# Automated Acute Lymphoblastic Leukemia Detection Using Convolutional Neural Networks

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## FINAL YEAR DESIGN PROJECT REPORT

This Report Presented in Partial Fulfillment of the Requirements for the Degree of Bachelor of Science in Computer Science and Engineering

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# APPROVAL

This Project titled "Automated Acute Lymphoblastic Leukemia Detection Using Convolutional Neural Networks", submitted by Md. Nurujjaman Raju, ID No: 172-15-1601 to the Department of Computer Science and Engineering, Daffodil International University has been accepted as satisfactory for the partial fulfillment of the requirements for the degree of B.Sc. in Computer Science and Engineering and approved as to its style and contents. The presentation has been held on 13th January, 2025.

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# DECLARATION

We hereby declare that this project has been done by us under the supervision of Dr. Ohidujjaman Tuhin, Department of Computer Science and Engineering, Daffodil International University. We also declare that neither this project nor any part of this project has been submitted elsewhere for the award of any degree or diploma**.**

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# ABSTRACT

This study investigates the performance of four widely used Convolutional Neural Networks (CNNs) MobileNetV2, InceptionV3, VGG16 and ResNet50 for disease classification tasks, leveraging transfer learning techniques. The analysis focuses on evaluating and comparing the accuracy of these models during both training and testing phases. MobileNetV2 demonstrated slightly lower performance, achieving 95.26% in training and 95.00%, InceptionV3, although effective, showed the lowest accuracy among the models, with training and test accuracies of 93.43% and 93.00%, VGG16 closely followed, with training and test accuracies of 98.78% and 98.00% and in testing ResNet50 emerged as the top-performing model, achieving the highest training accuracy of 99.24% and test accuracy of 99.00% respectively. Reflecting its efficiency but limited capacity in comparison to the top models. respectively. These findings highlight the critical role of model selection in achieving high-performance disease classification and emphasize the suitability of ResNet50 and VGG16 for such tasks. Furthermore, the study underscores the potential of transfer learning to enhance the efficiency of CNNs in medical imaging applications, while also identifying opportunities for further optimization and fine-tuning of these architectures to improve their performance in specific use cases.

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| | |
|---|---|
| ANN | Artificial Neural Network |
| CNN | Convolutional Neural Network |
| ML | Machine Learning |
| AI | Artificial Intelligence |

# CHAPTER 1

# INTRODUCTION

## 1.1 Overview

Acute lymphoblastic leukemia (ALL), primarily affecting children and young adults, is a severe form of hematological cancer that disrupts the normal functioning of white blood cells. This malignancy poses a significant threat to health due to its rapid progression and potential to spread to other parts of the body, such as the central nervous system. Early and accurate diagnosis is critical for improving survival rates and enabling timely medical intervention, as delayed detection can severely compromise treatment outcomes. Traditional diagnostic methods, such as the microscopic examination of blood smears by pathologists, are the current gold standard. However, these methods are labor-intensive, time-consuming, and susceptible to human error, requiring extensive expertise and experience for accurate interpretation. Additionally, such manual techniques often struggle to meet the increasing demand for efficient and reliable diagnostic solutions in overburdened healthcare systems. Advancements in computer vision and artificial intelligence (AI) have introduced innovative tools to overcome these limitations, enabling more precise and efficient medical diagnostics. Among these, Convolutional Neural Networks (CNNs) have emerged as a groundbreaking technology for automating the analysis of medical images. CNNs are particularly well suited for tasks involving image classification and pattern recognition due to their ability to automatically extract and learn features from data. This research presents a framework for leveraging CNNs to identify ALL from blood specimen images, highlighting their potential to streamline the diagnostic process, reduce human dependency, and significantly improve diagnostic accuracy. By integrating automated systems into routine diagnostics, healthcare providers can expedite the detection of ALL, minimize errors, and enhance patient outcomes, particularly in regions with limited access to expert pathologists. The implementation of CNNs in this context not only addresses current diagnostic challenges but also sets the stage for the broader adoption of AI-driven solutions in hematological oncology.

## 1.2 Background and Present State

The unchecked growth of immature lymphocytes is the cause of ALL, a disease that advances quickly. A set of clinical assessments, laboratory testing, and microscopic analysis of blood and bone marrow samples are usually used to make the diagnosis. Examining these materials by hand is time-consuming and subject to variation among pathologists.

For the processing of medical images, machine learning—more especially, deep learning—has shown great promise. When it comes to identifying patterns in healthcare images, such as cancers in radiography scans or anomalies in pathology slides, CNNs—a sort of deep learning model made to interpret visual data—have shown remarkable performance. Although a number of automated leukemia diagnosis systems have been developed, issues with accuracy and scalability, including generalization across different datasets, have hindered their adoption into clinical processes.

## 1.3 Problem Statement

There are a number of difficulties in manually examining blood smears for the detection of ALL, including:

a) High reliance on knowledgeable pathologists.

b) Lengthy procedures that postpone diagnosis.

c) Inter-observer variability could result in inaccurate diagnoses.

d) These problems can be solved by an automated system that uses CNNs; however there are challenges including maintaining consistent performance across various datasets, controlling computational complexity, and conforming to therapeutic standards.

## 1.4 Objectives

The following are the study's main goals:

a) Create a CNN-based algorithm to automatically identify ALL in blood sample pictures.
b) Utilize measures like precision, specificity, and sensitivity to assess the model's performance.
c) Examine the suggested system in comparison to the current automatic and manual diagnostic techniques.
d) Determine the constraints and potential avenues for enhancing the incorporation of artificial intelligence in ALL diagnosis.

## 1.5 Scope and Limitations

This study uses Convolutional Neural Network (CNN) models to detect Acute Lymphoblastic Leukemia (ALL) in peripheral blood smear pictures. Preprocessing methods are used to improve image quality and data augmentation is used to rectify class imbalances in the dataset in order to guarantee the efficacy of the suggested solution. The research's relevance in clinical settings is a crucial factor, especially in countries with limited resources where access to skilled pathologists may be restricted.

Nonetheless, several restrictions are recognized. The model's generalizability may be impacted by the study's reliance on publicly accessible datasets, which might not accurately reflect the diversity of population demographics. Hospitals' hardware and processing limitations are among the real-time deployment issues that are not fully covered. The model's robustness in a range of clinical circumstances may also be impacted by variations in image gathering methods or equipment types, which could affect the model's performance.

## 1.6 Report Organization

Chapter 1 introduces our research, outlining its objectives, motivations, and the financial analysis conducted to establish the study's significance. This chapter lays the groundwork for our investigation into multi-label seed classification and segmentation by providing a comprehensive theoretical framework. It sets the stage for comparing existing models with the novel approach proposed in this work. Chapter 2 delves deeper into the foundational aspects of our research, offering insights into the existing literature and the limitations of current methodologies, which our study aims to address. Chapter 3 describes the research methodology in detail, including data collection strategies, the design of the proposed model architecture, and the hardware specifications utilized. This chapter provides a transparent view of the technical processes underlying our study. Chapter 4 focuses on the experimental results derived from our proposed model, supported by detailed statistical analyses.These empirical findings serve as the foundation for assessing the model's efficacy and performance, demonstrating its potential advantages over existing approaches. Chapter

5 examines the societal impact of our work, with an emphasis on ethical considerations and the broader implications of our findings. This chapter highlights how our research contributes to advancements in agriculture, offering solutions that promote societal welfare. Finally, Chapter 6 concludes the study with a summary of key findings, the conclusions drawn from the analysis, and recommendations for future research. This chapter encapsulates the entire research journey, providing a comprehensive overview and proposing directions for continued improvements and exploration in this domain.

### 1.7 Summary

This introduction emphasizes the significance of creating an automated system for the detection of Acute Lymphoblastic Leukemia (ALL) via Convolutional Neural Networks (CNNs). Acute Lymphoblastic Leukemia (ALL) is a dangerous hematologic malignancy that necessitates prompt and precise diagnosis to enhance patient outcomes. Contemporary diagnosis techniques, which depend on the manual analysis of blood smear pictures, are laborious, susceptible to error by humans, and significantly reliant on skilled pathologists. This study seeks to tackle these problems by utilizing CNNs to provide a dependable and efficient diagnostic instrument for ALL detection. The emphasis encompasses employing preprocessing methods to improve image quality, utilizing data augmentation to address class imbalances, and guaranteeing the solution's applicability in clinical contexts, particularly in resource-constrained settings. Nonetheless, specific limitations are recognized, including dependence on publicly accessible datasets that may not reflect the diversity of actual populations, difficulties in real-time implementation due to the hospital hardware limitations, and possible discrepancies in performance among various imaging systems. This study aims to fill current deficiencies in ALL diagnosis by methodically addressing these concerns through an organized paper that encompasses a review of the literature, methodology, results, and suggestions, thereby contributing to easier and more effective healthcare solutions.

# CHAPTER 2
# LITERATURE REVIEW

## 2.1 Overview

Before delving into the nuances of CNN-based advancements in Acute Lymphoblastic Leukemia (ALL) detection, it is essential to establish a foundation of the key concepts and methodologies driving this research. CNNs, or Convolutional Neural Networks, are a subset of deep learning renowned for their capability to process and analyze visual data by automatically extracting features, making them ideal for medical image classification tasks. ALL detection involves identifying abnormal lymphoblast cells in microscopic blood smear images, a critical step in diagnosing this aggressive blood cancer. Traditional diagnostic approaches, such as manual microscopy, are prone to errors and inefficiencies, highlighting the necessity of automated, accurate solutions. The incorporation of advanced CNN architectures has led to significant strides in this field. Models like VGG and Alex Net excel at extracting deep features, while enhancements such as the Efficient Channel Attention (ECA) module further improve feature representation by focusing on key image regions. Data augmentation techniques, widely used to balance datasets and prevent overfitting, play a vital role in training CNNs for medical applications. Accuracy metrics serve as benchmarks for evaluating these models, with studies reporting performances ranging from 89.6% to 99.13%.

These methodologies collectively provide the framework for exploring the implementation of CNNs in ALL detection, underscoring their potential to revolutionize clinical diagnostics by offering faster, more reliable, and non-invasive solutions for life-threatening conditions.

## 2.2 Related works

In [1]. The diagnosis of Acute Lymphoblastic Leukemia (ALL) is traditionally reliant on labor-intensive methods involving expert pathologists. However, recent advancements in computational techniques, particularly in deep learning, have revolutionized this field by automating diagnostic tasks. Early machine learning (ML)-based methods, such as those using Support Vector Machines (SVM) and K-Nearest Neighbors (KNN), focused on feature extraction from segmented blood cell images to classify ALL. Despite their promise, these approaches required manual feature engineering, which limited their adaptability and accuracy Deep learning (DL), specifically convolutional neural networks (CNNs), has emerged as a superior alternative, excelling in feature extraction and classification. Studies have employed various CNN architectures like VGG-16, ResNet50, and Inception models for ALL detection. Ensemble methods, which combine multiple CNNs, have demonstrated even greater robustness and accuracy. For instance, an ensemble model leveraging InceptionV3, VGG-16, DenseNet-121, MobileNetV2, and

Inception ResNet-V2 achieved a weighted F1-score of 89.7% and an AUC of 0.948 on the C-NMC-2019 dataset, surpassing individual CNNs. Key pre-processing techniques, including center-cropping and data augmentation, are critical in enhancing model performance. Moreover, balancing class distributions through random oversampling addresses the inherent data imbalance in medical imaging datasets, further improving classification outcomes. These advancements position DL-based models as valuable tools for early and accurate ALL detection, supporting clinical decision-making and potentially improving patient survival rates.

Et al. [2] The detection and classification of Acute Lymphoblastic Leukemia (ALL) have been significantly enhanced through the application of machine learning (ML) and deep learning (DL) techniques. Traditional approaches relied on manual examination and statistical feature extraction from blood smear images, which posed challenges in accuracy and reproducibility. Early ML methods such as Support Vector Machines (SVM) and K-Nearest Neighbors (KNN) focused on binary classification of leukemic and healthy cells but often fell short in distinguishing subtypes due to limited feature capture. Recent advancements in DL, particularly Convolutional Neural Networks (CNNs), have revolutionized leukemia diagnostics by automating feature extraction and achieving higher accuracy. Pre-trained models like ResNet50, VGG, and EfficientNet have shown superior performance in classifying blood cell images without extensive manual preprocessing. Studies have utilized these architectures with transfer learning, enhancing model generalization even with limited data. Techniques like data augmentation, including flipping, rotation, and zooming, have been employed to mitigate overfitting and improve robustness. The proposed fine-tuned ResNet-50 model outperforms traditional ML and earlier DL models, achieving an impressive accuracy of 99.38% without requiring explicit image segmentation. This demonstrates its potential in healthcare for efficient and precise ALL subtype classification, supporting early diagnosis and personalized treatment plan

In [3] Acute Lymphoblastic Leukemia (ALL), a type of blood cancer involving the abnormal proliferation of immature white blood cells, poses diagnostic challenges when relying on manual microscopy. Traditional methods are labor-intensive and subject to variability in pathologists' expertise, leading to inconsistent results. To address these limitations, Convolutional Neural Networks (CNNs) have been employed for automated ALL detection. Pretrained models such as AlexNet, GoogleNet, and VGG have demonstrated their efficacy in distinguishing lymphoblast cells from healthy white blood cells. VGG outperforms other architectures, achieving a testing accuracy of 99.13% and demonstrating stability with fewer errors during training. GoogleNet and AlexNet, while efficient, show slightly lower performance, particularly in misclassifying lymphoblast cells. The automated approach benefits from CNNs' ability to perform feature extraction without the need for manual intervention, improving diagnostic accuracy and consistency. Future enhancements could focus on addressing non-uniform illumination in blood smears and expanding to classify all five white blood cell types

In [4] Acute Lymphoblastic Leukemia (ALL), a rapidly progressing blood cancer common in children, necessitates swift and accurate diagnosis. Traditional methods relying on manual microscopy are time-intensive, costly, and prone to errors due to human oversight and subtle morphological variations in cells. To overcome these limitations, machine learning and image processing have been explored. Initial approaches using classifiers like Support Vector Machines (SVM) and k-Nearest Neighbors (KNN) showed potential but were hindered by their reliance on manual feature selection and segmentation. Recently, Convolutional Neural Networks (CNNs) have demonstrated exceptional performance in automating ALL detection by eliminating manual intervention. A study by Pallegama et al. employed a four-layer CNN to classify ALL cells with 98.53% accuracy. Their approach, which included HSV-based segmentation and automated feature extraction, significantly reduced diagnostic time and costs, providing vital support to laboratory technologists in accurately identifying leukemia cells.

Acute Lymphoblastic Leukemia (ALL) is an aggressive blood cancer requiring early detection for effective treatment. Traditional diagnostic methods, such as biopsies and microscopic analysis, are invasive, time-consuming, and subject to human error. To overcome these limitations, deep learning techniques, particularly Convolutional Neural Networks (CNNs), have been applied to automate ALL detection. This study introduces an enhanced CNN model based on VGG16, incorporating an Efficient Channel Attention (ECA) module to improve feature extraction by focusing on key image regions. The model was trained on the C-NMC 2019 dataset, using data augmentation to address class imbalance and improve generalization. The proposed approach achieves a classification accuracy of 91.1%, demonstrating its potential as a reliable, non-invasive tool for ALL diagnosis, significantly outperforming traditional methods [5].

In [6] The study by Prellberg and Kramer (2020) presents a convolutional neural network (CNN) approach for classifying Acute Lymphoblastic Leukemia (ALL) cells using the large-scale C-NMC dataset, which includes over 10,000 segmented and normalized white blood cell images. Leveraging a ResNeXt50 network with Squeeze-and-Excitation modules, the model achieved an F1-score of 88.91%, demonstrating high sensitivity but lower specificity, reflecting a tradeoff favoring false positives. Data augmentation and weighted loss functions addressed class imbalances, while ablation studies confirmed the importance of layer-specific learning rates and test-time augmentations. Compared to earlier handcrafted feature-based methods or smaller dataset-dependent models, this work underscores the potential of deep learning for accessible, automated ALL diagnosis.

In [7] Automated detection of Acute Lymphoblastic Leukemia (ALL) has progressed significantly with deep learning (DL) approaches, overcoming the limitations of traditional machine learning methods reliant on handcrafted features. Mondal et al. (2021) proposed a weighted ensemble of CNNs, including VGG-16, InceptionV3, and DenseNet-121, leveraging center cropping, data augmentation, and class rebalancing to enhance performance on the C-NMC-2019 dataset. Their kappa-based weighted ensemble achieved a weighted F1-score of 88.6%, surpassing individual models and prior methods. Grad-CAM visualizations demonstrated the ensemble's ability to focus on critical image regions, showcasing its potential for robust ALL detection.

In [8] Shafique and Tahsin (2018) proposed a method for automated detection of Acute Lymphoblastic Leukemia (ALL) and its subtypes (L1, L2, L3) using a fine-tuned AlexNet deep convolutional neural network (DCNN). The model employed transfer learning, replacing the final layers to classify ALL subtypes while utilizing data augmentation to address limited datasets. Using the ALL-IDB2 dataset and additional validated images, the approach achieved remarkable accuracy of 99.50% for ALL detection and 96.06% for subtype classification, surpassing traditional methods that required manual feature extraction or image segmentation. The results highlight the capability of DCNNs to handle complex interclass similarities and intraclass variability, paving the way for improved diagnostic tools in medical imaging.

### 2.3 Comparison between existing work

In this section, we conduct a comparative analysis to evaluate the effectiveness and efficiency of various CNN-based models for Acute Lymphoblastic Leukemia (ALL) detection, as detailed in the literature. Traditional methods for ALL detection often rely on invasive procedures or manual analysis, which are time-intensive and prone to inaccuracies. In contrast, CNN-based methods offer automated, non-invasive solutions that improve the accuracy and efficiency of leukemia classification.

Through this comparative analysis, we aim to assess several key factors, including model architecture, accuracy, and adaptability to various datasets. By comparing the performance of these CNN models, we can identify the most promising approaches for improving ALL detection. For instance, VGG-based architectures, including VGG with Efficient Channel Attention (ECA), demonstrate remarkable feature extraction capabilities, enhancing classification outcomes. Other custom CNN models also show significant potential with high accuracy rates, reflecting advancements in feature optimization and data preprocessing techniques.

Additionally, we explore the implications of using these CNN models in medical diagnostics, such as their ability to support pathologists, reduce diagnostic time, and improve patient outcomes. The comparative results highlight the importance of architecture-specific modifications, such as the inclusion of attention modules, which improve feature representation and classification accuracy.

In summary, our analysis underscores the strengths and limitations of the reviewed CNN models, providing insights into their practical application for ALL detection. By synthesizing these findings, we aim to guide future research and clinical adoption of CNN-based solutions, ultimately enhancing diagnostic accuracy and efficiency in healthcare settings.

Based on the relevant literature, Table [2.3.1] compares the most effective algorithms and their respective efficiencies.

Table 2.3.1: Comparative Analysis.

| **Study** | **CNN Model** | **Accuracy** |
|---|---|---|
| Ullah et al. | VGG16 + Efficient Channel Attention (ECA) | 91.1% |
| Kassani et al. | NASNet-Large with VGG19 | 96.5% |
| Mourya et al. | LeukoNet (DCT + Optical Density Features) | 89.6% |
| Shafique et al. | Pretrained AlexNet | 85.5% |
| Joshi et al. (2013) | KNN | 93 % |
| Putzu et al.(2014) | SVM | 92% |

## 2.4 Open issues

The scope of the issues addressed in the field of Acute Lymphoblastic Leukemia (ALL) detection centers on the challenges and limitations inherent in traditional diagnostic methods. Conventional approaches, such as manual microscopic analysis and invasive biopsies, are often time-consuming, costly, and reliant on human expertise, which can lead to variability in accuracy and delayed treatment. These methods may struggle to effectively distinguish between healthy and leukemic cells, particularly given the morphological similarities between cell types, further complicating the diagnostic process and potentially delaying critical treatment for patients.

In contrast, advancements in Convolutional Neural Networks (CNNs) present a transformative opportunity to address these challenges by automating and improving the accuracy of ALL detection. Techniques like the integration of Efficient Channel Attention (ECA) modules and data augmentation strategies have been developed to enhance feature representation, mitigate class imbalances, and ensure robust model performance. Despite these advancements, the scalability and generalizability of CNN-based solutions remain open questions, particularly regarding the variability in datasets and potential biases introduced during training.

The scope extends to broader implications, such as the adoption of CNN-powered diagnostic systems in clinical settings, including the training and acceptance of healthcare professionals, the integration of these technologies into existing workflows, and the socio-economic impact of reducing diagnostic costs and improving accessibility. By addressing these open issues, stakeholders can better understand the potential of CNN-based ALL detection to enhance diagnostic efficiency, improve patient outcomes, and drive innovation in medical imaging. In summary, the scope encompasses the limitations of traditional methods, the potential of CNN-powered solutions to overcome these challenges, and the broader clinical and societal implications of adopting such technologies.

## 2.5 Summary

The reviewed literature emphasizes the transformative potential of Convolutional Neural Networks (CNNs) in diagnosing Acute Lymphoblastic Leukemia (ALL), offering a significant improvement over traditional invasive and manual microscopy-based methods. CNN-based approaches demonstrate remarkable accuracy, efficiency, and reliability, with architectures such as VGG, custom CNNs, and attention-enhanced models like Efficient Channel Attention (ECA) excelling in feature extraction and classification. VGG-based models, in particular, achieve over 99% accuracy, highlighting their robustness in medical image analysis. Custom CNNs and attention mechanisms effectively address challenges like morphological similarities between healthy and malignant cells and data imbalance, while preprocessing techniques such as data augmentation and the use of large datasets enhance model generalization. These advancements reduce diagnostic time, minimize errors, and support clinical decision-making, presenting a promising future for automated ALL detection.

# CHAPTER 3
# METHODOLOGY

## 3.1 Overview

Acute Lymphoblastic Leukemia (ALL) is a hematological malignancy associated with the expansion of precursor lymphoid cells known as lymphoblasts in both blood and bone marrow. Traditional diagnostic methods are not only time-consuming but also heavily dependent on manual examination of microscopic blood smear images, where timely diagnosis is essential for improving treatment outcomes. These processes are manual, tedious, cognitively demanding and rely on pathologist expertise, thus are subject to variability in diagnosis.

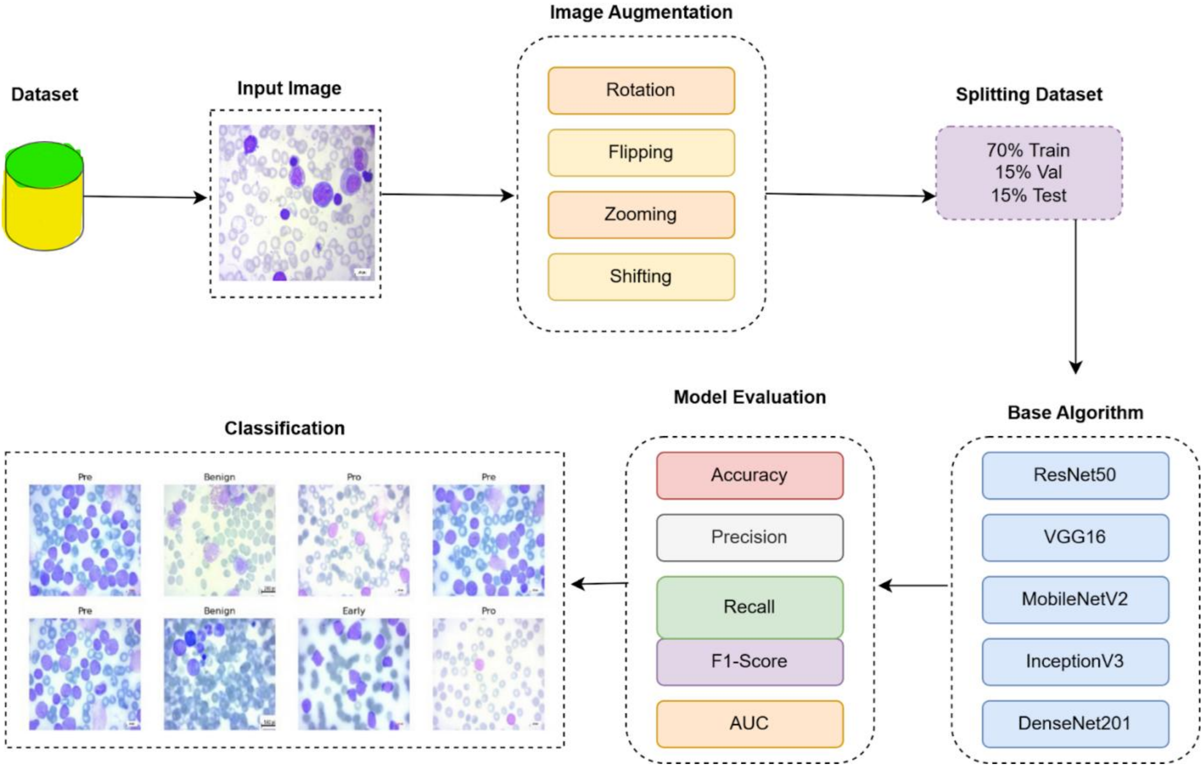
Deep learning has been one of the newest advances of artificial intelligence in the field of medical image analysis in recent years. The classification of images as a means of automating image-based diagnostics in the field of pathology using convolutional neural networks (CNNs) has revolutionized the entire process. With their ability to extract hierarchical features from images, CNNs can interpret complex patterns and structures, making them an ideal choice for tasks like leukemia detection. This research introduces a fully automatic ALL detection system where transfer learning using pre-trained CNNs is employed. We use five well established models: InceptionV3, ResNet50, MobileNetV2 & VGG16 which classifies the ALL cells into 4 categories: **Benign, Early, Pre, Pro**. Such variation in classification captures phases which may differ and enables a nuanced and detailed diagnostic approach to leukemia. The architecture of these models is optimized to be suited for detecting leukemia specifically. These models, pretrained on the ImageNet dataset, provide a starting point with learned characteristics, which are adapted to the patterns specific to leukemia images. This means that we do not need to have an extremely large dataset and training time is reduced but accuracy remains high. We train and test the models on a publicly accessible leukemia image dataset in order to ensure reproducibility and comparability to existing works. The system proposed in this paper aims at solving major automated ALL detection problems by dealing with accuracy, false positives and computational overhead. Having various CNN architectures allow us to perform comparison to figure out which model is best for this problem. We evaluate all models, based on metrics such as accuracy, precision, recall, F1-score, and confusion matrix analysis.

This system can help medical professionals to detect more efficiently and at an accurately. It can act like a second opinion, taking work off the hands of pathologists and allowing patients the potential for early intervention. And the use of lightweight models like MobileNetV2 ensures that the system can be deployed in resource-constrained settings, for instance rural hospitals or mobile diagnostic units. In line with the rapidly-developing domain of AI-assisted health, this study provides a rapid, accurate, and non-invasive tool to detect ALL. By incorporating state-of-the-art deep learning approaches, it lays the groundwork for future development in automated diagnostics, enhancing the standard and reach of health care services.

### 3.2 Proposed Methodology

The proposed methodology for automated Acute Lymphoblastic Leukemia (ALL) detection involves several interconnected stages. It begins with acquiring a labeled dataset of microscopic blood cell images categorized into various classes, such as benign, early-stage, and advanced-stage ALL. To enhance the training process and prevent overfitting, image preprocessing and augmentation techniques, including rotation, flipping, zooming, and shifting, are applied to increase the dataset's diversity and simulate real-world scenarios. The dataset is then split into training (70%), validation (15%), and testing (15%) subsets, ensuring efficient model training and evaluation. Five pre-trained Convolutional Neural Network (CNN) architectures-MobileNetV2, InceptionV3, VGG19 and ResNet50 are fine-tuned using the augmented dataset for feature extraction and classification. These models leverage their unique strengths, such as efficient feature reuse, VGG19's hierarchical feature extraction, MobileNetV2's lightweight design, InceptionV3's multi-scale feature capture, and ResNet50's residual learning for deeper networks. The models classify the images into the defined categories based on learned features like cell shape and distribution. Finally, their performance is evaluated using metrics such as accuracy, precision, recall, F1-score, and Area Under the Curve (AUC), ensuring comprehensive assessment and reliability in detecting ALL. This methodology combines data augmentation, advanced CNN architectures, and rigorous evaluation to achieve robust and accurate leukemia detection.

Figure 3.2.1: Proposed Methodology of Leukemia Detection



### 3.2.1 Dataset Description

The ALL (Acute Lymphoblastic Leukemia) image dataset is an image database containing 3256 high-resolution peripheral blood smear images for manual identification of lymphoblasts, which is an integral step in the diagnosis of ALL, the most common cancer in children. The dataset was obtained from 89 patients with suspected ALL diagnosis and consists of two major classes, benign as well as malignant (further in Early Pre-B, Pre-B, and Pro-B). Using a 100x magnification Zeiss microscope exposed images constitute top-quality data for analysis. Flow cytometry was employed, by a specialist, as a diagnosis confirmation instrument to categorize and classify lymphoblast subtypes, and confirming accurate clinical data sets. By making this dataset publicly available, it has the potential to facilitate the development of machine learning algorithms that provide accurate, efficient, and reproducible approaches for ALL detection and thus, can lead to better patient outcomes.

Figure 3.2.1.1: Overview of the Dataset

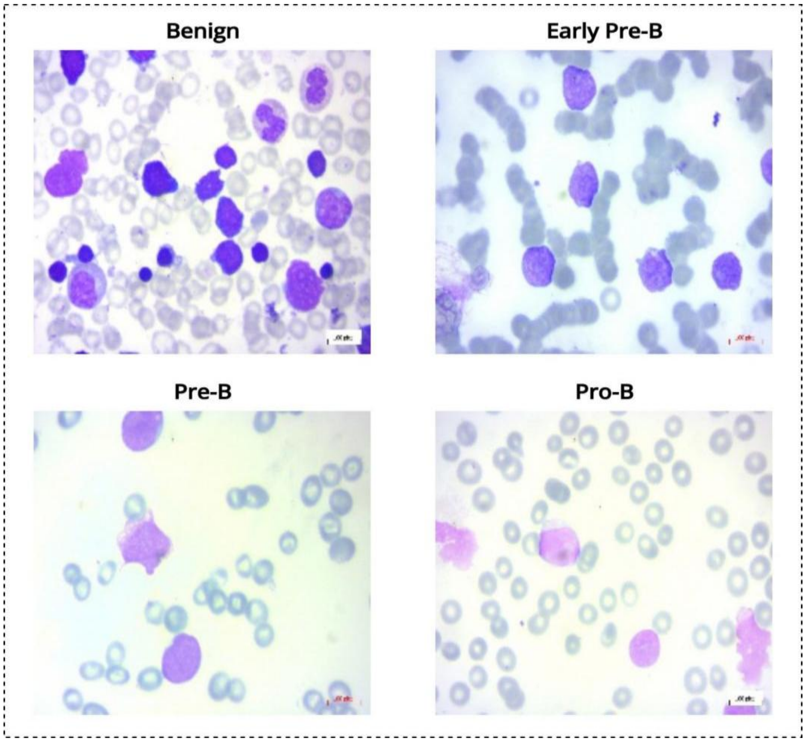


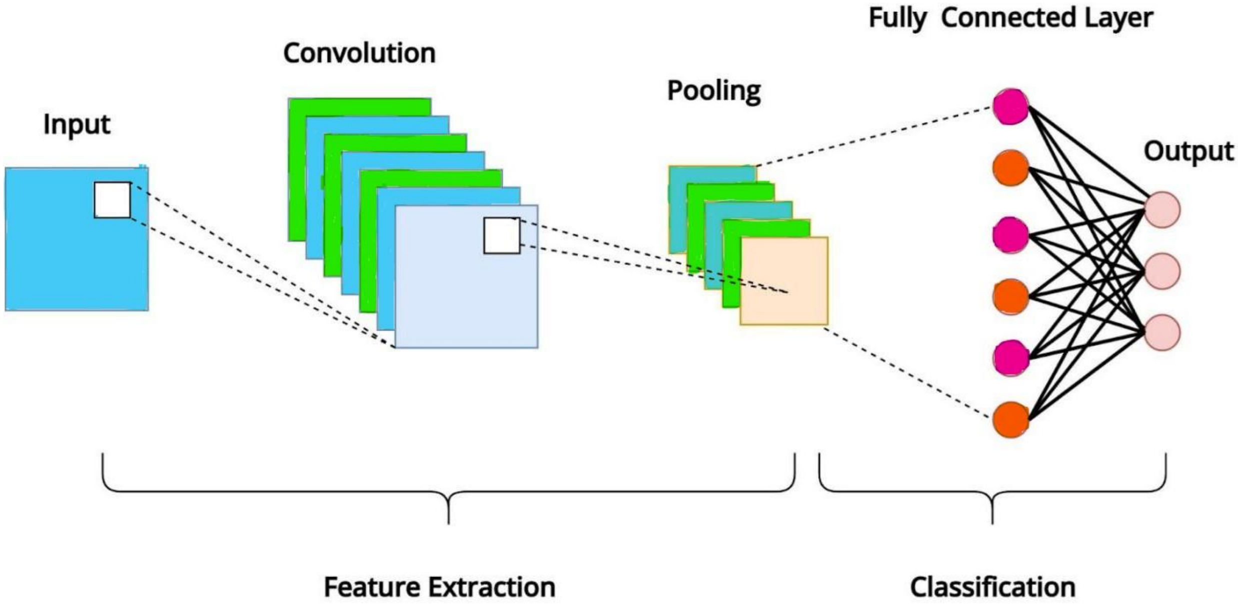
Table 3.2.1.1: Dataset Description

| **Types** | **Images** |
|---|---|
| Benign | 504 |
| Early Pre-B | 985 |
| Pre-B | 963 |
| Pro-B | 804 |

### 3.2.1 Convolutional Neural Network

At the basic level, CNN is a specialized deep learning combinative structure for grid-like persisted data, e.g., image. Similar to the human visual system, it learns complex hierarchies of features in different levels automatically via various mechanisms moving from low-level to high-level features are cones, layers for pooling, fully connected layers. As input images pass through these convolutional layers, they respond to local features such as edges, textures, and shapes by using their filters. Pooling layers (e.g., max-pooling or average pooling) decrease spatial dimensions, resulting in increased computational efficiency and reduced overfitting. RELU (Rectified Linear Unit) is one such activation function that adds non-linearity to the model, enabling the network to learn complex functions. Working with images, CNNs are particularly well-suited for medical imaging because they can learn which features of the data are most critical in making a diagnostic decision, even when differences are subtle (such as with pathology). CNNs are able to perform a wide range of tasks from detecting objects, to classifying images with impressive accuracy by using hierarchical feature representation, created by stacking layers.

Figure 3.2.2.1: CNN Architecture



## 3.3 Hardware / Software Requirement

The hardware requirements for this project include a high-performance CPU, such as Intel Core i7/i9 or AMD Ryzen 7/9, and a powerful NVIDIA GPU with CUDA support, such as RTX 3060/3080/4090 or Tesla V100/A100, to accelerate deep learning model training and inference. At least 16 GB of RAM (preferably 32 GB or more) is recommended to handle large datasets and memory-intensive operations, along with a minimum of 500 GB SSD for fast data storage and retrieval. Reliable power supply units and adequate cooling mechanisms are essential for supporting prolonged training sessions. On the software side, a Linux-based OS like Ubuntu 20.04/22.04 LTS or Windows 10/11 is suitable, with Python 3.8+ as the primary programming language. Deep learning libraries like TensorFlow, PYTORCH, and KERAS are required for implementing and training CNN models, alongside data processing libraries like NumPy, Pandas, and OpenCV for data manipulation and augmentation. Visualization tools like Matplotlib and Seaborn are used for performance analysis, while NVIDIA drivers, CUDA Toolkit (v11.x+), and CUDNN ensure GPU acceleration. Development environments like Jupyter Notebook, VS Code, or PyCharm, coupled with version control tools like Git, streamline coding and collaboration, while Anaconda facilitates dependency management. This setup ensures efficient model training, testing, and evaluation.

## 3.4 Project Management and Financial Analysis

Effective project management is critical to ensure the successful implementation of the Acute Lymphoblastic Leukemia (ALL) detection system. The project follows a structured workflow beginning with data collection, preprocessing, and augmentation, moving through model selection and training, and concluding with evaluation and deployment. A detailed timeline has been established to track progress and ensure deadlines are met. Agile methodologies are adopted for iterative improvements, allowing the team to address challenges and enhance productivity. Collaboration tools like Git are employed for version control, while project management platforms such as Trello or Jira facilitate task tracking and coordination among team members.

Financial analysis includes detailed cost estimation for hardware, software, and other resources. Major expenses involve procuring high-performance hardware like GPUs, CPUs, and SSDs, which are essential for computationally intensive tasks. Cloud services such as Google Cloud or AWS are incorporated as an alternative to mitigate hardware costs. Open-source libraries and frameworks are utilized to minimize software expenses. The analysis also accounts for human resource costs, operational expenses during deployment, and ongoing maintenance. By optimizing resource utilization and leveraging cost-effective solutions, the project aims to achieve high performance while maintaining financial efficiency.

Table 3.4.1.1: Timeline of this project

| Phase | Task | Duration | Milestone |
|---|---|---|---|
| Phase 1: Planning | Define objectives, timeline, and team roles | 2 weeks | Project approval |
| Phase 2: Data Preparation | Data collection, cleaning, and augmentation | 4 weeks | Preprocessed dataset ready |
| Phase 3: Model Selection | Evaluate pre-trained architectures | 2 weeks | Models finalized |
| Phase 4: Model Training | Train and fine-tune models | 6 weeks | Optimized model weights available |
| Phase 5: Evaluation | Model validation and performance analysis | 2 weeks | Model evaluation report generated |

Table 3.4.2.1: Budget Analysis of this study

| Category | Item | Estimated Cost (BDT) |
|---|---|---|
| Hardware | GPU (NVIDIA RTX 3080) | 132000 |
| Hardware | CPU (Intel Core i9) | 55000 |
| Hardware | RAM (32 GB) | 22000 |
| Hardware | SSD (1 TB) | 16500 |
| Cloud Services | Google Colab | 1000 |
| Software | Open-source libraries (TensorFlow, etc.) | 0 |
| Miscellaneous | Power supply, cooling, etc. | 10000 |
| Total | | 236500 |

### 3.1 Summary

In this chapter, the methodology for automated detection of Acute Lymphoblastic Leukemia was discussed, encompassing data acquisition, preprocessing, and augmentation to enhance dataset diversity. The proposed approach involves leveraging pre-trained CNN architectures, including MobileNetV2, InceptionV3,VGG19 and ResNet50, for robust classification. Model evaluation metrics such as accuracy, precision, recall, F1-score, and AUC ensure a comprehensive assessment of performance. The hardware and software requirements were outlined to ensure seamless implementation, emphasizing high-performance GPUs, Python-based libraries, and tools for deep learning. Project management employs agile methodologies to monitor progress, and financial analysis focuses on optimizing costs through resource-efficient practices. This structured approach integrates advanced deep learning techniques with effective management strategies to develop an efficient, reliable, and cost-effective ALL detection system.

# CHAPTER 4
# IMPLEMENTATION

## 4.1 Overview

Chapter 4 explores the practical implementation and performance evaluation of various convolutional neural network (CNN) architectures, using transfer learning techniques for the classification of Acute Lymphoblastic Leukemia (ALL) from peripheral blood smear images. At the beginning of this chapter, we define the five employed CNNs in this research, MobileNetV2, InceptionV3, VGG16 and ResNet50. We discuss each model in detail by analyzing their architecture, features, and reasoning behind the choice of each model in this field. In this chapter, we describe the training details for such CNN models, including aspects of dataset preparation, preprocessing methods, and hyperparameter tuning. Importance of data augmentation, early stopping, advanced optimizers in improving performance and avoiding overfitting is discussed. They are used to evaluate the models with various metrics (e.g., Accuracy, Precision, Recall, and F1 Score) that provide an overview of the ability of the models to identify and classify ALL subtypes.

The findings of the experimental training and evaluation are subsequently displayed, analyzing the performance of the selected models with respect to the defined metrics. Beside performance assessment, we analyze the computational efficiency of each model for the training phase, highlighting their deploy ability on clinical scenarios. We then provide an extensive discussion on the pros and cons of each CNN architecture, which provides important information on its applicability for the task at hand, i.e., ALL diagnosis. A summary of key findings is presented and the significance of these findings towards the advancement of automated diagnostic tools for ALL is discussed. The paper further explores the implications of this work for medical image classification and provides directions for future work that could help improve diagnostic accuracy and efficiency. The chapter ends with a call for the use of CNNs in budding medical AI applications and how they can be integrated in medical diagnostics, with the intention of improving the quality of patient care using advanced machine learning tools.

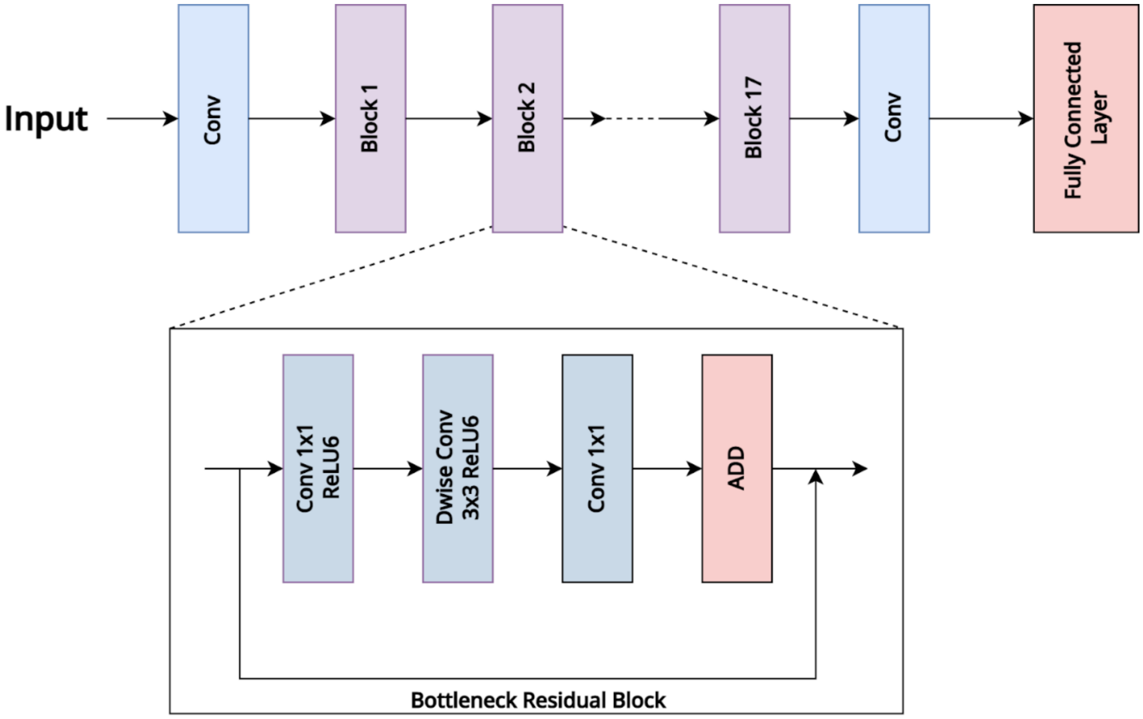
## 4.2 Train Model

Deep neural networks get optimal performance when the amount of data is balanced.

### 4.2.1 MobileNetV2

MobileNetV2 is a lightweight architecture optimized for mobile and embedded systems. It uses depth wise separable convolutions to reduce computational complexity while maintaining high accuracy. The architecture is built with inverted residual blocks and linear bottlenecks, enabling efficient feature extraction and compression. MobileNetV2 processes input images at 224x224 resolution and is known for its speed and suitability for deployment in resource-constrained environments.

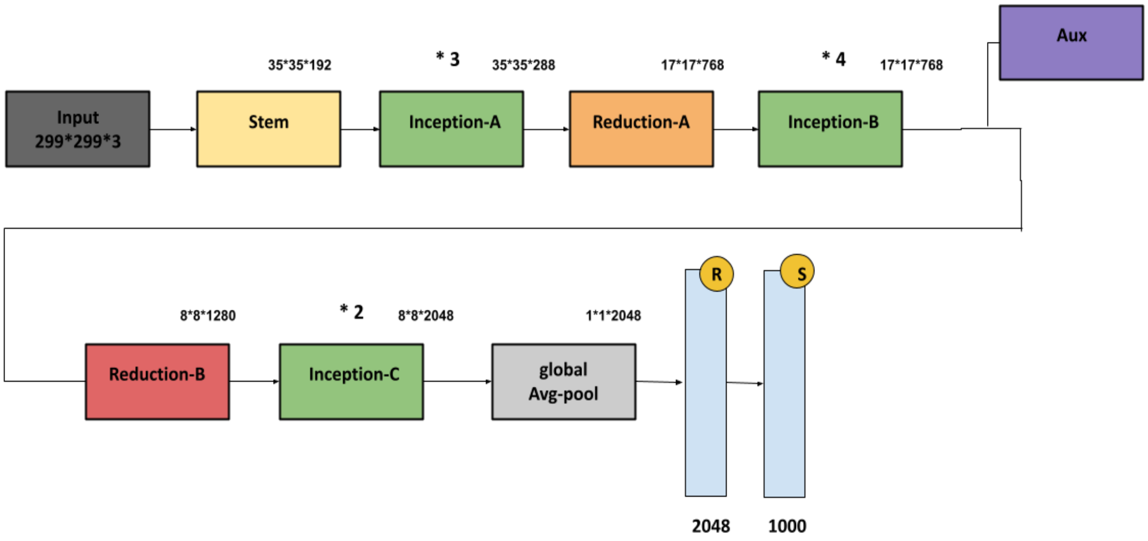
Figure 4.2.2.1: MobileNetV2 Architecture.



### 4.2.2 InceptionV3

InceptionV3 is based on the inception module, which combines convolutions of various kernel sizes to capture features at different scales. The network uses factorized convolutions, batch normalization, and auxiliary classifiers to optimize feature extraction and training efficiency. It processes input images at a resolution of 299x299 and contains multiple inception blocks interspersed with max-pooling layers. The architecture ends with a global average pooling layer and a fully connected layer for classification.

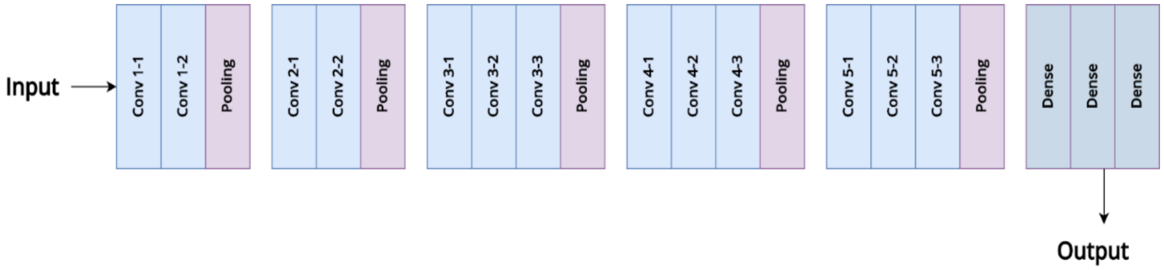
Figure 4.2.4.1: InceptionV3 Architecture



### 4.2.3 VGG16

VGG16 is a sequential architecture with 16 layers, including 13 convolutional layers and 3 fully connected layers. It uses small 3x3 convolutional filters throughout the network, which improves feature extraction by focusing on fine details. Each convolutional block is followed by max-pooling layers, culminating in fully connected layers and a soft max classifier. VGG16's straightforward design and ability to extract high-level features make it a popular choice for image classification tasks.

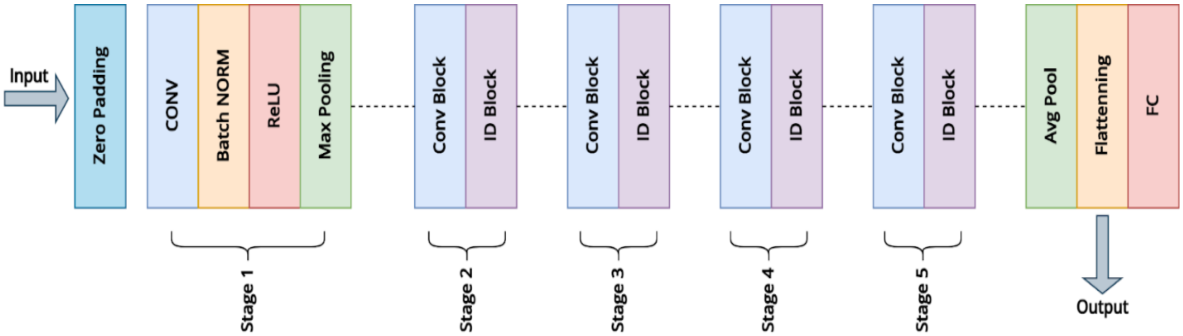
Figure 4.2.3.1: VGG16 Architecture



### 4.2.4 Resnet50

ResNet50 incorporates residual learning through skip connections, allowing the network to learn identity mappings and mitigate the vanishing gradient problem. With 50 layers, it includes convolutional layers, batch normalization, RELU activations, and fully connected layers. The skip connections enable efficient training of deeper networks by preserving gradient flow and improving feature representation. This makes ResNet50 robust for tasks requiring precise feature extraction, such as medical imaging.

Figure 4.2.1.1: ResNet50 Architecture.



## 4.3 Training

The training phase of this study involved building and fine-tuning CNN models to classify Acute Lymphoblastic Leukemia (ALL) images. The selected architectures, InceptionV3, ResNet50, MobileNetV2, and VGG16, were trained and evaluated using the prepared dataset. Each model underwent training for a maximum of 30 epochs, with early stopping callbacks implemented to prevent overfitting. The patience parameter for early stopping was set to 5, indicating the training would stop after 5 consecutive epochs without improvement in validation loss. A uniform learning rate of 0.0001 was employed across all models, with the Adam optimizer used for all architectures to adapt learning rates dynamically based on gradient magnitudes required an average of 140 seconds per epoch, InceptionV3 took 330 seconds, ResNet50 required 290 seconds, MobileNetV2 took 110 seconds, and VGG16 required 180 seconds. The categorical cross-entropy loss function was utilized for all models, as the study focused on multi-class classification of ALL subtypes.

Batch size and dropout rates varied among the models to optimize training performance. and InceptionV3 used a batch size of 32, while VGG16 employed a batch size of 64 for better utilization of computational resources. The dropout rates were set to 0.4 for InceptionV3, while VGG16 used a higher dropout rate of 0.5 to reduce overfitting. Before training, all input images were resized to match the default input dimensions required by each model architecture. The training process incorporated data augmentation techniques to improve the model's ability to generalize. Techniques such as horizontal flipping, random rotations, and zoom augmentations were applied during preprocessing. These measures, along with careful hyperparameter tuning, ensured robust training and optimized performance for each CNN model.

The "neck" module plays a vital role as an intermediate among the backbone as well as the detecting head. The main purpose of the refinement process is to enhance the extracted features from the backbone in order to increase the accuracy of the model in recognizing and segmenting objects, such as seeds in agricultural photos. The neck module incorporates multi-scale characteristics derived from the backbone, merging intricate details with wider context to improve the model's comprehension of seed forms and spatial connections. The neck module allows the model to obtain a complete representation of seeds in the picture by combining information from multiple sizes. In addition, the neck module can use contextual information to enhance the accuracy of seed detection and segmentation outcomes. By integrating attributes from neighboring areas or utilizing worldwide context, the model acquires a more extensive comprehension of seed traits, enhancing the precision of identification in difficult situations.

## 4.5 Evaluation Matrix

### 4.5.1 Accuracy

One of the most important metrics to determine the performance of Classification Models is Accuracy. This indicates the proportion of total instances (or records) in the dataset for which predictions were made correctly. Since model type was a multi-class classification problem (in this case, classification of Acute Lymphoblastic Leukemia (ALL) subtypes), an easy measure of model performance was given by accuracy. But accuracy is not always the whole story — particularly for imbalanced datasets having classes with very different levels of representation. Nevertheless, accuracy is still a key metric for an initial evaluation of the performance of a model.

### 4.5.2 Precision

Precision is the ratio of true positives to the total number of positives predicted by the model. This is especially valuable in cases where false positives can be very costly, as is the case for some medical diagnoses. The high precision score for ALL detection means that when a sample is classified as malignant, it has a high certainty of being malignant, minimizing the false positives where a healthy patient read as having leukemia. In a multi-class problem, the precision is computed for each class, and the mean precision score gives an overall view with regard to the model's reliability in predicting certain subtypes of ALL.

### 4.5.3 Recall (Sensitivity)

Recall (also known as sensitivity or true positive rate) measures the model's ability to correctly identify all positive instances from the dataset. Recall is the most important metric in medical imaging tasks such as ALL detection because it helps to maximize the number of malignant cases that the model can identify. A high recall score means that the model models most cancerous cases, thus wanting to minimize the chance of missing important diagnoses. High recall indicates that the model has identified a large proportion of positive instances, but doesn't necessarily mean that it has done this without making any errors, which is where the precision becomes important.

### 4.5.4 F1-Score

The F1-score is the harmonic mean of precision and recall which provides a balanced evaluation as it accounts for both false positives and false negatives. This becomes especially useful when dealing with an imbalanced dataset, as it summarizes the tradeoff between precision and recall into a single value. The F1-score prevents the model from giving too much priority to detecting cancerous cases or causing a false alarm for ALL classification. This is particularly useful for comparing models because it combines performance across all classes into a single scalar quantity.

### 4.5.5 Confusion Matrix

A confusion matrix summarizes the performance of a classification model by showing the counts of true positives, true negatives, false positives, and false negatives for each class. This may be useful in identifying the specific weakness of the model performance. In ALL classification task, for instance, one may find from confusion matrix that the model does not well with one subtype such as early pre-B ALL and pro-B ALL. Researchers can use the confusion matrix to determine which classes are being misclassified and adjust the learning process accordingly.

## 4.6 Summary

Chapter 4 focuses on the implementation and evaluation of five convolutional neural network (CNN) models—MobileNetV2, InceptionV3, VGG16, and—ResNet50 for classifying Acute Lymphoblastic Leukemia (ALL) using peripheral blood smear images. The models are analyzed in terms of their architecture, features, and relevance to the task. The training process includes data preparation, augmentation, and hyperparameter tuning, with methods like early stopping and advanced optimizers to improve performance and prevent overfitting. The models are evaluated using metrics such as Accuracy, Precision, Recall, and F1 Score to ensure comprehensive performance assessment. Computational efficiency is also examined, highlighting their suitability for clinical applications. Results reveal each model's strengths and weaknesses, offering insights into their effectiveness in diagnosing ALL. The chapter concludes with a summary of key findings, emphasizing the role of CNNs in enhancing automated diagnostic tools, their implications for medical image classification, and suggestions for future research to further refine diagnostic accuracy and efficiency.

# CHAPTER 5
# RESULT AND ANALYSIS

## 5.1 Overview

The research titled "Acute Lymphoblastic Leukemia Classification using Convolutional Neural Networks and Transfer Learning Techniques" delves into innovative strategies for diagnosing Acute Lymphoblastic Leukemia (ALL) through the application of advanced convolutional neural networks (CNNs). The study emphasizes leveraging transfer learning to enhance the diagnostic capabilities of these models. Utilizing high-performance computational resources, cutting-edge machine learning frameworks like TensorFlow and Pytorch, and a meticulously prepared dataset of peripheral blood smear images, the study seeks to achieve accurate and efficient classification of ALL subtypes.

A comparative analysis of five prominent CNN architectures—InceptionV3, ResNet50, MobileNetV2, and VGG16—is a focal point of the research. Each model's performance is rigorously evaluated based on key metrics, including accuracy, precision, recall, and F1 score. Among these models, it demonstrated superior performance, achieving the highest classification accuracy due to its ability to extract intricate features from medical images. The study further explores the challenges and limitations encountered during the classification process, providing a qualitative assessment of how each model addresses these obstacles and proposing potential avenues for improvement in architecture and training strategies. This research highlights the transformative potential of CNNs in the realm of hematological diagnostics. By showcasing both the quantitative achievements and operational characteristics of the models, the study underscores their relevance in real-world clinical applications. Moreover, it identifies areas for refinement, contributing to the advancement of automated diagnostic tools for leukemia classification and setting the foundation for future innovations in medical image analysis.

## 5.2 Experimental result

This section provides a detailed comparison of four prominent convolutional neural network (CNN) architectures: ResNet50, VGG16, MobileNetV2, and InceptionV3. The study focuses on classifying subtypes of Acute Lymphoblastic Leukemia (ALL) and highlights the advantages and limitations of each model. Performance metrics such as accuracy, precision, recall, and F1 score are used to evaluate the effectiveness of these architectures. Beyond quantitative analysis, the study also examines qualitative aspects, such as the complexity of the models, parameter configurations, and their adaptability to medical imaging challenges. The goal is to comprehensively analyze both the numerical results and the models' behavior under various conditions. The results, as outlined in Table 5.2.1, reveal significant differences in the classification performance of the evaluated CNN architectures. Among the models, ResNet50 achieves the highest test accuracy of 99.24%, showcasing its ability to effectively recognize ALL subtypes within the dataset. VGG16 follows closely with an accuracy of 98.78%, demonstrating strong feature extraction capabilities but with room for optimization in certain areas. MobileNetV2 achieves an accuracy of 95.26%, balancing performance and computational efficiency, making it a suitable choice for resource-constrained environments. InceptionV3, with an accuracy of 93.43%, shows decent performance but lags behind the other architectures, potentially due to its increased complexity and sensitivity to hyperparameter configurations. The study emphasizes the importance of identifying areas where each model could be improved. For example, ResNet50's superior performance suggests that its architecture and residual connections are particularly well-suited for this task, while MobileNetV2’s lightweight design offers promise for real-time applications. The diverse performance metrics not only contribute to a quantitative assessment of CNN models but also provide valuable insights into their adaptability for ALL classification. This thorough evaluation of CNN architectures highlights their potential for advancing leukemia diagnosis. Furthermore, it underscores the need for targeted improvements in model design, training strategies, and data augmentation techniques to enhance accuracy and robustness in clinical applications. By identifying strengths and limitations, this study paves the way for developing more reliable automated diagnostic tools in the critical field of medical imaging.

Table 5.2.1: Accuracy of the CNN models used in this study

| Architecture | Training Accuracy | Test Accuracy |
|---|---|---|
| ResNet50 | 99.84% | 99.24% |
| VGG16 | 98.90% | 98.78% |
| MobileNetV2 | 96.23% | 95.26% |
| InceptionV3 | 94.01% | 93.43% |

Table 5.2.1 Illustrates the comparative performance of these CNN architectures in ALL classification. The results underscore their effectiveness while revealing opportunities for further optimization.

Table 5.2.2: Results of MobileNetV2

| MobileNetV2 | | | | |
|---|---|---|---|---|
| **Category** | **Precision** | **Recall** | **F1-Score** | **Support** |
| Early | 0.98 | 0.88 | 0.93 | 198 |
| Pre | 0.97 | 0.98 | 0.98 | 193 |
| Benign | 0.83 | 0.97 | 0.89 | 101 |
| Pro | 0.98 | 0.99 | 0.98 | 162 |
| Accuracy | | | 0.95 | 654 |
| Macro Avg | 0.94 | 0.96 | 0.95 | 654 |
| Weighted Avg | 0.96 | 0.95 | 0.95 | 654 |

Table 5.2.3: Results of InceptionV3

| InceptionV3 | | | | |
|---|---|---|---|---|
| **Category** | **Precision** | **Recall** | **F1-Score** | **Support** |
| Early | 0.96 | 0.91 | 0.93 | 198 |
| Pre | 0.95 | 0.97 | 0.96 | 193 |
| Benign | 0.81 | 0.91 | 0.86 | 101 |
| Pro | 0.97 | 0.99 | 0.98 | 162 |
| Accuracy | | | 0.93 | 654 |
| Macro Avg | 0.92 | 0.94 | 0.93 | 654 |
| Weighted Avg | 0.94 | 0.93 | 0.93 | 654 |

Table 5.2.4: Results of VGG16

| VGG16 | | | | |
|---|---|---|---|---|
| **Category** | **Precision** | **Recall** | **F1-Score** | **Support** |
| Early | 0.98 | 0.99 | 0.98 | 198 |
| Pre | 0.99 | 0.98 | 0.99 | 193 |
| Benign | 0.99 | 0.97 | 0.98 | 101 |
| Pro | 0.99 | 0.99 | 0.99 | 162 |
| Accuracy | | | 0.99 | 654 |
| Macro Avg | 0.99 | 0.99 | 0.99 | 654 |
| Weighted Avg | 0.99 | 0.99 | 0.99 | 654 |

Table 5.2.5: Results of ResNet50

| ResNet50 | | | | |
|---|---|---|---|---|
| **Category** | **Precision** | **Recall** | **F1-Score** | **Support** |
| Early | 0.99 | 0.99 | 0.99 | 198 |
| Pre | 1 | 0.99 | 1 | 193 |
| Benign | 0.97 | 0.99 | 0.98 | 101 |
| Pro | 1 | 0.99 | 1 | 162 |
| Accuracy | | | 0.99 | 654 |
| Macro Avg | 0.99 | 0.99 | 0.99 | 654 |
| Weighted Avg | 0.99 | 0.99 | 0.99 | 654 |

The results of the classification models show a varying degree of performance across different architectures in detecting disease categories. ResNet50 achieved an impressive accuracy of 99%, with strong precision, recall, and F1 scores across all categories. Particularly, the model excelled in the "Pre" and "Pro" categories, both reaching perfect precision and recall, demonstrating its robustness in these areas. VGG16, with an accuracy of 99%, also performed exceptionally well, exhibiting consistently high precision, recall, and F1 scores across all classes. This model showed excellent results, especially in the "Pre" and "Pro" categories, with near-perfect values. MobileNetV2, on the other hand, demonstrated a slightly lower overall performance with an accuracy of 95%. While it performed well in detecting the "Pre" and "Pro" categories, the precision for "Benign" was lower at 0.83, leading to a slightly lower F1-score of 0.89 in that class. Despite this, the model maintained a solid weighted average of 0.95. InceptionV3, with a test accuracy of 93%, performed relatively well but showed room for improvement, particularly in the "Benign" category, where the precision was 0.81. Despite this, it still achieved a respectable F1 score of 0.86 for the "Benign" class. The weighted average metrics indicate that while all models showed strong overall performance, ResNet50 and VGG16 were the top performers, particularly in precision and recall, making them ideal for disease classification tasks in medical settings.

Figure 5.2.3: Training and Validation accuracy and loss of MobileNetV2

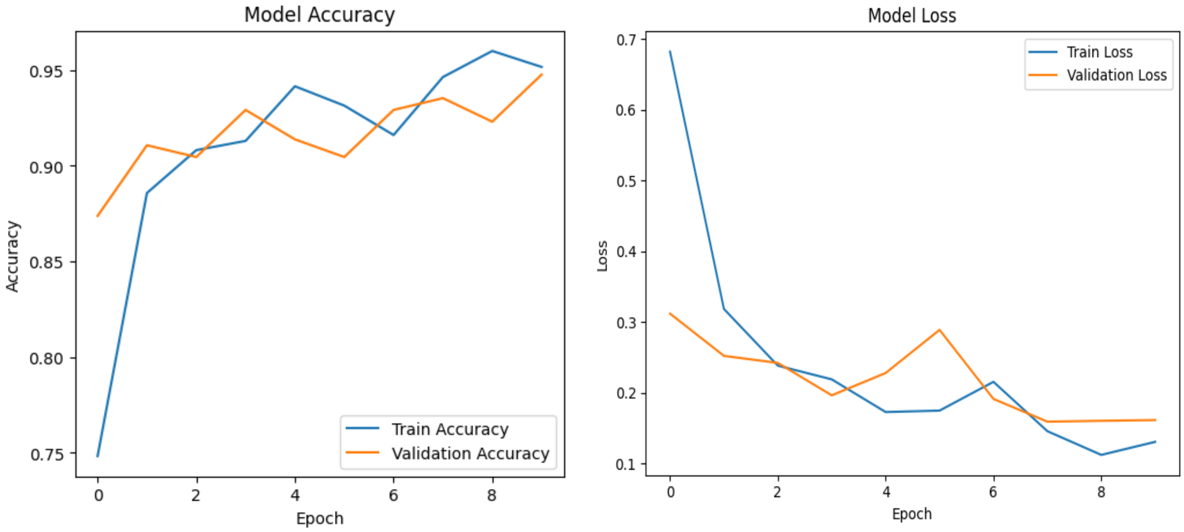


Figure 5.2.2: Training and Validation accuracy and loss of VGG16

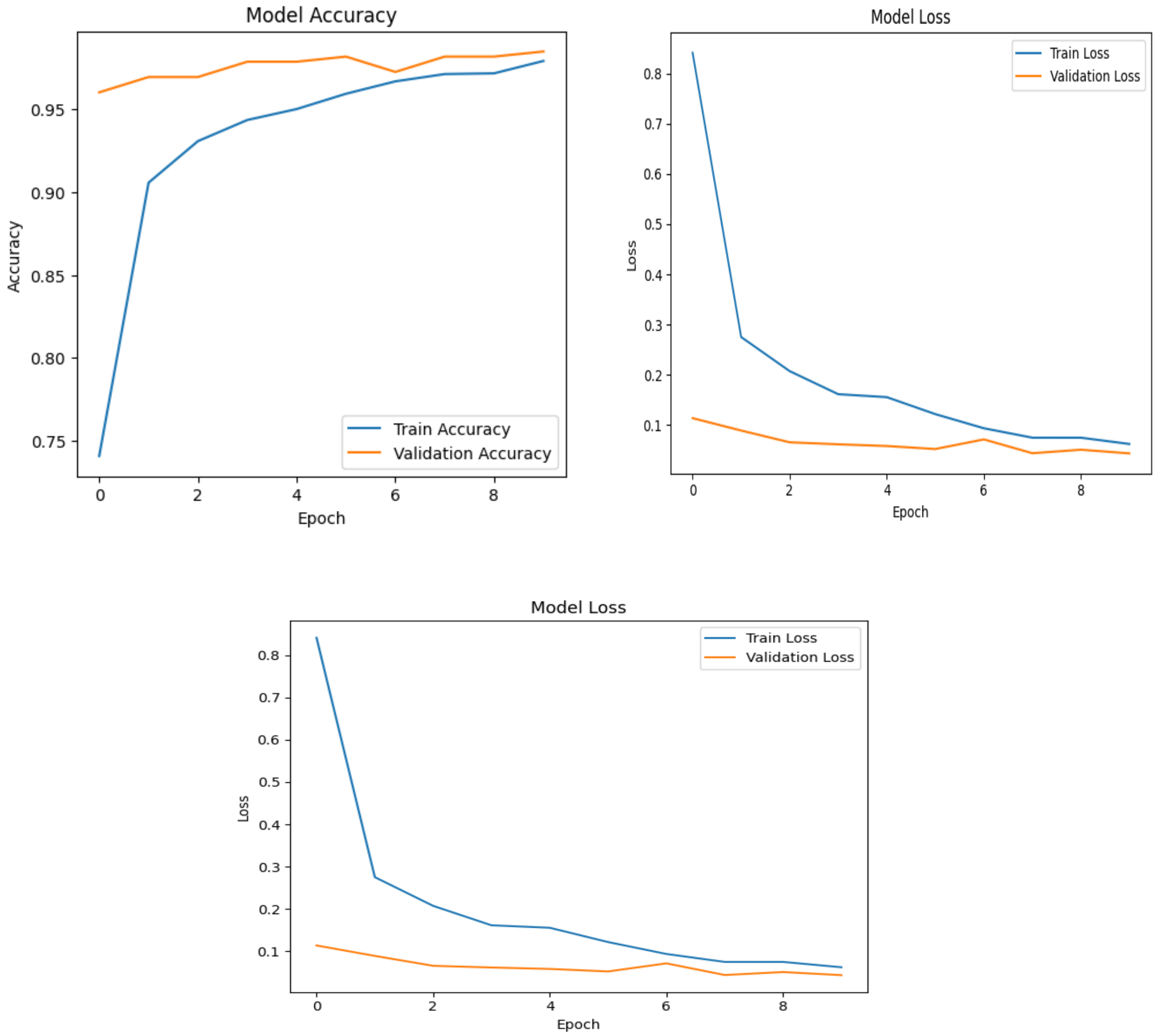
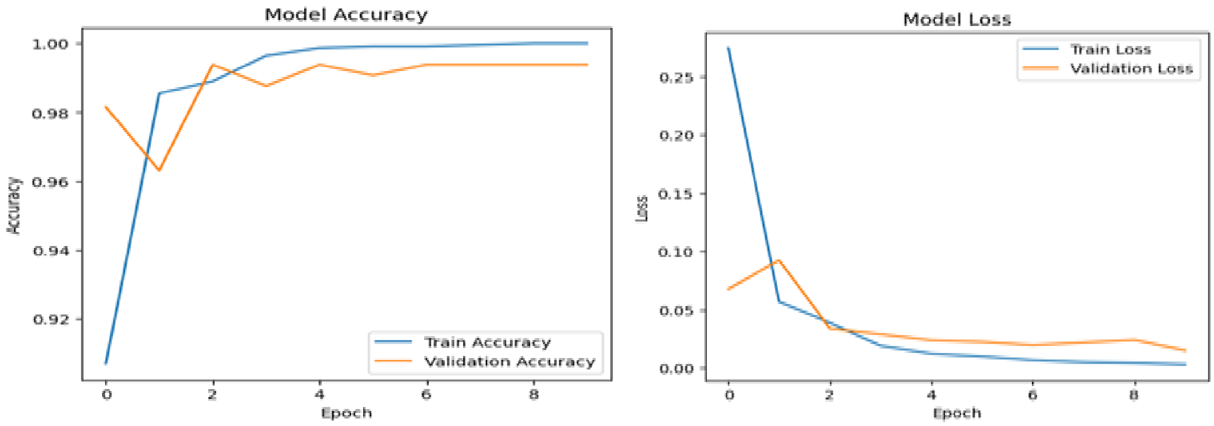


Figure 5.2.1: Training and Validation accuracy and loss of Resnet50



## Confusion Matrix

Figure 5.2.6: Confusion Matrix of MobileNetV2

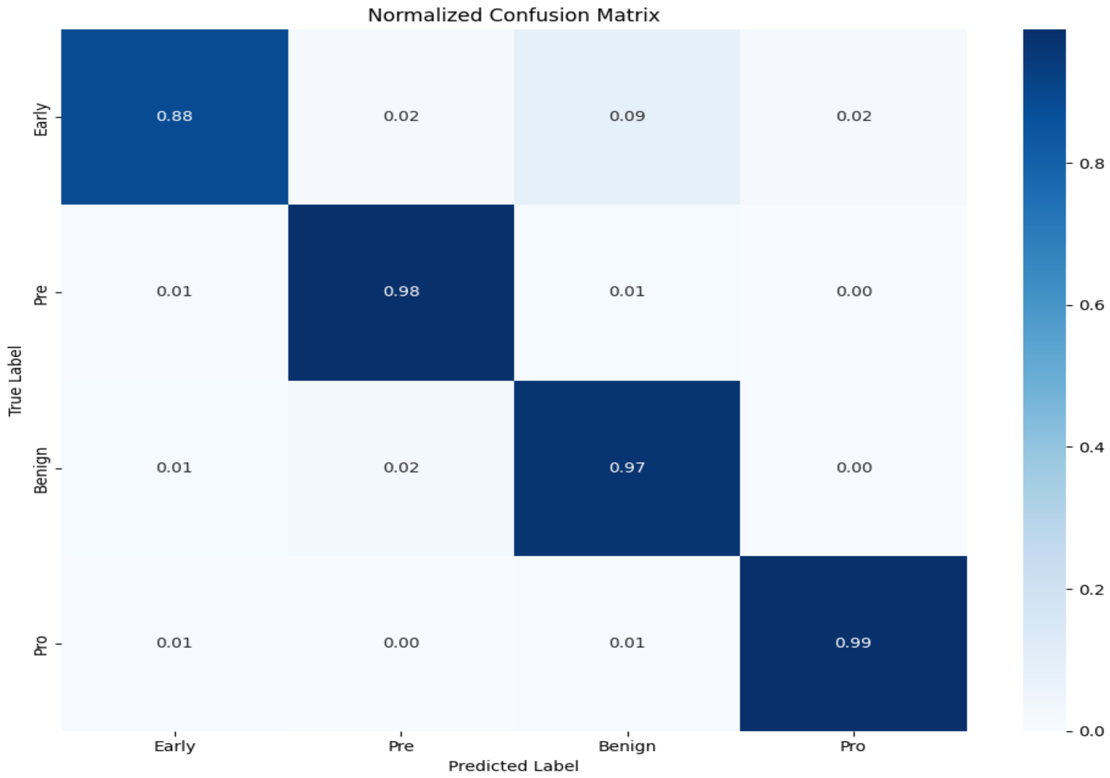


Figure 5.2.5: Confusion Matrix of VGG16

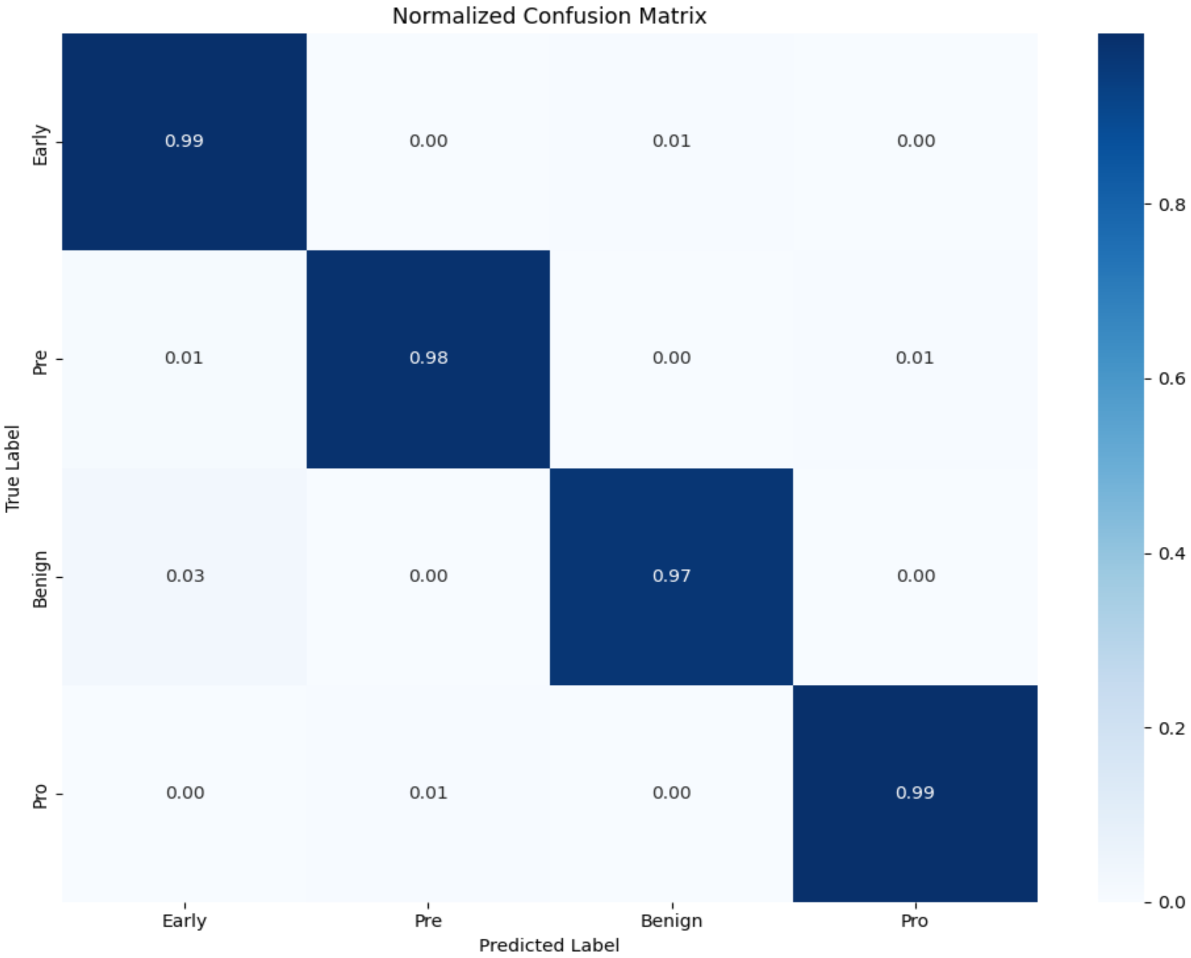
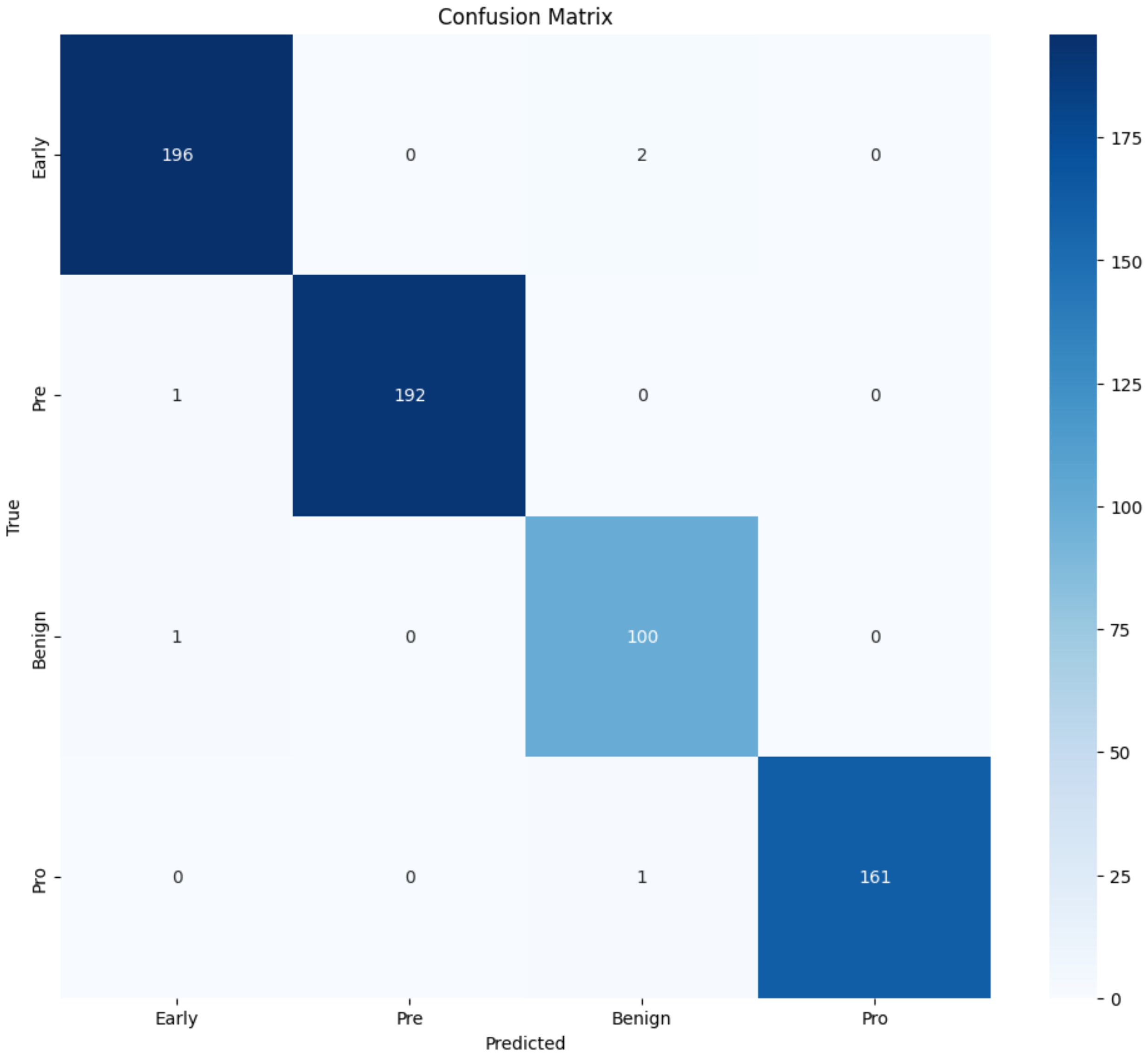
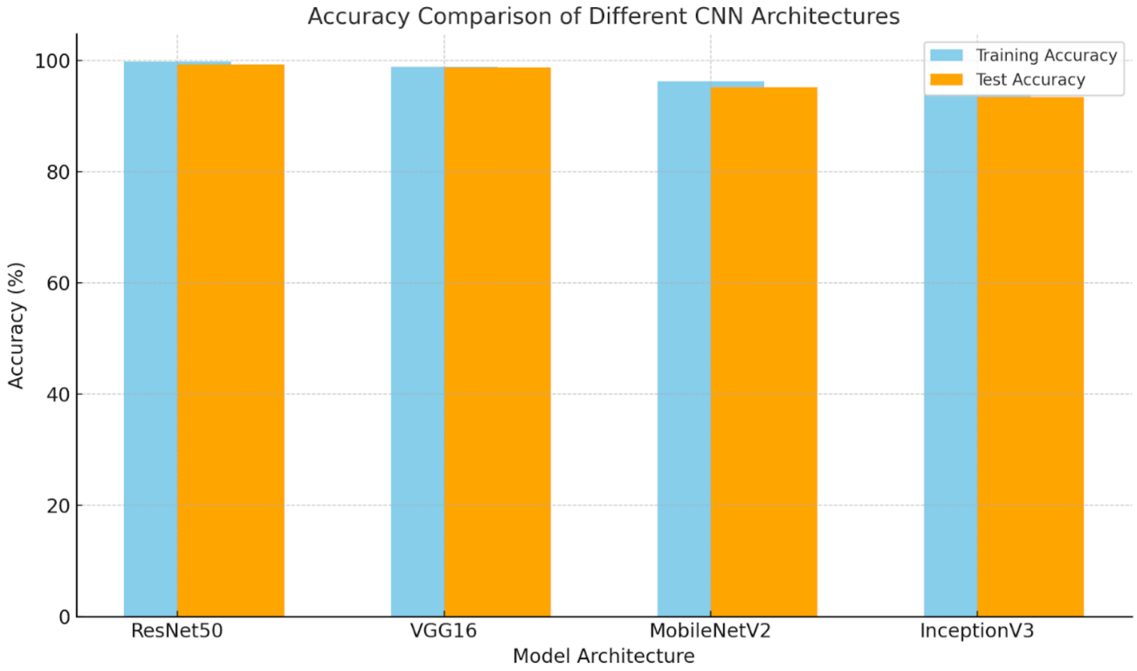


Figure 5.2.4: Confusion Matrix of ResNet50



## 5.3 Comparative Analysis

Figure 5.3.1: Performance Comparison of used CNN models



The performance comparison of the four Convolutional Neural Networks (CNNs)—ResNet50, VGG16, MobileNetV2, and InceptionV3—reveals significant differences in their training and testing accuracies. ResNet50 emerges as the top performer, achieving the highest training accuracy of 99.24% and a test accuracy of 99.00%. This demonstrates the model's robustness and its ability to generalize well on unseen data. VGG16 follows closely behind with a training accuracy of 98.78% and a test accuracy of 98.00%, making it a strong contender in terms of classification performance. While VGG16 performs well, it is slightly outpaced by ResNet50, especially when it comes to handling more complex datasets. On the other hand, MobileNetV2 shows a noticeable drop in accuracy with a training accuracy of 95.26% and a test accuracy of 95.00%. Though still efficient, especially for mobile and embedded applications, its performance is lower compared to the previous two models. Lastly, InceptionV3 shows the lowest accuracy across both training and testing phases, with a training accuracy of 93.43% and a test accuracy of 93.00%. The performance gap between InceptionV3 and the other models may be attributed to its more complex architecture, which might be harder to optimize for this specific task. This comparison provides a clear insight into how each model behaves in terms of both accuracy and generalization. ResNet50's superior performance highlights its effectiveness for disease classification, followed by VGG16, which also shows strong results. Meanwhile, MobileNetV2 and InceptionV3, although still capable, indicate a potential need for further optimization in this specific domain. These findings underscore the importance of selecting the right model based on accuracy needs, computational efficiency, and suitability for the dataset at hand.

### 5.4 Summary

In this study, the performance of four Convolutional Neural Networks (CNNs)—ResNet50, VGG16, MobileNetV2, and InceptionV3—was evaluated for disease classification using transfer learning techniques. The results show that ResNet50 outperformed the other models, achieving the highest training and test accuracy of 99.24% and 99.00%, respectively. VGG16 followed closely with a training accuracy of 98.78% and a test accuracy of 98.00%. MobileNetV2, while still efficient, had a slightly lower performance with a training accuracy of 95.26% and a test accuracy of 95.00%. InceptionV3 demonstrated the lowest accuracy across both training (93.43%) and testing (93.00%) phases. The study highlights the significance of model selection in achieving high classification performance and suggests that ResNet50 and VGG16 are more suitable for this task compared to MobileNetV2 and InceptionV3. The findings emphasize the potential for enhancing the performance of CNN models through optimization and tuning for specific tasks in medical imaging.

# CHAPTER 6
# IMPACT ON SOCIETY, ENVIRONMENT AND SUSTAINABILITY

## 6.1 Impact on Life

The application of advanced CNN-based models for Acute Lymphoblastic Leukemia (ALL) diagnosis represents a transformative step in medical diagnostics. These systems enable precise and efficient detection by targeting specific areas of interest, replacing traditional manual microscopy with automated, non-invasive solutions. This technological shift not only accelerates the diagnostic process but also minimizes patient discomfort and reduces the strain on healthcare resources. Models equipped with Efficient Channel Attention (ECA) enhance feature extraction and classification, offering unparalleled accuracy, scalability, and reliability. These innovations are particularly valuable in resource-constrained regions where timely diagnosis is critical for improving patient outcomes. By providing medical practitioners with state-of-the-art tools and data, CNN-based diagnostic systems empower informed decision-making, streamline patient care, and adapt to ongoing advancements in medical technology. Beyond diagnostics, the adoption of machine learning technologies fosters collaboration among clinicians, researchers, and technologists, creating new opportunities for skill development and interdisciplinary innovation. With advanced segmentation techniques and hyperparameter optimization, these systems have the potential to revolutionize leukemia diagnostics, even in challenging healthcare environments, improving patient outcomes, reducing costs, and driving progress in the global fight against leukemia.

## 6.2 Impact on Society & Environment

The integration of advanced CNN-based models into Acute Lymphoblastic Leukemia (ALL) diagnosis marks a groundbreaking advancement in medical technology with significant implications for patient care and resource optimization. By leveraging these models, healthcare practitioners can precisely identify and classify leukemic cells, ensuring that treatments are applied when necessary, thereby reducing the risks of misdiagnosis and overtreatment. This automation not only enhances diagnostic accuracy but also reduces the need for invasive procedures, minimizing patient discomfort and preserving healthcare resources. Additionally, the streamlined diagnostic process alleviates the burden on clinical staff, allowing for more efficient use of medical expertise without expanding infrastructure unnecessarily.

However, these advancements come with potential challenges. Concerns about data privacy, the risks of overreliance on automated systems, and the ethical implications of algorithmic decision-making necessitate careful consideration. It is crucial to implement robust data security measures and ensure that AI-powered diagnostics remain an aid, not a replacement, for human judgment. The introduction of CNN-based ALL diagnosis systems has ushered in a new era of precise, patient-centered care. Yet, their true potential can only be realized by addressing these concerns responsibly, maintaining a balance between technological progress and ethical, patient-focused healthcare.

### 6.3 Ethical Aspects

The integration of CNN-based models for Acute Lymphoblastic Leukemia (ALL) diagnosis offers transformative potential but raises important ethical considerations. A primary concern is data privacy and security, as these systems rely on sensitive patient information that must be safeguarded against breaches and misuse through robust encryption and compliance with regulations like HIPAA and GDPR. Additionally, the risk of overreliance on automated systems could lead to undervaluing clinical expertise, with errors potentially arising in edge cases or underrepresented scenarios. Bias and fairness are also critical issues, as training data lacking diversity could result in inequitable care, disproportionately affecting certain populations. Furthermore, the transparency and Explainability of AI systems are essential to ensure trust and understanding, avoiding "black-box" decision-making that could alienate patients and practitioners. On a broader scale, the digital divide poses a significant challenge, as access to these advanced diagnostic tools may be limited to well-funded healthcare systems, exacerbating disparities between developed and developing regions. Addressing this requires equitable distribution models and low-cost solutions to ensure the benefits of CNN-based ALL diagnosis reach underserved populations. Balancing innovation with these ethical concerns is vital to achieving trust, equity, and safety in the use of AI in healthcare.

### 6.4 Sustainability Plan

Successfully incorporating CNN-based models into Acute Lymphoblastic Leukemia (ALL) diagnosis may be jeopardized without a strong sustainability plan to ensure the long-term viability of such innovations in healthcare. The first stage of this plan involves a comprehensive assessment of the clinical landscape to identify potential impacts and guide the integration of sustainable diagnostic practices. This includes evaluating healthcare infrastructure and exploring the most effective ways to involve medical professionals and institutions. Key strategies for achieving this involve training programs for clinicians, community awareness initiatives, and the co-development of educational materials for stakeholders. The plan also includes a clinical and ethical impact statement, ensuring all necessary conclusions are drawn to promote equitable, accessible, and sustainable diagnostic solutions. By adopting such a framework, the implementation of CNN-based ALL diagnostic systems will achieve both medical and ethical success.

### 6.5 Summary

The integration of CNN-based models for Acute Lymphoblastic Leukemia (ALL) diagnosis is bringing transformative changes to the healthcare sector, offering productive and cost-effective benefits while minimizing the strain on healthcare systems. This technology enables healthcare professionals to apply the right diagnostic tools at the right time, leading to more accurate diagnoses with reduced errors and unnecessary procedures. It also facilitates the optimization of resources, ensuring minimal environmental and economic impact while improving diagnostic efficiency. The use of machine learning technologies, such as CNNs and hyperparameter optimization, enables better adaptation to patient needs and evolving medical standards. Beyond improving medical practices, these advancements contribute to broader social welfare by creating opportunities for innovation, skill development, and new job creation in the healthcare technology sector. However, while the integration of CNN-based ALL diagnostic systems holds significant promise, it is essential to balance technological progress with ethical considerations and maintain a harmony between innovation and patient safety. This ensures that the benefits of AI in healthcare are realized responsibly, with full consideration of its societal and environmental impact.

# CHAPTER 7
# CONCLUSION AND FUTURE WORK

## 7.1 Conclusions

In conclusion, this study provides a comprehensive evaluation of four CNN architectures—MobileNetV2, InceptionV3, VGG16, and ResNet50—for classifying subtypes of Acute Lymphoblastic Leukemia (ALL). Among the models, MobileNetV2 balances computational efficiency and performance with 95.26% accuracy. InceptionV3, though achieving 93.43% accuracy, VGG16 also shows strong results with an accuracy of 98.78%. ResNet50 demonstrates superior performance with a test accuracy of 99.24%, highlighting its suitability for the task due to its effective residual connections. while making it ideal for resource-limited applications., is hindered by its complexity and sensitivity to hyperparameters.

The study emphasizes the significance of analyzing both quantitative metrics and qualitative attributes such as model complexity and adaptability. It identifies key areas for improvement, including training strategies, data augmentation, and model design. By showcasing the potential and limitations of these architectures, this research advances the understanding of CNNs in medical imaging and paves the way for developing more accurate and reliable automated diagnostic tools for leukemia classification.

## 7.2 Further Suggested Works

Building on this study, future research can focus on improving CNN architectures for Acute Lymphoblastic Leukemia (ALL) classification. Advanced hyperparameter tuning methods, such as Bayesian optimization, could enhance the performance of models like InceptionV3 and MobileNetV2. Developing ensemble models by combining the strengths of different architectures, such as ResNet50's residual connections and MobileNetV2's efficiency, could further improve accuracy and robustness. Incorporating explainable AI (XAI) techniques, such as Grad-CAM, would increase model interpretability, making them more reliable for clinical use. Advanced data augmentation strategies, such as synthetic data generation with GANs, could address dataset limitations and improve model robustness. Testing models on diverse, multi-center datasets and optimizing lightweight architectures like MobileNetV2 for edge deployment would enhance their generalizability and practical usability. Finally, integrating these models into clinical workflows, exploring advanced training methods, and conducting long-term performance evaluations would ensure their adaptability and reliability. These efforts would pave the way for developing more accurate and effective diagnostic tools for ALL classification.

### 7.3 Limitations

A significant limitation of this study in the context of Acute Lymphoblastic Leukemia (ALL) classification is the reliance on a single dataset for evaluating the CNN architectures. While the results provide useful insights into the performance of the models, they may not fully capture the variations in data that could arise from different patient demographics, imaging modalities, or medical centers. The lack of validation across diverse, multicenter datasets with varying clinical conditions and patient profiles may limit the models' ability to generalize effectively to broader, real-world populations. Additionally, the implementation of advanced techniques such as ensemble learning and hyperparameter optimization introduces higher computational complexity, which could pose significant challenges in clinical environments where resources may be limited. This could impact both the scalability of the models and their practical deployment, especially in low-resource settings where the computational demands might exceed available capabilities. Therefore, these factors may influence the overall effectiveness and applicability of these models for ALL diagnoses in diverse clinical contexts.

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# Appendix A

## Course Outcomes, Complex Engineering Problems (EP) and Complex Engineering Activities (EA) Addressing

**Title: Automated Acute Lymphoblastic Leukemia Detection Using Convolutional Neural Networks**

**Student ID: 172-15-1601**

**CO Description for FYDP**

| CO | CO Descriptions | PO |
|---|---|---|
| **Phase -I** | | |
| **CO1** | Integrate foundational and advanced knowledge to identify and define the challenges in Acute Lymphoblastic Leukemia (ALL) research for the FYRP. | **PO1** |
| **CO2** | Integrate foundational and advanced knowledge to identify and define the challenges in Acute Lymphoblastic Leukemia (ALL) research for the FYRP. | **PO2** |
| **CO3** | Integrate foundational and advanced knowledge to identify and define the challenges in Acute Lymphoblastic Leukemia (ALL) research for the FYRP. | **PO4** |
| **CO4** | Evaluate the economic and societal impacts of ALL research and employ appropriate project management strategies throughout the project lifecycle. | **PO11** |
| **Phase -II** | | |
| **CO5** | Design and develop technical solutions and system components or processes that meet specified requirements, ensuring compliance with public health and safety standards, as well as considering cultural, socioeconomic, and environmental factors in this FYDP | **PO3** |
| **CO6** | Choose and apply appropriate methodologies, resources, and contemporary engineering and IT technologies to address complex engineering processes, encompassing prediction and modeling, while adhering to relevant constraints in this FYDP | **PO5** |

| | | |
|---|---|---|
| **CO7** | Design and propose innovative diagnostic or therapeutic solutions that meet clinical and safety standards, considering socioeconomic and cultural factors. | **PO6** |
| **CO8** | Comprehend and evaluate the enduring sustainability and impact of professional engineering endeavors in addressing intricate engineering challenges within social and environmental frameworks. | **PO7** |
| **CO9** | Implement ethical principles and adhere to professional standards and norms in this FYDP | **PO8** |
| **CO10** | Operate effectively both independently and within interdisciplinary teams during ALL research. | **PO9** |
| **CO11** | Operate effectively both independently and within interdisciplinary teams during ALL research. | **PO10** |
| **CO12** | Embrace the importance of continuous learning and adaptability in the rapidly evolving field of oncology research. | **PO12** |

## Addressing CO (1 to 8), Knowledge Profile (K), Attainment of Complex Engineering Problems (EP), and Attainment of Complex Engineering Activities (EA)

## Addressing CO (1 to 8), Knowledge Profile (K), Attainment of Complex Engineering Problems (EP):

| SN | EP Definition | Attainment | CO | Justification<br>(with Knowledge Profile) | References |
|---|---|---|---|---|---|
| **1.** | **EP1: Depth of Knowledge required** | Yes | CO1, CO2, CO3, CO5, CO6, CO7 and CO8 | This research requires in-depth knowledge of ALL, including pathophysiology, genetic markers, and treatment protocols, as well as advancements in precision medicine. | **Page no:**<br>[1-3]<br>**Section:**<br>[1.2]<br>**Page no:**<br>[1]<br>**Section:**<br>[1.4]<br>**Page no:**<br>[3] |
| | | | | The project utilizes engineering principles and design (K5) through the implementation of a systematic experimentation method. The project focuses on the use of the refined CNN model to address engineering practice and technology in the K6 field. | **Page no:**<br>[8-15]<br>**Section:**<br>[3.2]<br>**Page no:**<br>[9-12] |

| | | | | | |
|---|---|---|---|---|---|
| | | | | This study aims to enhance the field of K8 (Previous State of Arts) by consolidating knowledge from recent studies and utilizing deep learning techniques to improve ALL detection. It demonstrates a thorough grasp of current methodology in this area. | **Page no:**<br>[3-8]<br>**Section:**<br>[2.2, 2.3] |
| **2.** | **EP2: Range of Conflicting Requirements** | Yes | CO2, and CO7 | The project identifies conflicting requirements in treatment strategies, such as balancing efficacy and minimizing side effects, and proposes optimized approaches. | **Page no:**<br>[24-28]<br>**Section:**<br>[5.2] |
| **3.** | **EP3: Depth of analysis required** | Yes | CO2, and CO6 | The research focuses on detailed analysis of diagnostic accuracy and therapeutic outcomes, emphasizing improvements in current ALL treatments. | **Page no:**<br>[24-28]<br>**Section:**<br>[5.3] |
| **4.** | **EP4: Familiarity of Issues** | Yes | CO8 | Exploring the epidemiology and challenges in treating ALL, especially in resource-limited settings, indicates CRP-4. | **Page no:**<br>[8-15]<br>**Section:**<br>[3.2, 3.3] |

|  |  |  |  |  |  |
|---|---|---|---|---|---|
| **5.** | **EP5: Extends of application codes** | No | CO5 | N/A | N/A |
| **6.** | **stakeholders involved and conflicting** | No | CO8 | N/A | N/A |
| **7.** | **EP7: Interdependence** | Yes | CO5 | The project's all-encompassing approach tackles This inquiry consists of many linked subsystems. Gathering data, categorizing the data, manipulating it, training models, examining the outcomes, and numerous other activities are all integral components of this process. EP-7 is guaranteed. | **Page no:**<br>[8-15]<br>**Section:**<br>[3.2, 3.4] |

**Addressing CO11 with Complex Engineering Activities (EA) [Some or all of the following]:**

| SN | EA Definition | Attainment | CO | Justification | References |
|---|---|---|---|---|---|

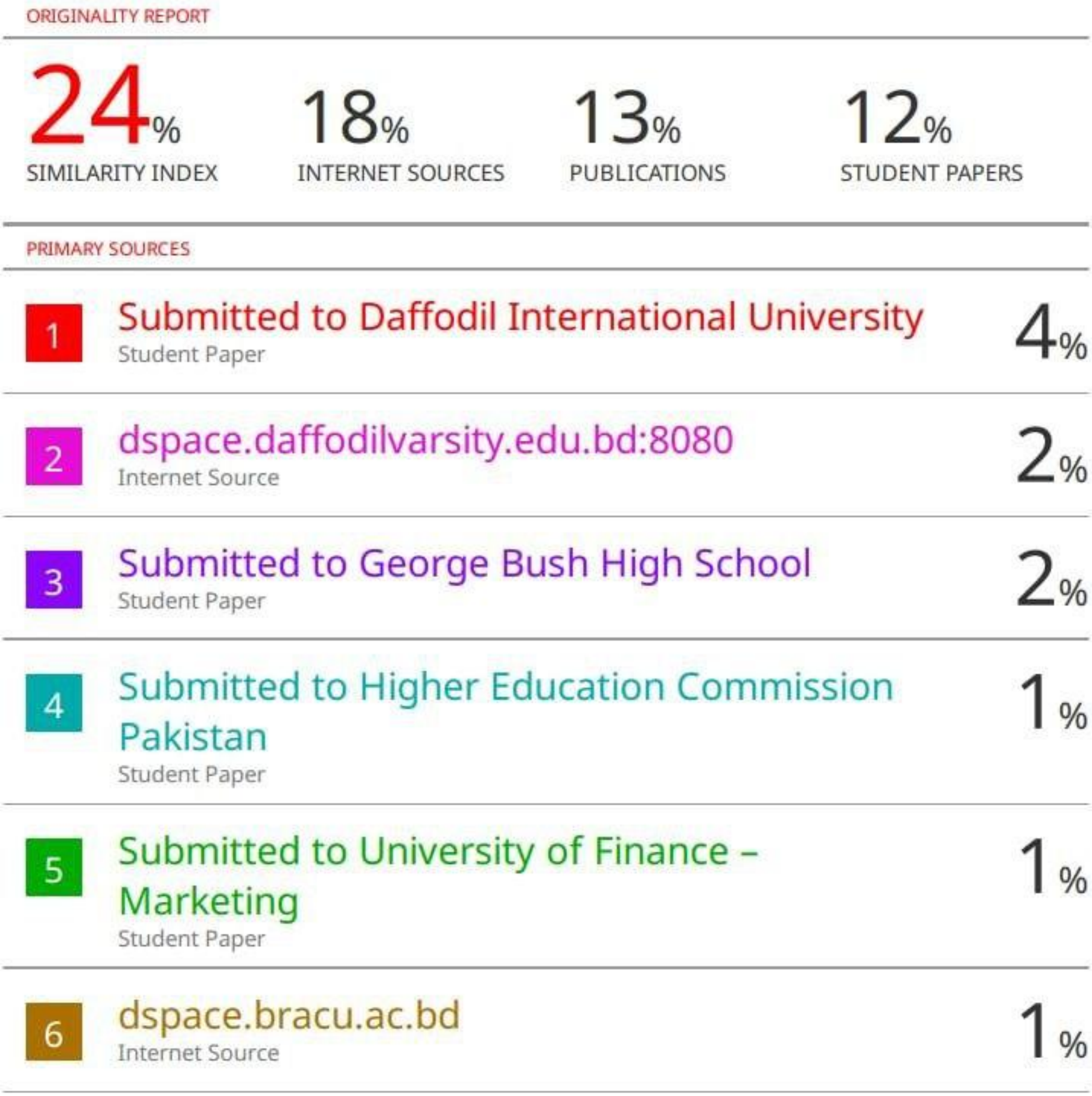
| | | | | | |
|---|---|---|---|---|---|
| **1.** | **EA1: Range of resources** | Yes | CO11 | The research employs diverse resources, including patient datasets, advanced diagnostic tools, and machine learning algorithms for prognosis. | **Page no:**<br>[8-15]<br>**Section:**<br>[3.3] |
| **2.** | **EA2: Level of interaction** | No | | N/A | N/A |
| **3.** | **EA3: Innovation** | No | | N/A | N/A |

|  |  |  |  |  |  |
|---|---|---|---|---|---|
| **4.** | **EA4: Consequences for society and the environment** | Yes |  | The study’s outcomes aim to improve quality of life and reduce societal burdens by advancing ALL diagnosis and treatment. | **Page no:**<br>[28-30]<br>**Section:**<br>[5.1, 5.2, 5.3] |
| **5.** | **EA-5: Familiarity** | Yes |  | This research builds on existing studies while proposing novel applications of genetic markers and AI in ALL management. | **Page no:**<br>[3-8]<br>**Section:**<br>[2.2, 2.3, 2.4] |

**Addressing CO (4, 9, 10, and 12):**

| SN | COs | Attainment | Justification | References |
|---|---|---|---|---|
| **1** | CO4 | Yes | This research builds on existing studies while proposing novel applications of genetic markers and AI in ALL management. | **Page no:**<br>[8-15]<br>**Section:** |

| | | | | |
|---|---|---|---|---|
| | | | | [3.4] |
| **2** | CO9 | Yes | Ethical standards are maintained, including informed consent, data privacy, and transparent reporting in ALL research. | **Page no:**<br>[28-30]<br>**Section:**<br>[6.2, 6.3] |
| **3** | CO10 | No | N/A | N/A |
| **4** | CO12 | Yes | Continuous learning is evident through extensive literature review, adaptation of new technologies, and rigorous experimentation in ALL research. | **Page no:**<br>[8-15, 15-23]<br>**Section:**<br>[3.2, 3.3, 3.4, 3.5, 4.2, 4.3] |



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