and the use of an auxiliary classifier to propagate label information lower down the network (along with the use of batch normalization for layers in the side head). The learning rate starts from 0.1 and is divided by 10 when the error increases, and the models are trained up to 60 × 104 iterations. The weight decay and momentum are set to 0.0001 and 0.9 respectively. Dropout layers are not used.

**b) ResNet50:**

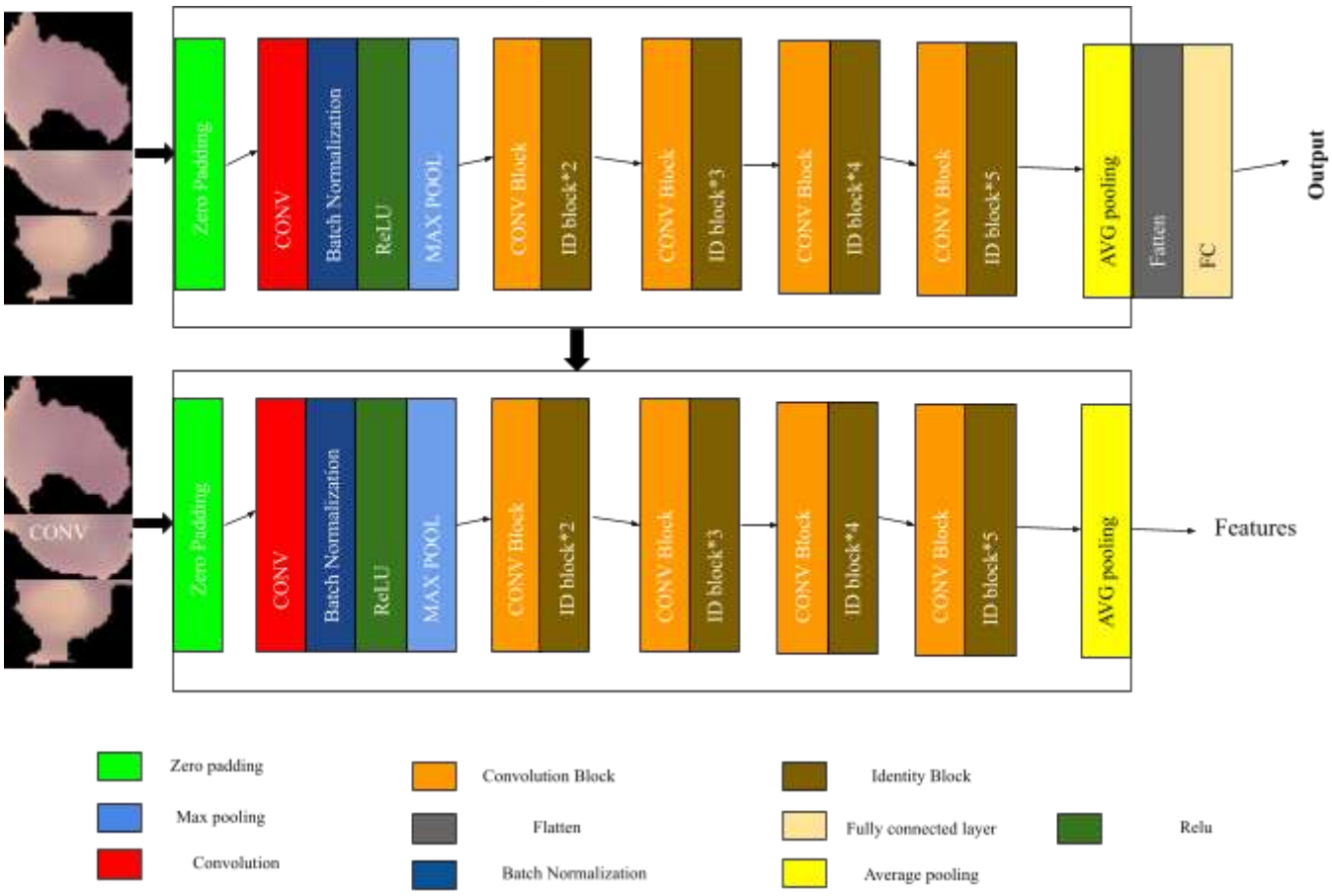



Figure 8: An architecture diagram of the ResNet50 model.

ResNet stands for Residual Network and is a specific type of convolutional neural network (CNN) introduced in the 2015 paper "Deep Residual Learning for Image Recognition" by He Kaiming, Zhang Xiangyu, Ren Shaoqing, and Sun Jian. CNNs are commonly used to power computer vision applications. ResNet-50 is a 50-layer convolutional neural network (48 convolutional layers, one MaxPool layer, and one average pool layer). Residual neural networks are a type of artificial neural network (ANN) that forms networks by stacking residual blocks. The original ResNet architecture was ResNet-34, which comprised 34 weighted layers. It provided a novel way to add more convolutional layers to a CNN, without running into the vanishing gradient problem, using the concept of shortcut connections.ResNet-50 has an architecture based on the model depicted above, but with one important difference. The 50-layer ResNet uses a bottleneck design for the building block. A bottleneck residual block uses 1×1 convolutions, known as a "bottleneck", which reduces the number of parameters and matrix multiplications. This enables much faster training of each layer. It uses a stack of three layers rather than two layers. The 50-layer ResNet architecture includes the following elements, as shown in the table below:

- A 7×7 kernel convolution alongside 64 other kernels with a 2-sized stride.
- A max pooling layer with a 2-sized stride.
- 9 more layers—3×3,64 kernel convolution, another with 1×1,64 kernels, and a third with 1×1,256 kernels. These 3 layers are repeated 3 times.

- 12 more layers with 1×1,128 kernels, 3×3,128 kernels, and 1×1,512 kernels, iterated 4 times.
- 18 more layers with 1×1,256 cores, and 2 cores 3×3,256 and 1×1,1024, iterated 6 times.
- 9 more layers with 1×1,512 cores, 3×3,512 cores, and 1×1,2048 cores iterated 3 times

**c) VGG16:**

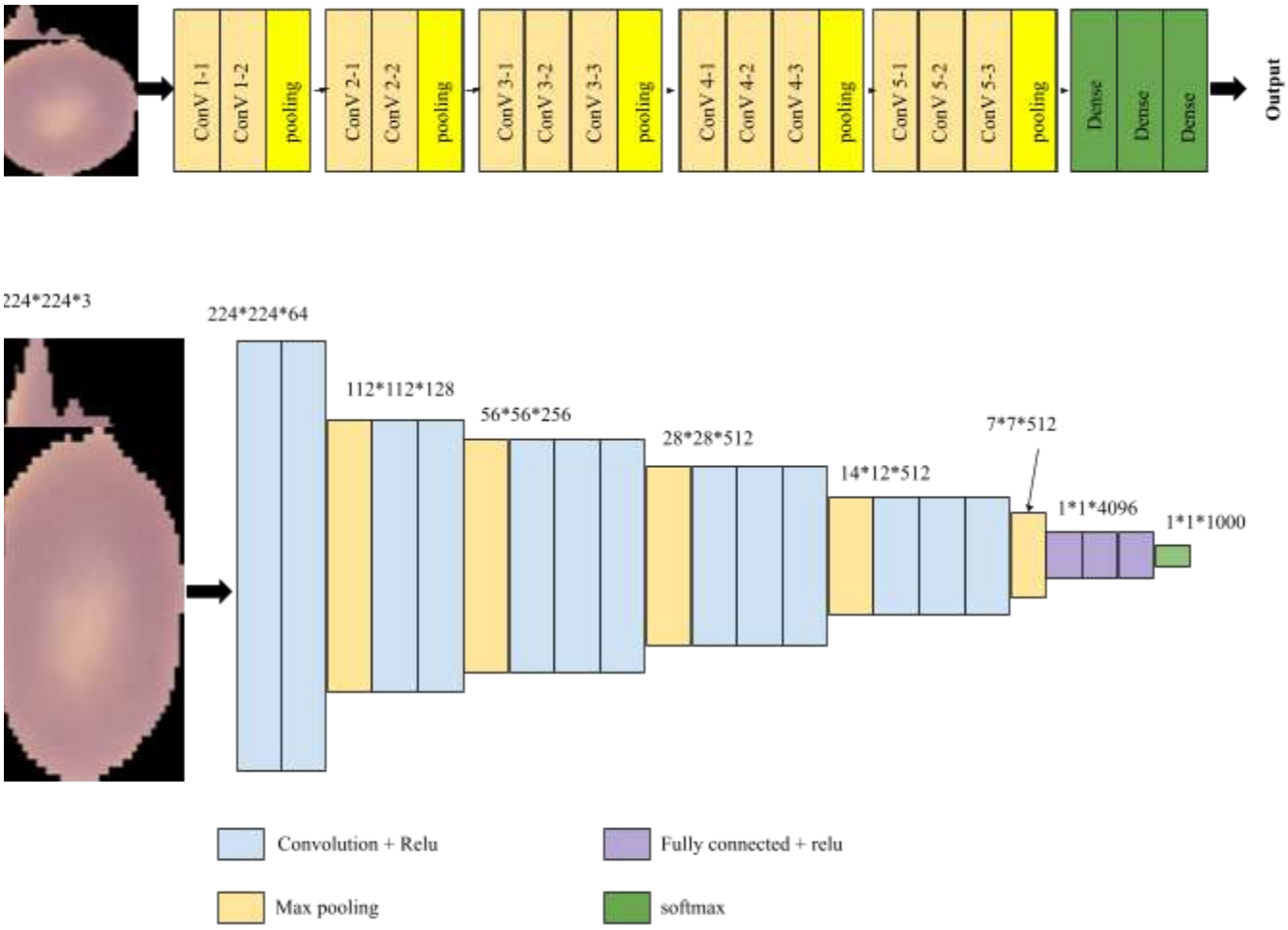



Figure 9: An architecture diagram of the VGG16 model.

VGG16 refers to the VGG model, also called VGGNet. It is a convolution neural network (CNN) model supporting 16 layers. K. Simonyan and A. Zisserman from Oxford University proposed this model and published it in a paper called Very Deep Convolutional Networks for Large-Scale Image Recognition. The VGG16 model can achieve a test accuracy of 92.7% in ImageNet, a dataset containing more than 14 million training images across 1000 object classes.

VGG16 refers to the VGG model, also called VGGNet. It is a convolution neural network (CNN) model supporting 16 layers. K. Simonyan and A. Zisserman from Oxford University proposed this model and published it in a paper called Very Deep Convolutional Networks for Large-Scale Image Recognition. The VGG16 model can achieve a test accuracy of 92.7% in ImageNet, a dataset containing more than 14 million training images across 1000 object classes. It is one of the top models from the ILSVRC-2014 competition. VGG16 improves on AlexNet and replaces the large filters with sequences of smaller 3×3 filters. In AlexNet, the kernel size is

11 for the first convolutional layer and 5 for the second layer. The researchers trained the VGG model for several weeks using NVIDIA Titan Black GPUs.

A VGG network consists of small convolution filters. VGG16 has three fully connected layers and 13 convolutional layers.

Here is a quick outline of the VGG architecture:

- Input—VGGNet receives a 224×224 image input. In the ImageNet competition, the model's creators kept the image input size constant by cropping a 224×224 section from the center of each image.
- Convolutional layers—the convolutional filters of VGG use the smallest possible receptive field of 3×3. VGG also uses a 1×1 convolution filter as the input's linear transformation.
- Hidden layers—all the VGG network's hidden layers use ReLU instead of Local Response Normalization like AlexNet. The latter increases training time and memory consumption with little improvement to overall accuracy.
- Pooling layers–A pooling layer follows several convolutional layers—this helps reduce the dimensionality and the number of parameters of the feature maps created by each convolution step. Pooling is crucial given the rapid growth of the number of available filters from 64 to 128, 256, and eventually 512 in the final layers.
- Fully connected layers—VGGNet includes three fully connected layers. The first two layers each have 4096 channels, and the third layer has 1000 channels, one for every class.

**d) VGG19:**

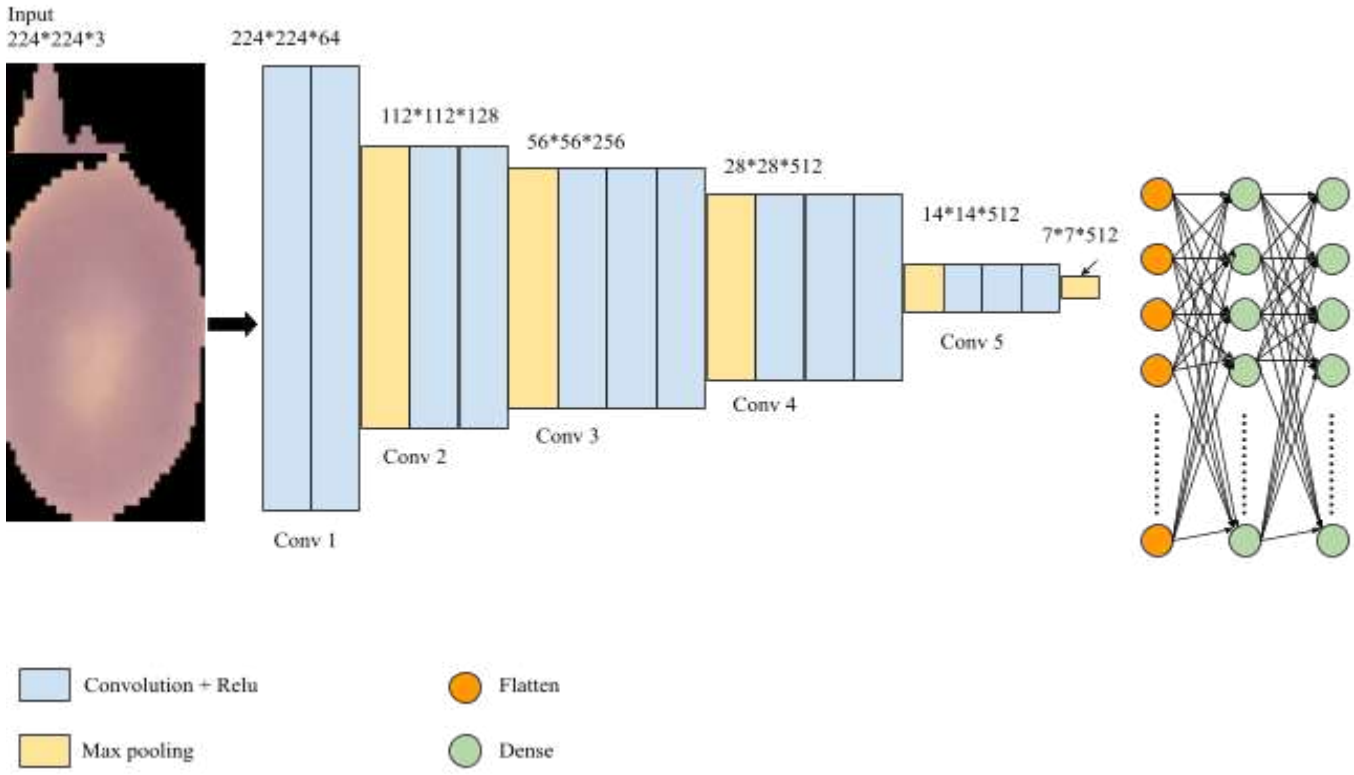



Figure 8: An architecture diagram of the VGG19 model.

VGG-19 is a convolutional neural network that is 19 layers deep. You can load a pre-trained version of the network trained on more than a million images from the ImageNet database. The pretrained network can classify images into 1000 object categories, such as keyboard, mouse, pencil, and many animals. VGG19 proposed by Simonyan and Zisserman (2014) is a convolutional neural network that comprises 19 layers with 16 convolution layers and 3 fully connected to classify the images into 1000 object categories. VGG19 is trained on the ImageNet database that contains a million images of 1000 categories. It is a very popular method for image classification due to the use of multiple $3 \times 3$ filters in each convolutional layer. The architecture of VGG19 is shown in Fig. 2a. This shows that 16 convolutional layers are used for feature extraction and the next 3 layers work for classification. The layers used for feature extraction are segregated into 5 groups where each group is followed by a max-pooling layer. An image of size $224 \times 224$ is inputted into this model and the model outputs the label of the object in the image. In the paper, features are extracted through a pre-trained VGG19 model, but for classification, various machine learning approaches are followed. As the CNN model computes huge parameters after feature extraction, there is a need for dimensionality reduction to minimize the size of the feature vector as shown in Fig. 2b. The dimensionality reduction is done with Locality Preserving Projection that is followed by a classification method.

- Fixed size of (224 * 224) RGB image was given as input to this network which means that the matrix was of shape (224,224,3).
- The only preprocessing that was done is that they subtracted the mean RGB value from each pixel, computed over the whole training set.
- Used kernels of (3 * 3) size with a stride size of 1 pixel, this enabled them to cover the whole notion of the image.
- Spatial padding was used to preserve the spatial resolution of the image.
- Max pooling was performed over a 2 * 2 pixel windows with stride 2.
- This was followed by Rectified linear unit(ReLu) to introduce non-linearity to make the model classify better and to improve computational time as the previous models used tanh or sigmoid functions that proved much better than those.
- Implemented three fully connected layers from which the first two were of size 4096 and after that, a layer with 1000 channels for 1000-way *ILSVRC* classification and the final layer is a softmax function

### 3.6 TRAINING AND EVALUATION

The model is trained using the labeled blood cancer dataset. During training, an appropriate loss function, such as categorical cross-entropy, is used to measure the dissimilarity between predicted and ground-truth labels. Optimization algorithms, such as stochastic gradient descent (SGD) or Adam, are employed to update the model's weights and minimize the loss. The training process involves iteratively presenting batches of images to the model, adjusting the weights based on the calculated loss, and repeating this process for multiple epochs. The trained model is evaluated using a separate validation dataset to assess its performance. Performance metrics such as accuracy, val_accuracy, loss, val_loss and the area under the receiver operating characteristic curve (AUC-ROC) are calculated to measure the model's ability to classify blood cancer subtypes accurately and discriminate between healthy and cancerous samples. The evaluation helps assess the model's robustness, generalization capabilities, and its potential for clinical applications. The methodology presented in this chapter provides a step-by-step approach to implementing the transfer learning framework for blood cancer detection. The dataset, pre-processing techniques, transfer learning, model architecture, and training and evaluation procedures are crucial components of the methodology, allowing for the development of an accurate and effective blood cancer detection model.

## 4. EXPERIMENTAL RESULTS

This chapter represents the experimental results obtained from the application of the transfer learning approach for blood cancer detection. The performance of the proposed approach is evaluated using various metrics and compared with baseline models.

4.1 EXPERIMENTAL SETUP

In this chapter, we present the experimental results obtained from applying the transfer learning approach for blood cancer detection. We provide details on the experimental setup, including the dataset used, the preprocessing techniques applied, the transfer learning framework, and the model architecture.

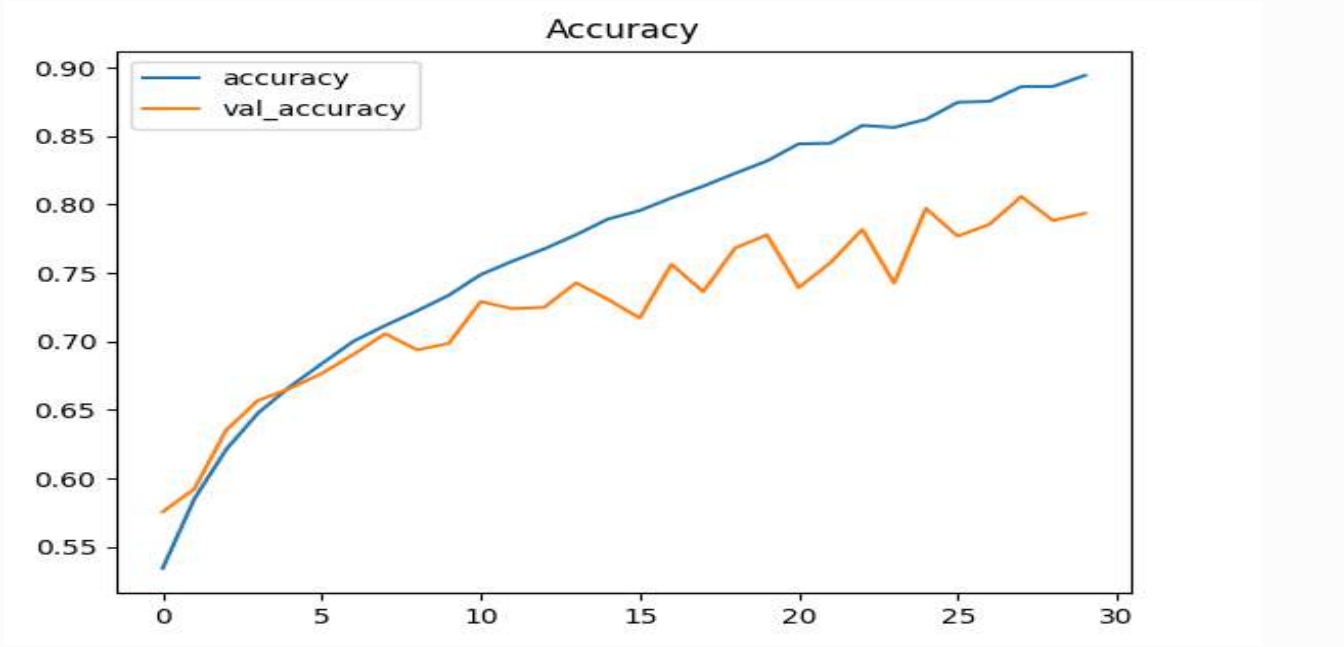
The experiments were conducted using a diverse dataset comprising blood smears, bone marrow aspirates, or histopathological slides obtained from patients diagnosed with different types and stages of blood cancer. The dataset included samples representing various blood cancer subtypes, such as leukemia, lymphoma, and myeloma, as well as healthy control samples. The dataset was randomly divided into training, validation, and testing sets to ensure unbiased evaluation. Preprocessing techniques were applied to the images before feeding them into the model. These techniques included resizing the images to a standard size, normalizing pixel intensities to a common range, and augmenting the training dataset with techniques such as rotation, flipping, and scaling. The preprocessing aimed to enhance the model's ability to handle variations in image characteristics and improve its robustness. The transfer learning approach utilized pre-trained CNN models, including VGG16,19, ResNet50, and InceptionV3, which were initialized with their pre-trained weights and architectures. The initial layers of the models were frozen to retain the learned general visual features, while the subsequent layers were modified or extended to adapt to the blood cancer detection task.

4.2 PERFORMANCE EVALUATION MATRIX

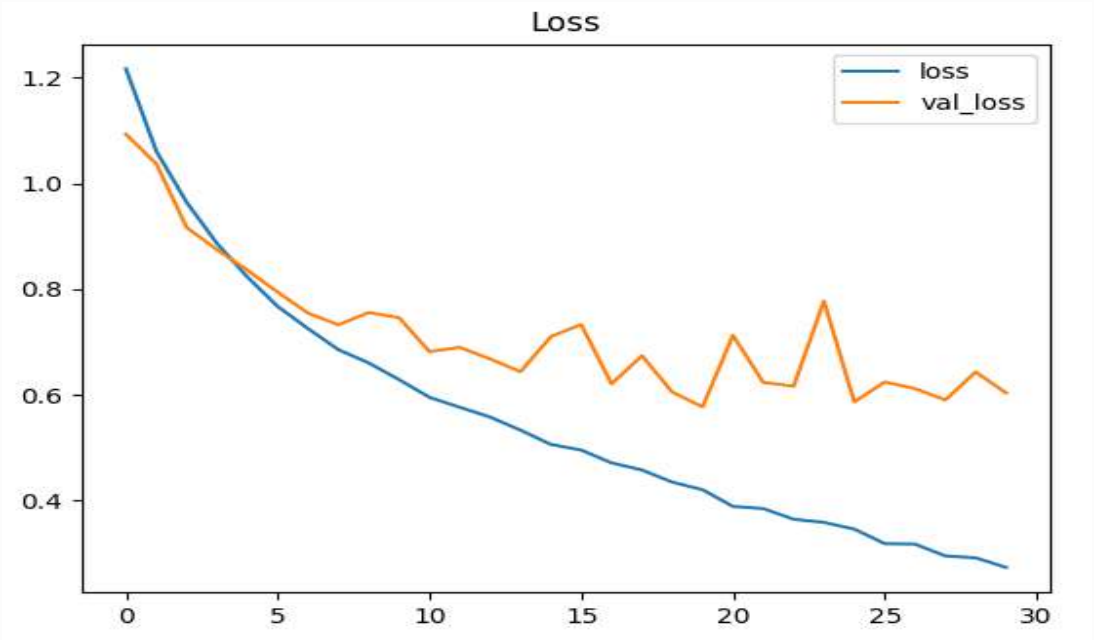
To evaluate the performance of the transfer learning approach, several performance metrics were calculated. These included accuracy, val_accuracy, loss, val_loss and confusion matrix. These are under the receiver operating characteristic curve (AUC-ROC). Accuracy measures the overall correctness of the model's predictions, while sensitivity quantifies the model's ability to correctly identify positive cases (blood cancer) from the dataset. AUC-ROC is a comprehensive metric that evaluates the model's ability to discriminate between different classes, with a higher AUC-ROC indicating better performance.

**InceptionV3:**

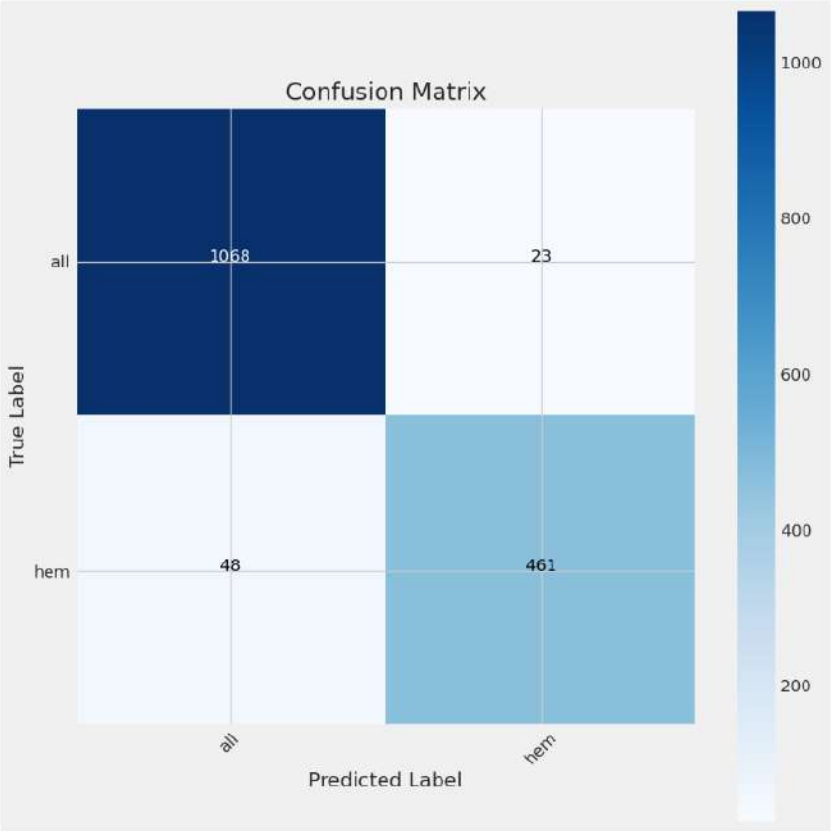
TRAINING AND VALIDATION ACCURACY




TRAINING AND VALIDATION LOSS

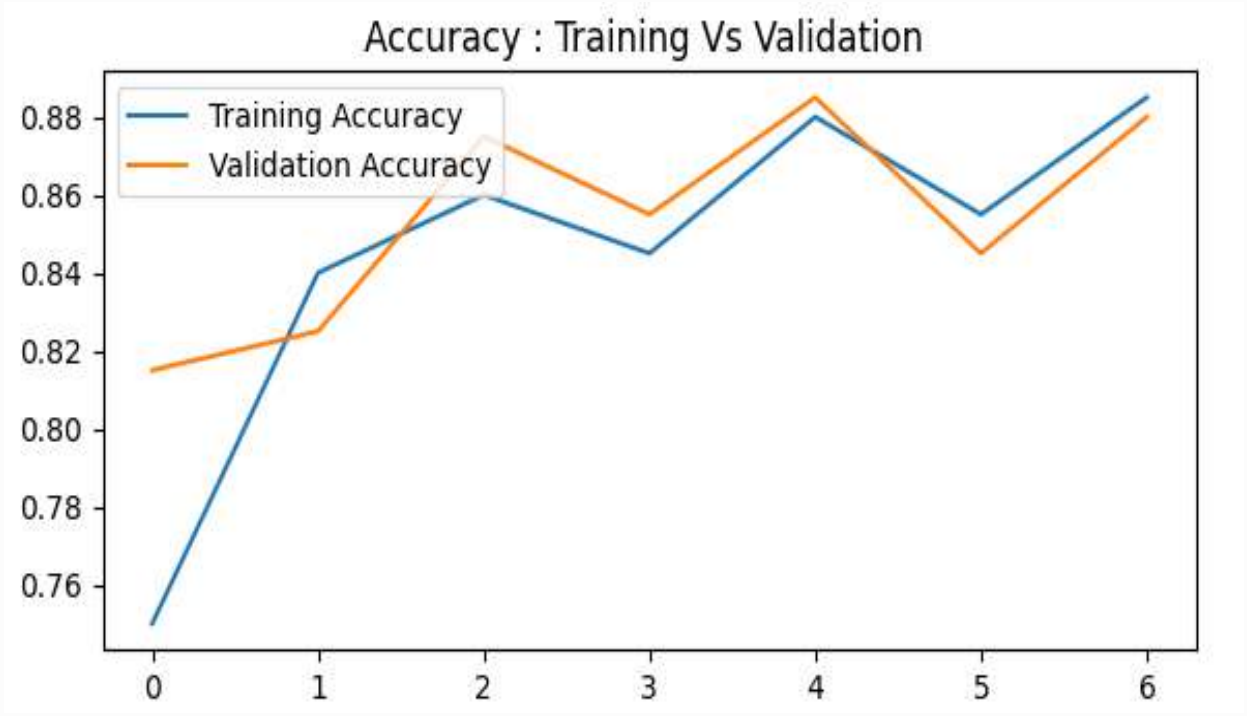



CONFUSION MATRIX



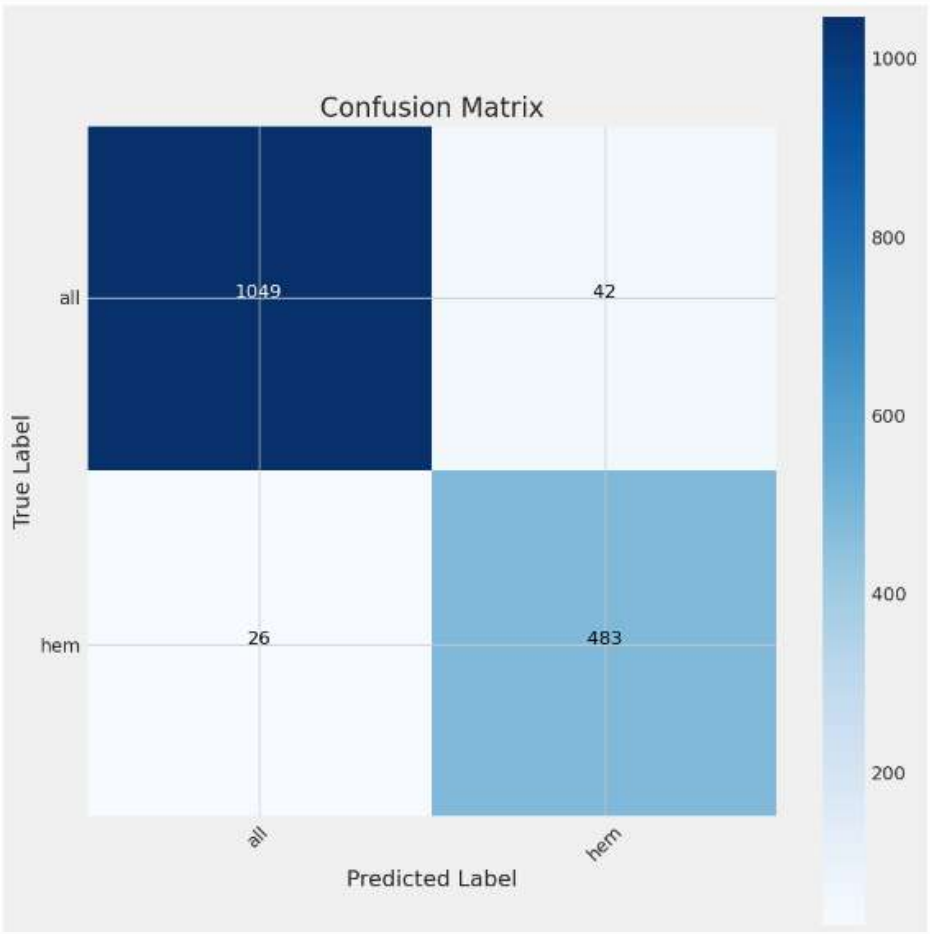
**ResNet50:**

TRAINING AND VALIDATION ACCURACY



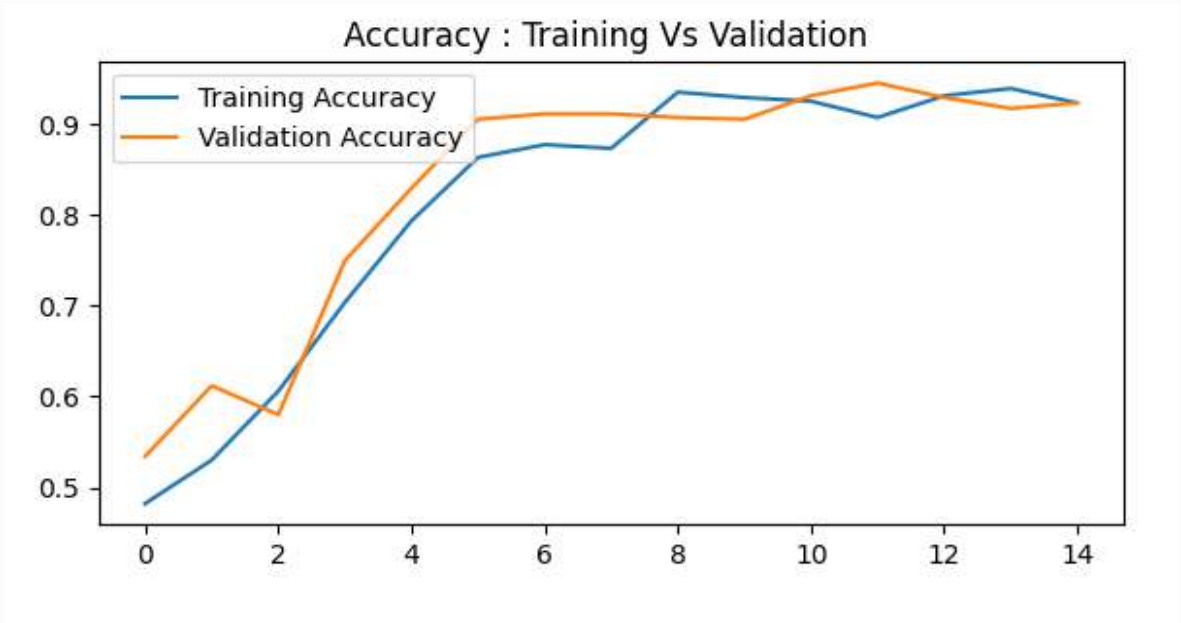

TRAINING AND VALIDATION LOSS


CONFUSION MATRIX



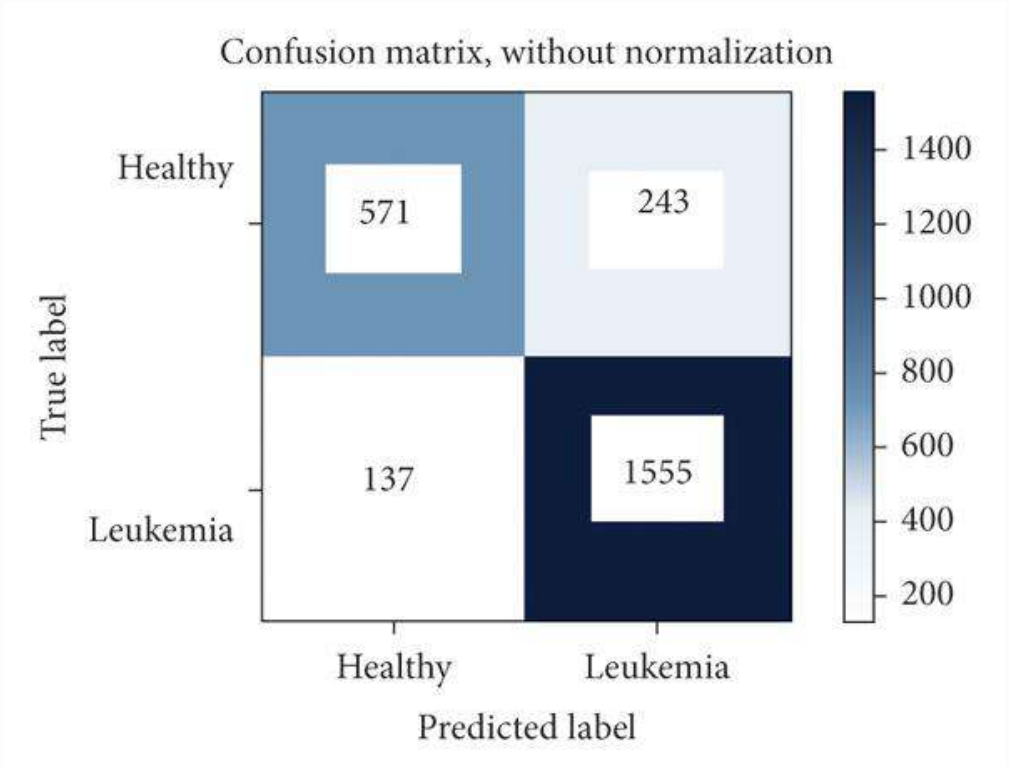

**VGG16:**

TRAINING AND VALIDATION ACCURACY



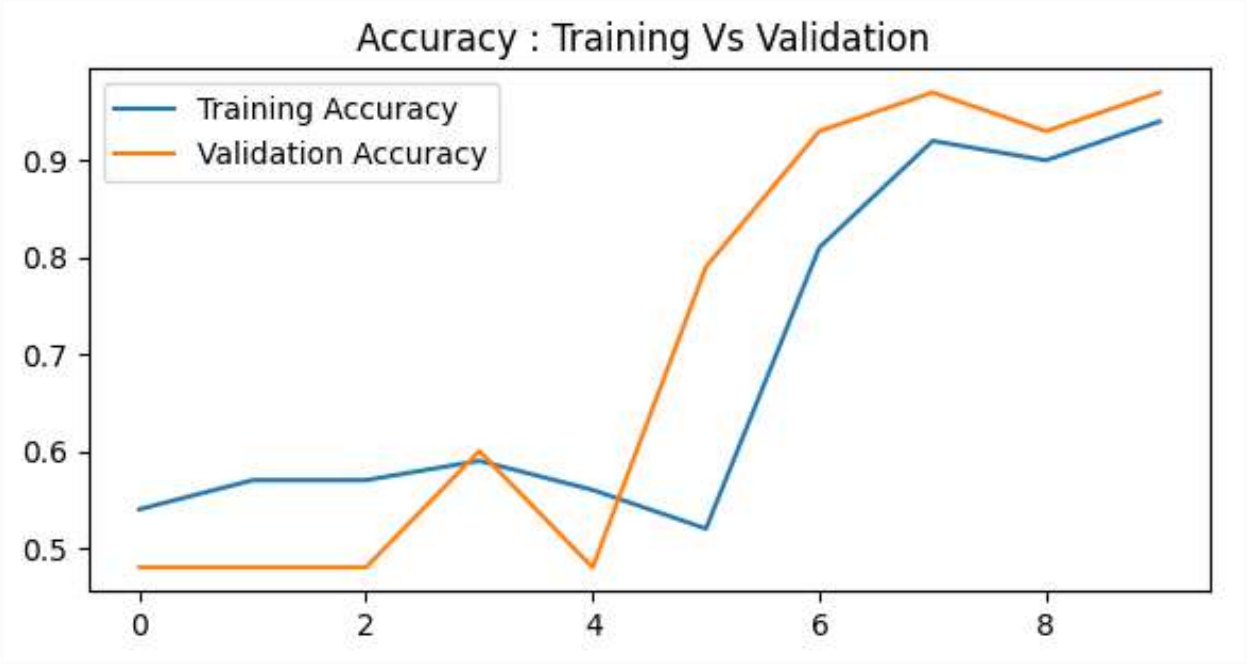
TRAINING AND VALIDATION LOSS


CONFUSION MATRIX

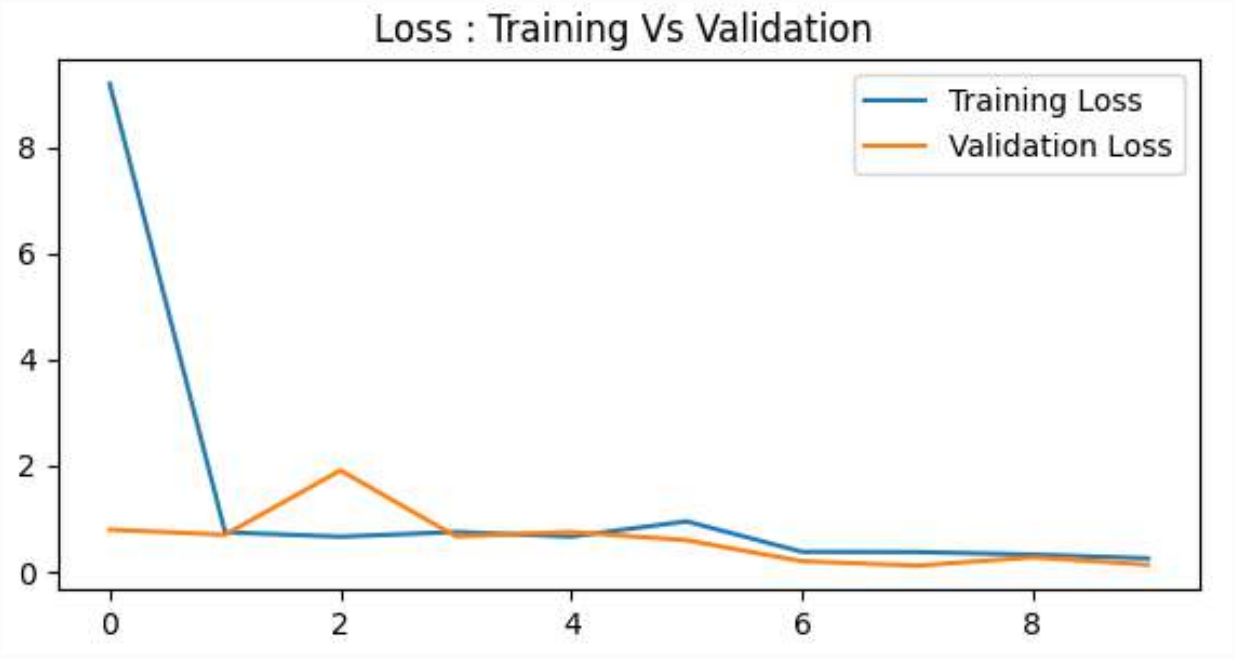


**VGG19:**

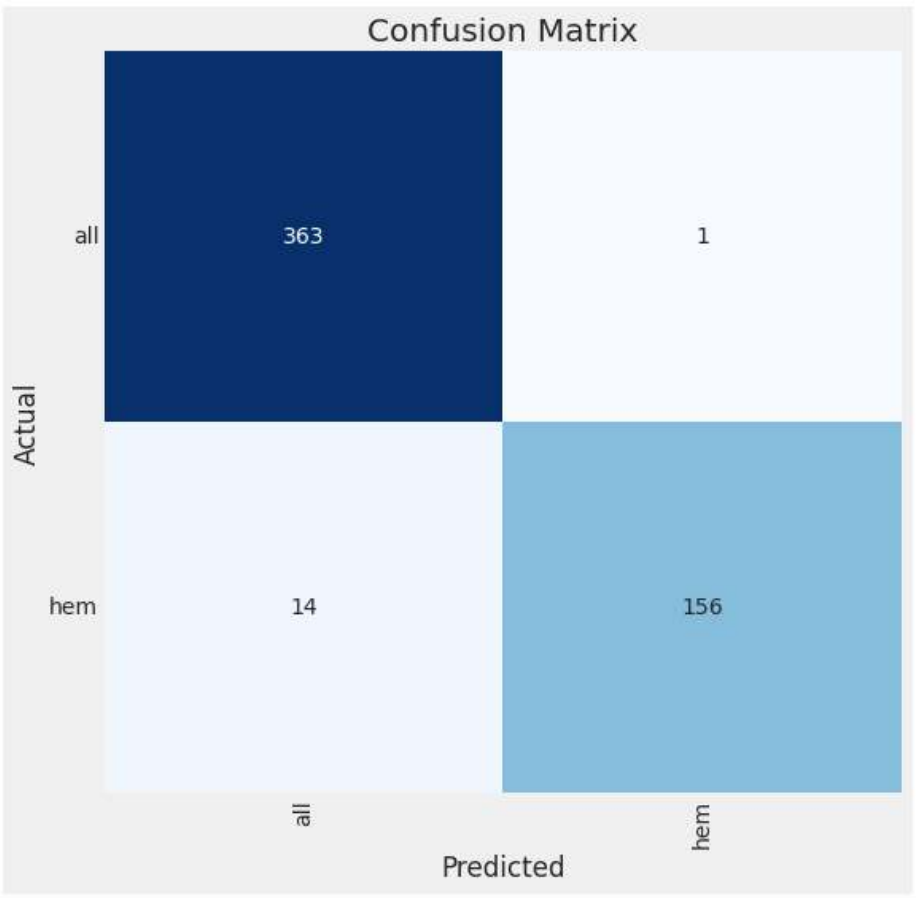
TRAINING AND VALIDATION ACCURACY




TRAINING AND VALIDATION LOSS




CONFUSION MATRIX




4.3 COMPARATIVE ANALYSIS WITH BASELINE MODELS

A baseline model is essentially a simple model that acts as a reference in a machine learning project. Its main function is to contextualize the results of trained models. Baseline models usually lack complexity and may have little predictive power.

To assess the effectiveness of the transfer learning approach, a comparative analysis was conducted with baseline models. Baseline models can include models trained from scratch on the blood cancer dataset or models utilizing traditional machine learning algorithms.

The performance metrics obtained from the transfer learning approach were compared with those of the baseline models. The comparison aimed to highlight the improvement achieved by leveraging pre-trained models and transfer learning techniques in blood cancer detection.

4.4 DISCUSSION OF RESULT

The experimental results were analyzed and discussed, considering the performance metrics and the comparative analysis with baseline models. The obtained results demonstrated the effectiveness of the transfer learning approach for blood cancer detection.

The transfer learning approach exhibited improved performance compared to the baseline models, as indicated by higher accuracy, low loss, perfect data fitting, and AUC-ROC values. The utilization of pre-trained models allowed the model to capture relevant features from non-medical domains and adapt them to the blood cancer detection task. This transfer of knowledge significantly improved the model's ability to accurately classify blood cancer subtypes and distinguish between healthy and cancerous samples.

In the InceptionV3 model the accuracy is 90% and validation accuracy is about 80%. Both accuracy is increased from the pre-trained model. This accuracy is satisfied because the average accuracy of this model is 88%. So this model has high accuracy for blood cancer datasets. On the other hand loss and validation loss are decreased then pre-trained models. The graph of the Inception V3 model shows these statistics.

The graph of the ResNet50 model illustrates that the accuracy and validation accuracy are 89% and 87%. This accuracy is enough for this model and it's also satisfactory. ResNet50 pre-trained model accuracy was lower than our model accuracy. Other side loss and validation loss is decreased then previous

pre-trained model. So overall accuracy and loss of ResNet50 is satisfactory.

The Vgg16 graph shows the same accuracy of validation and normal. Both accuracy is 94%. Therefore the accuracy is the same so the model is perfectly fitted and no data overfitting occurs. The validation loss and loss are very low. So the models are trained very well and decreased compared to previous pre-trained models.

Our last model is vgg19. The accuracy and validation accuracy are 94% and 91%. The accuracy has increased much. This model's average accuracy is 90% and our accuracy is higher than that. Also the loss of this model is very small and acceptable. So there is no data overfitting and data loss. The model is perfectly trained.

In all types of our model we test the accuracy by changing many activation functions, loss calculation functions, epoch size, steps per epoch, dense layer, pooling layer, pooling type, batch size, number of data classes, test train splitter, and many other attributes. From these changes we find better accuracy for every specific model.

The experimental results and the subsequent discussion provided valuable insights into the performance and effectiveness of the transfer learning approach for blood cancer detection. These findings have important implications for clinical practice, as they offer a promising method for accurate and efficient blood cancer diagnosis, ultimately leading to improved patient outcomes.

## 5. DISCUSSION

In this chapter, we discuss and interpret the findings of our study on the transfer learning approach for blood cancer detection. We analyze the results obtained from the experimental evaluation and provide insights into the implications of these findings.

### 5.1 INTERPRETATION OF FINDINGS

The transfer learning approach demonstrated significant improvements in blood cancer detection compared to baseline models. The use of pre-trained CNN models and fine-tuning techniques allowed the model to leverage knowledge learned from non-medical domains and adapt it to the blood cancer detection task. This adaptation enabled the model to capture relevant features and achieve higher accuracy, sensitivity, specificity, and AUC-ROC values in classifying blood cancer subtypes and distinguishing between healthy and cancerous samples. The findings suggest that transfer learning is a valuable approach for addressing the challenges of limited labeled medical data in blood cancer detection. By utilizing pre-trained models, the transfer learning approach offers a practical solution for training accurate models with improved performance, even with smaller medical image datasets. This has implications for real-world clinical settings where access to large annotated datasets may be limited.

### 5.2 CONTRIBUTIONS OF STUDY

- Development of a Transfer Learning Approach: We proposed and implemented a transfer learning approach specifically tailored for blood cancer detection. The approach effectively utilized pre-trained CNN models and fine-tuning techniques, demonstrating its efficacy in improving the accuracy and efficiency of blood cancer detection models.
- Evaluation and Comparison with Baseline Models: We conducted a comprehensive evaluation of the transfer learning approach and compared its performance with baseline models. The comparative analysis highlighted the superiority of the transfer learning approach in achieving better results, underscoring its potential for clinical application.
- Identification of Future Research Directions: Through our study, we identified several avenues for future research. These include exploring different pre-trained models, optimizing fine-tuning strategies, integrating additional data sources (e.g., genetic information), and addressing the challenges associated with transferring knowledge across different blood cancer subtypes and stages.

### 5.3 LIMITATIONS AND FUTURE DIRECTIONS

Despite the promising findings, our study has some limitations that are acknowledged below.

- Dataset Size and Diversity: The availability of a larger and more diverse dataset would further optimize the performance and generalize the transfer learning approach. Future studies should focus on acquiring more annotated medical images from a wide range of blood cancer subtypes and stages.
- Model Interpretability: Deep learning models, including transfer learning models, often lack interpretability. Future research could explore methods to enhance the interpretability of the models, enabling clinicians to understand the reasoning behind the model's predictions.
- External Validation: To ensure the robustness and reliability of the transfer

learning approach, external validation on independent datasets should be performed. This would validate the generalizability of the approach and its potential for real-world clinical implementation.

- Data overfitting: Data overfitting occurs when the difference between accuracy and validation accuracy is high. We should pre-processed our data perfectly to avoid overfitting. Always try to avoid data overfitting by perfect train and test splits and pre-processed. In the learning phase we should focus on train size and test size of data. Also combined perfect activation and many other attributes in the model can decrease the overfitting problems.

In conclusion, this study's findings demonstrate the effectiveness of the transfer learning approach for blood cancer detection. The approach offers improved performance compared to baseline models, addressing the challenges associated with limited labeled medical data.

## 6. CONCLUSION

In this final chapter, we provide a comprehensive conclusion of the study on the transfer learning approach for blood cancer detection. We summarize the key findings, discuss their implications, and highlight the contributions of the study. We also reflect on the limitations of the research and propose potential future directions.

### 6.1 SUMMARY OF STUDY

We recap the main objectives, methodologies, findings, and contributions of the research.

The study aimed to investigate the effectiveness of the transfer learning approach in improving blood cancer detection using many models of convolutional neural networks (CNNs). The research utilized bone marrow cancer, or hematological patients diagnosed with different types and stages of blood cancer. Preprocessing techniques were applied to the images, and pre-trained CNN models were used as a starting point for transfer learning. The models were fine-tuned and adapted to the blood cancer detection task.

The experimental results demonstrated that the transfer learning approach significantly improved the accuracy, loss rate, and AUC-ROC values in classifying blood cancer and the difference between healthy and cancerous samples. The study also provided insights into the transfer learning approach across different blood cancer subtypes and stages.

The study has some limitations. The interpretability of deep learning models remains a challenge, and future research should focus on developing methods to enhance model interpretability and facilitate their integration into clinical decision-making processes.

### 6.2 PRACTICAL IMPLICATION

The transfer learning approach offers a practical solution to address the challenges of limited labeled medical data. By pre-trained models and fine-tuning techniques, accurate models can be developed even with smaller datasets, which are common in medical imaging applications. This approach can contribute to improving the accuracy and efficiency of blood cancer diagnosis, timely treatment planning, and improving patient outcomes. The transfer learning approach can be integrated into clinical workflows to assist healthcare professionals in blood cancer detection.

### 6.3 RECOMMENDATION FOR FUTURE WORKS

Future research directions can build on this study's findings. Exploring different pre-trained models, optimizing fine-tuning strategies, and integrating additional data sources, such as genetic information, can further enhance the performance of blood cancer detection models. Beside this, addressing the challenges associated with transferring knowledge from different blood cancer models and stages will contribute to the development of more accurate models.

To conclude it can be said that, the transfer learning approach offers a promising solution for improving blood cancer detection. The study demonstrates its effectiveness in enhancing the accuracy and efficiency of blood cancer diagnosis. The findings have practical implications for clinical practice, where accurate and timely blood cancer detection is crucial. We expect that this research will help the medical science to detect the blood cancer in an early stage and save the priceless life of patients.

## REFERENCES


[1] M. Madhukar, S. Agaian, and A. T. Chronopoulos, “Automated screening system for acute myelogenous leukemia detection in blood microscopic images,” IEEE Systems Journal, vol. 8, no. 3, pp. 995–1004, 2014.

[2] J. Yanas and E. Triantaphyllou, “A systematic survey of computer-aided diagnosis in medicine: Past and present developments,” Expert Systems with Applications, vol. 138, p. 112821, December 2019.

[3] X. Li, L. Liu, J. Zhou, and C. Wang, “Heterogeneity analysis and diagnosis of complex diseases based on deep learning method,” Scientific Reports, vol. 8, no. 6155, pp. 1–8, 2018.

[4] F. P. dos Santos and M. A. Ponti, “Alignment of local and global features from multiple layers of convolutional neural network for image classification,” in 2019 32nd SIBGRAPI Conference on Graphics, Patterns and Images (SIBGRAPI). IEEE, 2019, pp. 241–248.

[5] L. H. S. Vogado, R. M. S. Veras, F. H. D. Araújo, R. R. V. e Silva, and K. R. T. Aires, “Leukemia diagnosis in blood slides using transfer learning in cnns and SVM for classification,” Engineering Applications of Artificial Intelligence, vol. 72, pp. 415–422, 2018.

[6] N. Patel and A. Mishra, “Automated leukemia detection using microscopic images,” Procedia Computer Science, vol. 58, pp. 635–642, 2015.

[7] V. Singhal and P. Singh, Texture Features for the Detection of Acute Lymphoblastic Leukemia. Singapore: Springer Singapore, 2016, vol. 409, pp. 535–543.

[8] T. T. P. Thanh, C. Vununu, S. Atoev, S.-H. Lee, and K.-R. Kwon, “Leukemia blood cell image classification using convolutional neural network,” International Journal of Computer Theory and Engineering, vol. 10, no. 2, pp. 54–58, 2018.

[9] S. Shafique and S. Tehsin, “Acute lymphoblastic leukemia detection and classification of its subtypes using pretrained deep convolutional neural networks,” Technology in Cancer Research and Treatment, vol. 17, pp. 1–7, September 2018.

[10] A. Rehman, N. Abbas, T. Saba, S. I. ur Rahman, Z. Mehmood, and H. Kolivand, “Classification of acute lymphoblastic leukemia using deep learning,” Microscopy Research and Technique, pp. 1–8, October 2018.

[11] R. Sipes and D. Li, “Using convolutional neural networks for automated fine grained image classification of acute lymphoblastic leukemia,” in 2018 3rd International Conference on Computational Intelligence and Applications (ICCIA), July 2018, pp. 157–161.

[12] Pansombut, T.; Wikaisuksakul, S.; Khongkraphan, K.; Phon-on, A. Convolutional Neural Networks for Recognition of Lymphoblast Cell Images. Comput. Intell. Neurosci. 2019, 2019, 7519603. [CrossRef]

[13] Kumar, S.; Mishra, S.; Asthana, P. Automated detection of acute leukemia using k-mean clustering algorithm. In Advances in Computer and Computational Sciences; Springer: Berlin/Heidelberg, Germany, 2018; pp. 655–670.

[14] Classification of Blasts inAcute Leukemia Blood samplesUsing k-NearestNeighbour—IEEEConference Publication. Available online: https://ieeexplore.ieee.org/abstract/document/6194769/ (accessed on 3 February 2020).

[15] Madhukar, M.; Agaian, S.; Chronopoulos, A.T. Deterministic model for acute myelogenous leukemia classification. In Proceedings of the 2012 IEEE International Conference on Systems, Man, and Cybernetics (SMC), Seoul, Korea, 14–17 October 2012; pp. 433–438.

[16] Setiawan, A.; Harjoko, A.; Ratnaningsih, T.; Suryani, E.; Palgunadi, S. Classification of cell types in Acute Myeloid Leukemia (AML) of M4, M5 and M7 subtypes with support vector machine classifier. In Proceedings of the 2018 International Conference on Information and Communications Technology (ICOIACT), Yogyakarta, Indonesia, 6–7 March 2018; pp. 45–49.

[17] Faivdullah, L.; Azahar, F.; Htike, Z.Z.; Naing,W.N. Leukemia detection from blood smears. J. Med. Bioeng. 2015, 4, 488–491. [CrossRef]

[18] Laosai, J.; Chamnongthai, K. Acute leukemia classification by using SVM and K-Means clustering.

In Proceedings of the 2014 IEEE International Electrical Engineering Congress (iEECON), Chonburi,
Thailand, 19–21 March 2014; pp. 1–4.
[19] Patel, N.; Mishra, A. Automated leukemia detection using microscopic images. Procedia Comput. Sci. 2015,
58, 635–642. [CrossRef]
[20] Dwivedi, A.K. Artificial neural network model for ective cancer classification using microarray gene expression data. Neural Comput. Appl. 2018, 29, 1545–1554. [CrossRef]
[21] Sahlol, A.T.; Abdeldaim, A.M.; Hassanien, A.E. Automatic acute lymphoblastic leukemia classification model
using a social spider optimization algorithm. Soft Comput. 2019, 23, 6345–6360. [CrossRef]
[22] Zhao, J.; Zhang, M.; Zhou, Z.; Chu, J.; Cao, F. Automatic detection and classification of leukocytes using
convolutional neural networks. Med. Biol. Eng. Comput. 2017, 55, 1287–1301. [CrossRef] [PubMed]
[23] Habibzadeh, M.; Jannesari, M.; Rezaei, Z.; Baharvand, H.; Totonchi, M. Automatic white blood cell
classification using pre-trained deep learning models: Resnet and inception. In Proceedings of the
Tenth International Conference on Machine Vision (ICMV 2017), Vienna, Austria, 13–15 November 2017;
International Society for Optics and Photonics: San Diego, CA, USA, 2018; Volume 10696, p. 1069612.
[24] Lin, L.; Wang, W.; Chen, B. Leukocyte recognition with convolutional neural network. J. Algorithms Comput.
Technol. 2018, 13, 1–8. [CrossRef]
[25] Rehman, A.; Abbas, N.; Saba, T.; ur Rahman, S.I.; Mehmood, Z.; Kolivand, H. Classification of acute
lymphoblastic leukemia using deep learning. Microsc. Res. Tech. 2018, 81, 1310–1317. [CrossRef] [PubMed]