

CHAPTER 1

INTRODUCTION

1.1 OVERVIEW

Acute Lymphoblastic Leukemia (ALL) is a type of blood cancer that affects white blood cells and progresses rapidly if not diagnosed early. Traditional diagnostic techniques are often labor-intensive, require specialized medical expertise, and are prone to human error. This project aims to automate the detection of ALL using a deep learning ensemble system trained on microscopic blood smear images. The system extracts features using advanced convolutional neural networks such as EfficientNetB7, ResNet152V2, DenseNet201, and InceptionV3. These features are then combined and classified using a meta-learner like XGBoost to achieve high diagnostic accuracy and reduce diagnostic time, thereby assisting pathologists in making reliable and timely decisions.

1.2 BACKGROUND OF ACUTE LYMPHOBLASTIC LEUKEMIA

Acute Lymphoblastic Leukemia (ALL) is a malignant disorder of the hematopoietic system characterized by the uncontrolled proliferation of immature lymphoid cells known as lymphoblasts in the bone marrow and peripheral blood. These lymphoblasts interfere with the normal production of blood cells, leading to anemia, susceptibility to infections, and bleeding disorders.

ALL is the most common form of leukemia in children, especially between the ages of 2 to 5, though it also occurs in adults with less favorable prognoses. It accounts for approximately 25% of all childhood cancers. Based on the cell lineage, ALL is primarily classified into:

- **B-cell ALL:** The most common form, involving B lymphocytes.
- **T-cell ALL:** Less common but often more aggressive.

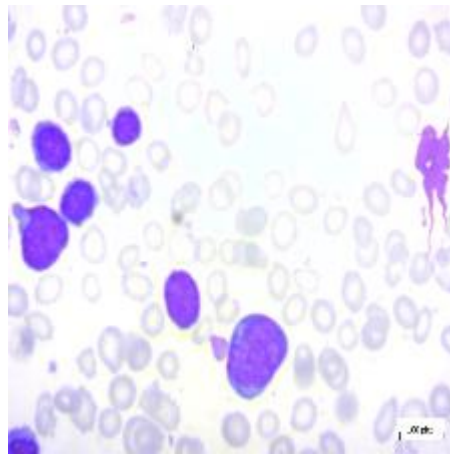


Figure 1.1. Blood Smear Image

Furthermore, for clinical and research purposes—particularly in image-based deep learning applications—ALL is commonly subclassified into four developmental stages of lymphoblasts:

- **Benign:** Non-leukemic or healthy samples used for baseline comparison.
- **Early Precursor (Early-ALL):** Initial abnormal lymphoid cell development, showing subtle morphological changes.
- **Pro-B (Pro-ALL):** More defined leukemic features, with immature B-cells showing blast proliferation.
- **Pre-B (Pre-ALL):** Advanced stage in B-cell lineage with more aggressive cell multiplication.

This 4-class categorization helps in granular classification of disease progression and is particularly relevant in AI-based diagnostic models, where distinguishing between these stages improves early intervention and treatment planning.

1.2.1 Pathogenesis

The disease originates in the bone marrow, where a series of genetic mutations lead to the transformation of normal precursor lymphocytes into malignant clones. These immature cells fail to differentiate and rapidly accumulate, eventually spilling into the bloodstream and infiltrating other organs such as the liver, spleen, lymph nodes, and central nervous system (CNS).

1.2.2 Clinical Symptoms

The clinical presentation of ALL is often acute and nonspecific, making early diagnosis challenging. Common symptoms include:

- Persistent fatigue and weakness
- Frequent infections
- Pale skin and easy bruising
- Bone pain and joint discomfort
- Swollen lymph nodes or abdomen

1.2.3 Diagnostic Techniques

The diagnosis of ALL involves a combination of clinical examination, laboratory investigations, and imaging. Common diagnostic tools include:

- **Complete Blood Count (CBC):** Shows abnormal white cell counts and presence of blasts
- **Peripheral Blood Smear:** Reveals the morphology of abnormal lymphoblasts
- **Bone Marrow Aspiration and Biopsy:** Confirms the infiltration of marrow by lymphoblasts

- **Flow Cytometry:** Determines the immunophenotype (B-cell or T-cell)
- **Cytogenetics and Molecular Testing:** Identifies chromosomal abnormalities and mutations
- **Lumbar Puncture:** Assesses central nervous system involvement

While these techniques are effective, they often require significant time, expert analysis, and laboratory infrastructure.

1.3 THE NEED FOR EARLY DETECTION

Early detection of Acute Lymphoblastic Leukemia (ALL) plays a vital role in reducing mortality and improving long-term outcomes. Due to the aggressive progression of the disease, identifying ALL in its early stages can significantly increase the chances of effective treatment and remission.

1.3.1 Importance of Timely Diagnosis

Prompt diagnosis allows clinicians to initiate treatment before the disease spreads to critical areas such as the central nervous system or results in complications like infections, anemia, or bleeding disorders. In pediatric ALL, early detection contributes to survival rates exceeding 85%, while in adults, it is crucial for minimizing relapse rates and tailoring treatment intensity.

1.3.2 Challenges in Early Diagnosis

Several challenges hinder early diagnosis:

- **Non-Specific Symptoms:** Fatigue, fever, and joint pain are common to many illnesses, often leading to delayed suspicion.
- **Lack of Awareness:** Patients and even some general practitioners may overlook warning signs.

- **Limited Access to Specialized Care:** In many regions, especially rural or underdeveloped areas, access to hematology experts and diagnostic labs is limited.

1.3.3 Diagnostic Delay and Its Consequences

Delayed diagnosis often results in:

- Disease progression to more advanced and less treatable stages.
- Higher risk of treatment failure or relapse.
- Increased burden on healthcare systems due to longer and more intensive therapy.

1.4 ROLE OF AI IN MEDICAL IMAGING

Artificial Intelligence (AI), especially deep learning, is transforming medical diagnostics by providing efficient, accurate, and scalable solutions. In the context of Acute Lymphoblastic Leukemia (ALL), AI-based approaches, particularly those using medical image analysis are proving invaluable for early detection and classification.

1.4.1 Introduction to AI in Healthcare

AI refers to the simulation of human intelligence processes by machines, especially computer systems. In healthcare, AI is utilized for predictive analytics, personalized medicine, robotic surgeries, and medical imaging. Machine learning (ML) and deep learning (DL), subfields of AI, are particularly adept at learning patterns from large datasets, making them well-suited for disease diagnosis tasks.

1.4.2 Medical Imaging in Leukemia Diagnosis

Traditional diagnosis of ALL involves examination of blood smears and bone marrow samples using microscopy. These imaging techniques capture cell morphology, which can be leveraged by AI systems to differentiate between normal and leukemic cells. AI algorithms trained on such medical images can aid hematologists in identifying ALL cases with high accuracy.

1.4.3 Advantages of AI in ALL Detection

- **Speed and Scalability:** Rapid analysis of thousands of images in seconds.
- **Objectivity:** Reduces human bias in interpretation.
- **Consistency:** Offers uniform performance across different cases.
- **Accessibility:** AI models can be deployed in low-resource settings to assist non-expert users.
- **Cost Reduction:** Minimizes the need for expensive molecular tests in initial screening.

1.4.4 Limitations and Ethical Considerations

Despite its advantages, AI in medical imaging must overcome certain limitations:

- **Data Privacy:** Patient data security must be ensured.
- **Interpretability:** AI decisions must be explainable to gain clinician trust.
- **Dataset Bias:** Models must be trained on diverse datasets to avoid generalization issues.
- **Regulatory Compliance:** Deployment in clinical settings requires regulatory approvals and validation.

CHAPTER 2

LITERATURE SURVEY

2.1 INTRODUCTION

To develop an effective and generalizable diagnostic system for ALL classification, it is essential to understand prior contributions in the domain of medical image analysis. This section reviews recent advancements in deep learning approaches applied to leukemia detection, focusing on hybrid CNN models, transfer learning strategies, and ensemble classifiers. These studies offer valuable insights into existing challenges, methodologies, and performance benchmarks that inform the architecture of the proposed model.

2.2 RELATED WORK

1. DL4ALL: A Multi-Task, Cross-Dataset Transfer Learning Framework for Acute Lymphoblastic Leukemia Detection

Authors: Genovese et al.

Year: 2023

Genovese et al. (2023) proposed DL4ALL, a multi-task, cross-dataset transfer learning framework designed to enhance Acute Lymphoblastic Leukemia (ALL) detection. This model employs EfficientNet-B0, known for its computational efficiency and high performance in image classification tasks. The integration of classification and segmentation tasks using a multi-task learning approach makes DL4ALL particularly versatile. By training on publicly available datasets like ALL-IDB1 and ALL-IDB2, the model ensures greater generalizability across diverse image conditions and patient demographics. The primary strength of this model lies in its ability to simultaneously handle

classification and segmentation tasks, which are crucial for detecting and delineating leukemia cells. The study shows that models trained on a variety of datasets perform better when adapted to new clinical environments. This framework demonstrates the importance of robust, adaptable models in real-world applications, particularly in clinical settings where datasets may be heterogeneous and limited in size. The approach also highlights the growing need for cross-domain transfer learning in medical imaging to improve model accuracy and ensure reliability across varied patient populations.

2. Deep Transfer Learning for Leukemia Cell Detection Using ResNet50 and VGG16

Authors: Fata et al.

Year: 2023

Fata et al. (2023) addressed the issue of data scarcity in medical imaging by leveraging a deep transfer learning strategy with ResNet50 and VGG16 architectures. Pre-trained on the ImageNet dataset, these models were fine-tuned on leukemia cell datasets to detect abnormal cells. The study emphasizes that using pre-trained networks can significantly improve classification performance, even with small and imbalanced datasets, which is often a challenge in medical imaging. The key advantage of this approach is its ability to minimize training time and computational costs while still retaining high diagnostic accuracy. The models demonstrated robust performance in identifying leukemia cells, achieving high accuracy despite the relatively small number of training images. This technique not only addresses data limitations but also proves to be computationally efficient, making it a suitable approach for low-resource clinical settings. The study validates the importance of leveraging pre-trained deep learning models to reduce the burden of data collection and training time, especially in the context of specialized medical image classification tasks.

3. Hybrid CNN-ML Classifier for Leukemia Detection

Authors: Ahmed et al.

Year: 2023

Ahmed et al. (2023) introduced a hybrid diagnostic system that combines deep learning and traditional machine learning algorithms for leukemia detection. The study used features extracted from various CNN architectures, including VGG19, DenseNet121, and InceptionV3, which were then fused and classified using traditional machine learning classifiers such as Support Vector Machine (SVM), Random Forest, Decision Tree, and k-Nearest Neighbors (k-NN). The fusion of CNN-extracted features with ensemble machine learning classifiers enhances the robustness and accuracy of the model, making it highly effective in handling varied imaging conditions and complex morphological variations found in medical images. The results showed that this hybrid framework achieved significantly higher accuracy than single-model approaches. The study suggests that combining the strengths of deep learning feature extraction and traditional classifiers is particularly beneficial for medical applications, where variations in image quality and morphology are common. This hybrid approach also makes the model more flexible and adaptable, especially in settings where the computational power is constrained.

4. ALLNet: A Specialized CNN for Acute Lymphoblastic Leukemia Detection

Authors: Mattapalli and Athavale

Year: 2023

Mattapalli and Athavale (2023) introduced ALLNet, a custom-designed Convolutional Neural Network (CNN) optimized specifically for detecting Acute Lymphoblastic Leukemia (ALL) from white blood cell images. Unlike standard

CNN architectures, ALLNet was tailored for leukemia detection, focusing on computational efficiency and optimized feature extraction. The model's architecture incorporates multiple convolutional and pooling layers, along with skip connections to preserve important spatial information, which is often lost in deeper layers of traditional CNNs. This specialization allowed ALLNet to outperform pre-trained networks like ResNet in terms of both accuracy and sensitivity for leukemia cell classification. The study showed that ALLNet achieved an accuracy rate of 96%, making it a promising tool for use in clinical practice. The tailored design and high performance of this model underscore the importance of domain-specific architectures in medical image analysis, especially when working with complex and highly variable biological data.

5. Comparative Study of Machine Learning Algorithms for Acute Lymphoblastic Leukemia Detection

Authors: Kocatürk et al.

Year: 2022

In a comprehensive study, Kocatürk et al. (2022) compared the performance of several traditional machine learning algorithms—including Naïve Bayes, Decision Trees, Random Forest, k-Nearest Neighbors (k-NN), and Support Vector Machine (SVM)—for Acute Lymphoblastic Leukemia (ALL) detection. The authors evaluated these models on a common dataset to ensure consistency and comparability. While deep learning models typically outperformed traditional machine learning methods, this study demonstrated that optimized traditional classifiers could still achieve competitive results, especially when data resources are limited. Among the traditional classifiers, Random Forest was found to perform the best, achieving an accuracy of 90%. The study emphasized that, in low-resource environments where computational power may be constrained, these machine learning models are still viable alternatives,

providing high classification performance without the need for extensive training data or advanced hardware. This comparative analysis highlights the ongoing relevance of classical machine learning approaches in medical imaging, particularly in settings where deep learning might be impractical due to resource constraints.

6. Leukemia Diagnosis Using Deep Learning in Clinical Environments

Authors: Zhou et al.

Year: 2021

Zhou et al. (2021) developed a leukemia diagnosis system using deep learning CNN architectures trained in real clinical environments, as opposed to relying solely on pre-collected datasets. This model incorporated advanced preprocessing and augmentation strategies, followed by CNN-based classification. The framework was trained and validated using data collected from actual hospital laboratories, enhancing the model's relevance and practical applicability. The study emphasized the challenges of implementing deep learning systems in clinical settings, where real-world data may have inconsistencies in quality, annotation, and variability. Despite these challenges, the model showed promising results in diagnosing leukemia, achieving a high classification accuracy of 94%. The study underscored the need for practical and robust deep learning models that can handle real-world data, providing valuable insights into the operationalization of AI in healthcare.

7. AI-Based Deep Learning for Early Leukemia Classification Using ResNet50

Authors: Rezayi et al.

Year: 2021

Rezayi et al. (2021) proposed an AI-based deep learning method using ResNet50, a deep residual network designed to overcome the vanishing gradient problem in very deep networks. The focus of the study was on the early and accurate classification of leukemia cells in blood smear images. The authors preprocessed the images using normalization and data augmentation techniques, which helped to improve the model's robustness and performance despite the limited size of medical datasets. The ResNet50 model, after training on the preprocessed images, was able to achieve a classification accuracy of 95%, demonstrating the effectiveness of deep residual networks in medical image classification. This study highlighted how ResNet50 can be used for both feature extraction and classification, providing an efficient solution for detecting leukemia in clinical applications, especially when data is scarce.

8. Multi-Task Pre-Training of Deep Neural Networks for Digital Pathology

Authors: Mormont et al.

Year: 2021

Mormont et al. (2021) explored the concept of multi-task pre-training for deep neural networks, specifically using ResNet50, on various digital pathology datasets. While their work was not limited to leukemia, it demonstrated the potential of multi-task learning in improving the adaptability and performance of deep learning models in pathology. The study introduced a framework where the model was trained to perform multiple related tasks, such as cell segmentation and disease classification, on the same dataset. This approach enabled better

generalization and feature extraction, which can be transferred to new and unseen tasks in clinical settings. The findings of this study suggest that multi-task learning can be highly beneficial for hematopathology, as it allows models to learn more robust features from multiple related tasks. The study demonstrated the advantages of multi-task pre-training in increasing model versatility, which is crucial for practical, real-world applications.

9. Weighted Ensemble Learning for Leukemia Detection

Authors: Mondal et al.

Year: 2021

Mondal et al. (2021) employed a weighted ensemble learning approach to combine the strengths of three prominent CNN architectures—VGG16, ResNet50, and InceptionV3—for leukemia detection. The study trained each model separately on leukemia image data, then aggregated their predictions using a weighted voting mechanism, where the weights were based on each model's individual performance. The ensemble method aimed to capitalize on the unique strengths of each individual network, while reducing the potential weaknesses of any single model. The authors found that this weighted ensemble approach significantly outperformed the individual models in terms of both accuracy and robustness. Specifically, the ensemble method showed a notable improvement in precision and recall when compared to single-model techniques, achieving an overall classification accuracy of 98%. This method proved particularly effective for medical image classification, where individual models may struggle with certain image features or noise. The study concludes that ensemble learning offers a reliable solution to improve the stability and reliability of medical diagnosis models, especially for complex diseases like leukemia.

10. Early CNN-Based Approach for Leukemia Detection from Bone Marrow Images

Authors: Deepika Kumar et al.

Year: 2020

Deepika Kumar et al. (2020) were among the earlier researchers to apply basic CNN architectures for detecting white blood cancer from bone marrow images. The study employed a standard CNN pipeline consisting of convolutional layers, pooling layers, and fully connected layers to learn discriminative features from microscopic bone marrow images. Despite its simplicity compared to more recent models, this CNN-based approach was one of the first to show the potential of deep learning for hematological imaging. The authors highlighted the model's capacity to automatically learn and detect complex cell structures from high-resolution images, which is a key advantage of CNNs in medical applications. The model achieved a classification accuracy of 87%, demonstrating that even simple CNN models can be effective in diagnosing leukemia from bone marrow images. Although the model was basic compared to more sophisticated architectures, the study laid the groundwork for future advancements in the field and established the feasibility of using deep learning in the detection of hematological diseases.

CHAPTER 3

EXISTING WORK

3.1 INTRODUCTION TO EXISTING WORK

The existing work presents a novel approach to improving the accuracy and generalizability of automated Acute Lymphoblastic Leukemia (ALL) detection using deep learning. Traditional transfer learning methods for ALL detection involve pretraining a model on a large source domain (such as ImageNet or histopathology datasets) followed by fine-tuning on a smaller target domain (such as white blood cell images). While this method can be effective, it has several drawbacks including overfitting to the source domain, insufficient adaptation to the target domain, and lack of support for leveraging unlabeled data.

To address these limitations, the DL4ALL framework introduces a multi-task learning architecture that replaces the traditional single-output layer with two fully connected layers—one for the source domain and one for the target domain. This dual-head structure enables the system to learn from both domains simultaneously, thus improving generalization and reducing overfitting.

Three innovative cross-dataset transfer learning strategies were proposed and implemented in this work:

1. Regular Cross-Dataset Transfer Learning – Alternates batches from source and target domains during training, using a weighted sum of their respective losses to update shared parameters.

2. Greedy Cross-Dataset Transfer Learning – Selectively updates weights using the source domain only if it results in a reduced loss on the target domain, ensuring that learning from the source supports the end goal.

3. Self-Supervised Cross-Dataset Transfer Learning –

Eliminates the need for manually labeled data in the source domain by assigning pseudo-labels based on metadata (e.g., WSI index), making the method more scalable and cost-effective.

The proposed DL4ALL framework was evaluated on a combination of publicly available datasets: the Atlas of Digital Pathology (ADP) as the source domain, and the C_NMC_2019 dataset from the ISBI 2019 ALL challenge as the target domain. Experiments were conducted using both ResNet18 and Vision Transformer (ViT) architectures. Results showed that DL4ALL outperforms traditional transfer learning approaches in terms of accuracy, sensitivity, and specificity, with the greedy learning method using ViT achieving the highest performance.

Furthermore, qualitative analysis using t-SNE and Grad-CAM confirmed that DL4ALL learned more discriminative and relevant features compared to conventional methods. These improvements are especially significant in medical contexts, where labeled data is scarce, and diagnostic accuracy is critical.

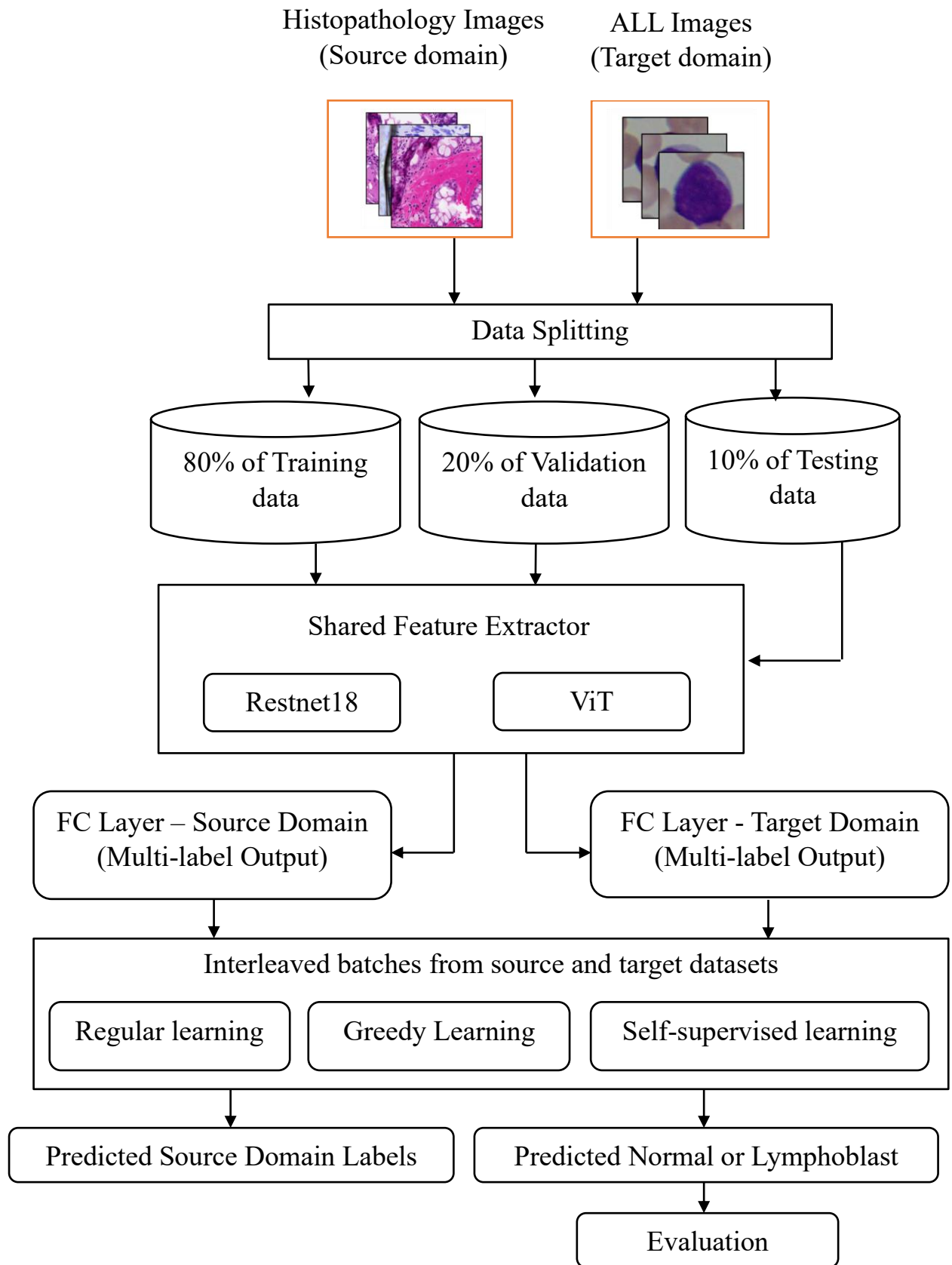


Figure 3.1. Existing Work Architecture

3.2 DISADVANTAGES OF THE EXISTING WORK

Although the DL4ALL framework presents an innovative approach to cross-dataset transfer learning for ALL detection, several critical limitations affect its practicality and scalability. These disadvantages are outlined below:

1. High Computational Requirement: DL4ALL involves computationally intensive processes, including training deep neural networks (e.g., ResNet18 or ViT) with interleaved batches from two datasets and maintaining dual output heads. Additionally, strategies like greedy learning and self-supervised optimization add to the training time and GPU memory consumption. This level of complexity demands high-end hardware, which may not be accessible in many clinical or research environments.

2. Requirement of Large Data: The model depends on both a labeled target domain and a large-scale source domain (e.g., histopathology datasets like ADP). These datasets typically include tens of thousands of image patches, often extracted from whole-slide images (WSIs), requiring significant preprocessing, storage, and bandwidth. The need for large, diverse, and structured data sources creates a barrier for rapid deployment or use in data-limited settings.

3. High Complexity in Training Procedure: The training workflow is complex, involving simultaneous optimization of source and target objectives, batch normalization handling across domains, loss balancing, and sometimes rollback logic (as in greedy learning). This makes implementation, debugging, and tuning more challenging compared to conventional single-task deep learning models.

4. Single Backbone Limitation: DL4ALL uses only one backbone model at a time (e.g., ResNet18 or ViT) for feature extraction. While effective, this limits the diversity of features learned, potentially restricting model performance. It lacks the benefit of architectural ensemble diversity, which has been shown to

improve robustness and generalization in deep learning tasks, especially in medical imaging.

5. Dependency on Domain Label Quality: Even in its self-supervised variant, DL4ALL relies on structured or semi-structured labeling from the source domain, such as slide-level annotations or WSI identifiers. If these labels are noisy, missing, or poorly structured, the performance of the model may degrade. This dependence makes the approach less adaptable to messy or weakly labeled real-world data.

CHAPTER 4

PROPOSED WORK

4.1 INTRODUCTION TO PROPOSED WORK

The proposed work presents an ensemble learning approach for multi-class classification of blood cell images to support early detection of blood cancer. The dataset includes four diagnostic categories: Benign, Pre, Pro, and Early. Images were preprocessed by resizing them to a consistent resolution, and assigning appropriate class labels. The data was divided into training, validation, and test sets to enable structured model development and evaluation. To enhance generalization and robustness, data augmentation techniques such as image rotation, flipping, and contrast adjustment were applied. Deep features were extracted from four pre-trained convolutional neural network architectures, namely EfficientNetB7, ResNet152V2, DenseNet201, and InceptionV3, without retraining the entire models. These features were combined and used as input to a meta-learning classifier based on XGBoost, which performed the final classification. This ensemble learning strategy effectively integrates the strengths of multiple convolutional models with the predictive power of gradient boosting, resulting in improved classification accuracy.

4.1.1 XGBoost Algorithm

XGBoost (Extreme Gradient Boosting) is a highly efficient and scalable implementation of gradient boosting algorithms. It builds an ensemble of decision trees in a sequential manner, where each new tree attempts to correct the errors made by the previous ones. XGBoost uses a second-order Taylor approximation of the loss function, allowing it to handle both linear and non-linear decision boundaries effectively.

In this system, XGBoost is employed as the meta-classifier that takes as input the concatenated deep features extracted from multiple pre-trained CNN models, including EfficientNetB7, ResNet152V2, DenseNet201, and InceptionV3. The algorithm excels in handling structured input data and is capable of modeling complex relationships without overfitting, especially when regularization techniques such as L1 and L2 penalties are applied.

Key advantages of using XGBoost in this context include:

- High predictive accuracy due to its ensemble nature
- Robustness to overfitting through regularization
- Support for handling imbalanced datasets using weighted loss
- Fast training and efficient memory usage, making it suitable for large feature sets derived from deep networks

The integration of XGBoost as a meta-learner complements the deep learning feature extractors by providing a powerful decision-making layer that enhances overall classification performance.

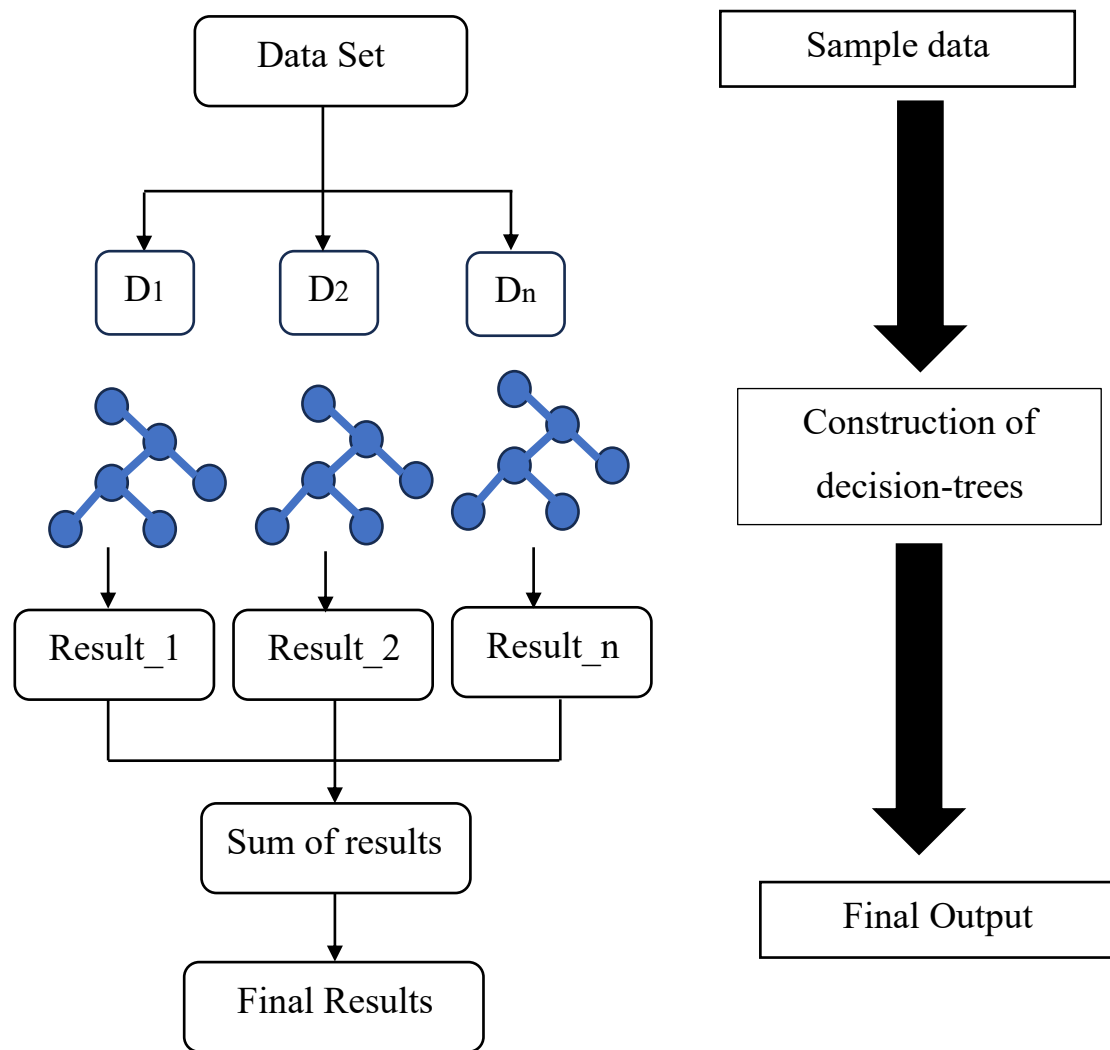


Figure 4.1. XGBoost Architecture

4.1.2 EfficientNetB7 Algorithm

EfficientNetB7 is the most advanced model in the EfficientNet family, designed using a compound scaling method that balances depth, width, and resolution for high accuracy and efficiency. It uses MBConv blocks with squeeze-and-excitation (SE) modules and Swish activation to enhance performance. In this study, images of size 224×224 were input to the model, and global average pooling was applied to extract a 2560-dimensional feature vector per image, making it well-suited for detailed medical image analysis.

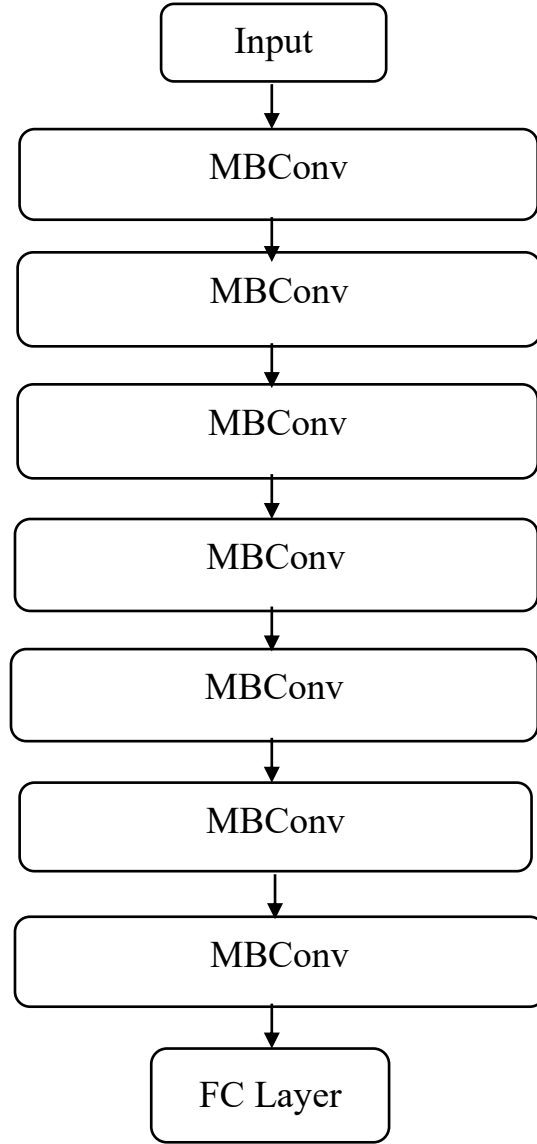


Figure 4.2. EfficientNetB7 Architecture

4.1.3 ResNet152 Algorithm

ResNet152V2 is a very deep convolutional neural network that uses residual learning with skip connections to address the vanishing gradient problem in deep architectures. It features improved identity mappings and batch normalization before activation, enhancing training stability and performance. The network consists of multiple residual blocks stacked together, enabling efficient learning of complex features. In this study, input images of size 224×224

were used, and global average pooling was applied to extract a 2048-dimensional feature vector per image, making ResNet152V2 well-suited for high-level feature extraction in medical imaging.

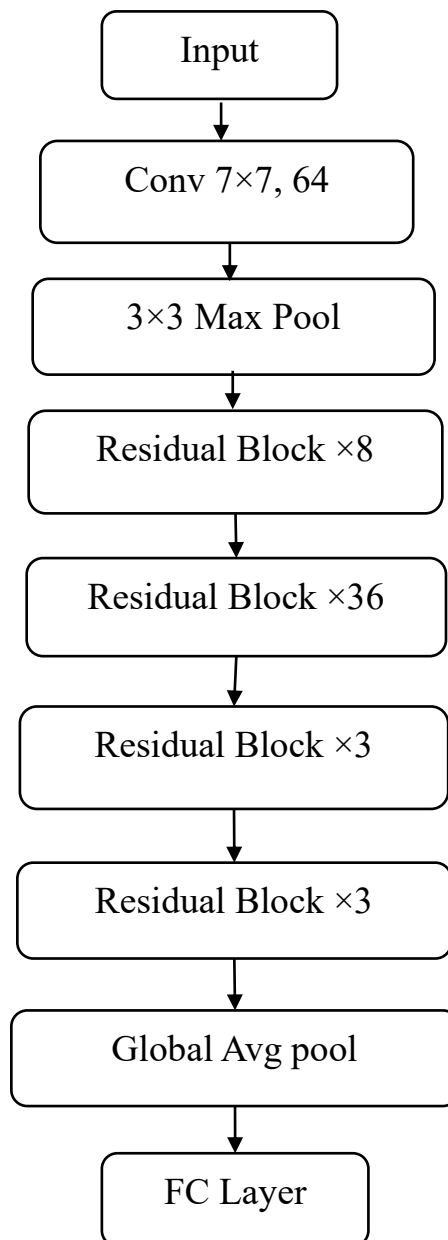


Figure 4.3. ResNet152 Architecture

4.1.4 DenseNet201 Algorithm

DenseNet201 is a deep convolutional neural network from the DenseNet family, known for its dense connectivity pattern where each layer receives input from all preceding layers. This design improves feature reuse, strengthens gradient flow, and reduces the number of parameters. It is composed of dense blocks and transition layers, using batch normalization and ReLU activation. In this study, input images of size 224×224 were used, and global average pooling was applied to extract a 1920-dimensional feature vector per image, making DenseNet201 effective for extracting rich features in medical imaging tasks.

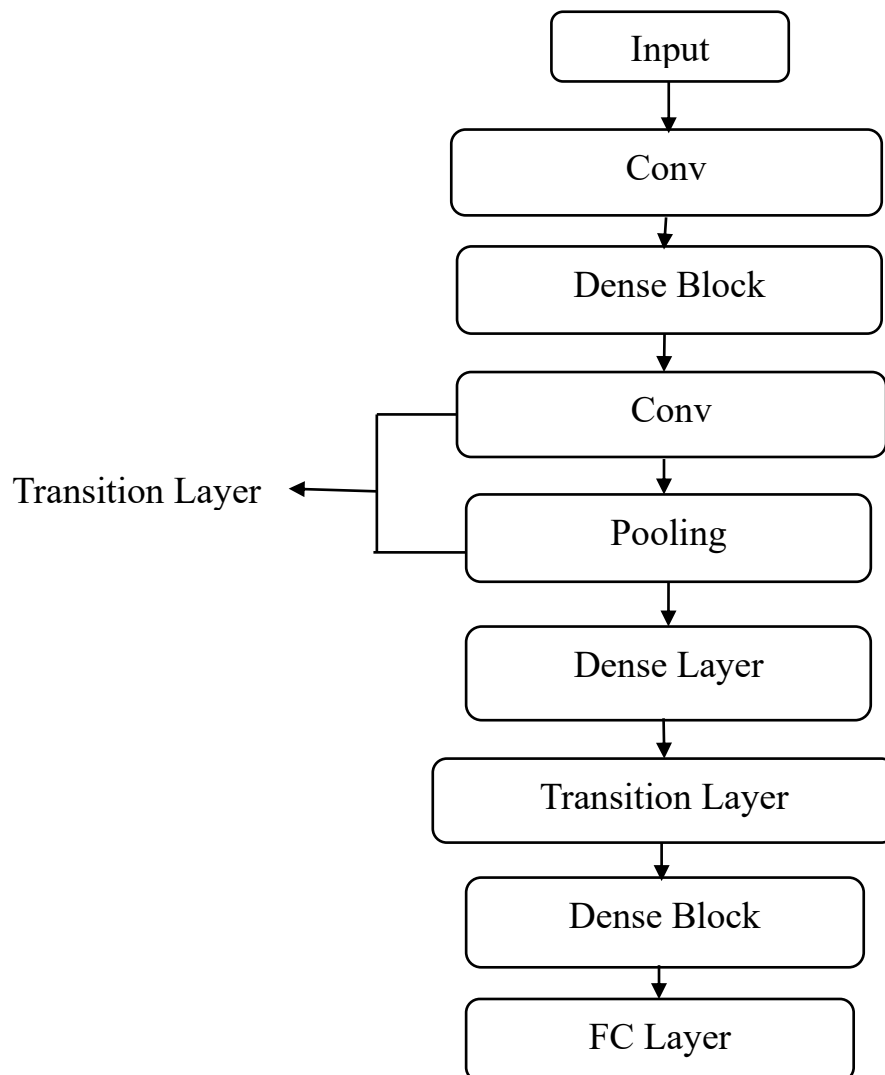


Figure 4.4. DenseNet201 Architecture

4.1.5 InceptionV3 Algorithm

InceptionV3 is a deep convolutional neural network known for its efficient architecture that uses parallel convolutional filters of different sizes within Inception modules to capture features at multiple scales. It employs techniques like factorized convolutions, auxiliary classifiers, and label smoothing to enhance performance and reduce computational cost. In this study, input images of size 224×224 were used, and global average pooling was applied to extract a 2048-dimensional feature vector per image, making InceptionV3 effective for detailed and scalable feature extraction in medical imaging.

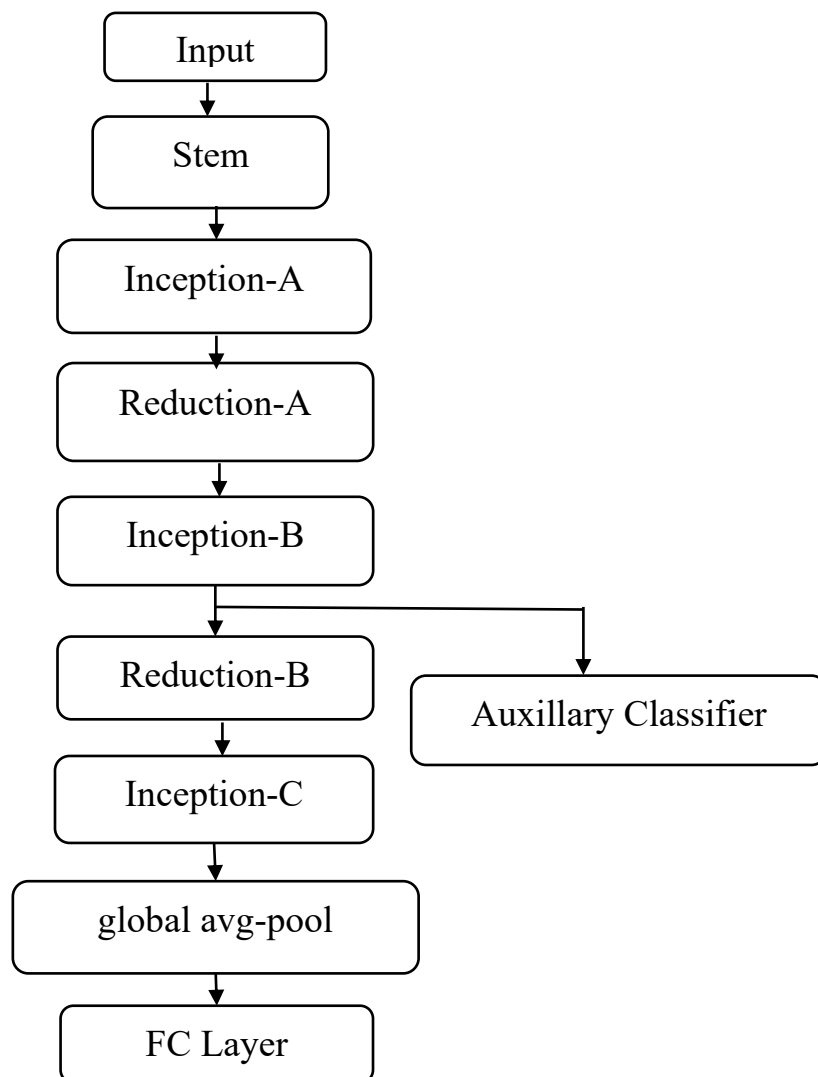


Figure 4.5. InceptionV3

4.2 PROPOSED WORK ARCHITECTURE

The proposed blood cell image classification system is designed as an ensemble learning model for multi-class classification, aimed at supporting the early detection of blood cancer. The system follows a modular approach, consisting of several stages, from raw image data processing to final classification. Each module is optimized for high accuracy, leveraging pre-trained Convolutional Neural Networks (CNNs) for robust feature extraction and XGBoost for meta-learning to perform the final classification.

The system architecture comprises the following key stages:

4.2.1 Data Ingestion

The input dataset includes images from blood cell samples, categorized into four diagnostic classes indicating different stages of blood cancer:

- **Benign:** Non-cancerous blood cells
- **Pre:** Pre-cancerous stage
- **Pro:** Pro-cancerous stage
- **Early:** Early stage of cancer

The images are sourced from a directory where each class has its subfolder. These images are read, converted to grayscale, resized to a uniform resolution of 224x224 pixels, and assigned appropriate labels. The data is then split into training, validation, and test sets for model development and evaluation.

4.2.2 Data Preprocessing

To prepare the dataset for effective training and improve model generalization, the following preprocessing steps were applied:

- **Resizing:** All images were resized to **224×224 pixels** to match the input requirements of the pre-trained convolutional neural networks (CNNs).

- **Data Augmentation:** To enhance the diversity of the training data and reduce overfitting, various augmentation techniques were applied using the Albumentations library:

- Random 90-degree rotations
- Horizontal flipping
- Brightness and contrast adjustments
- CLAHE (Contrast Limited Adaptive Histogram Equalization) for local contrast enhancement

- **Normalization:** Image pixel values were normalized by dividing by 255, scaling them to the $[0,1]$ range.

4.2.3 Data Splitting Strategy

The dataset consists of 3,266 labeled images, which are divided into three subsets using a two-phase stratified splitting approach to maintain class balance throughout the process:

Phase 1: Train-Test Split

- 80% of the dataset is allocated for training and validation: 2,449
- 20% is reserved for testing: 817

Phase 2: Train-Validation Split

From the 2,449 images in the training and validation set:

- 80% for training: 1959
- 20% for validation: 490

This results in approximately 60% training, 15% validation, and 25% testing. Such a three-way split ensures balanced representation of all classes, enabling robust training, effective hyperparameter tuning, and unbiased evaluation on unseen data.

4.2.4 Feature Extraction

Each image was passed through four pretrained CNN models: EfficientNetB7, ResNet152V2, DenseNet201, and InceptionV3 to extract rich and diverse high-level feature representations. All models had their top classification layers removed, and Global Average Pooling was applied to flatten the convolutional outputs:

- **EfficientNetB7** \rightarrow 2,560 features
- **ResNet152V2** \rightarrow 2,048 features
- **DenseNet201** \rightarrow 1,920 features
- **InceptionV3** \rightarrow 2,048 features.

4.2.5 Feature Concatenation and Label Encoding

The extracted feature vectors were then concatenated, resulting in a total of 8,576 features per image: $2560+2048+1920+2048 = 8576$ features

This concatenated vector forms a comprehensive and multi-perspective feature representation that leverages the complementary strengths of different CNN architectures for enhanced discrimination between blood cancer subtypes.

Features extracted from EfficientNetB7, ResNet152V2, DenseNet201, and InceptionV3 were concatenated into a single 8,576-dimensional vector for each image, combining diverse representations from all models. The categorical class labels were encoded using integer encoding (label encoding) to convert

them into numerical form, enabling multi-class classification with the XGBoost model.

4.2.6 Classification

The final classification is performed using an XGBoost meta-learner trained on the concatenated feature vectors extracted from four CNN models: EfficientNetB7, ResNet152V2, DenseNet201, and InceptionV3. The combined feature set is further split into training and validation subsets in an 80:20 ratio to monitor and evaluate the model's performance during training.

XGBoost is configured with optimized hyperparameters: `n_estimators=1600`, `learning_rate=0.05`, `max_depth=8`, `subsample=0.8`, and `colsample_bytree=0.8`. The `multi:softprob` objective function is employed for multi-class classification, enabling the model to output softmax-based probability distributions across the four diagnostic classes.

This approach effectively leverages the representational power of deep CNNs along with the strong classification performance of gradient boosting, allowing the model to capture complex patterns in the extracted features and deliver high-accuracy predictions.

4.2.7 Model Evaluation

Comprehensive evaluation is conducted to validate the model's performance. Key metrics include accuracy, precision, recall, F1-score, and AUC-ROC. These metrics are computed using scikit-learn and visualized using Matplotlib and Seaborn. Visual analysis includes training and validation accuracy/loss curves, confusion matrix heatmaps, and multi-class ROC curves. The system achieves a test accuracy of approximately 98, indicating highly reliable classification performance.

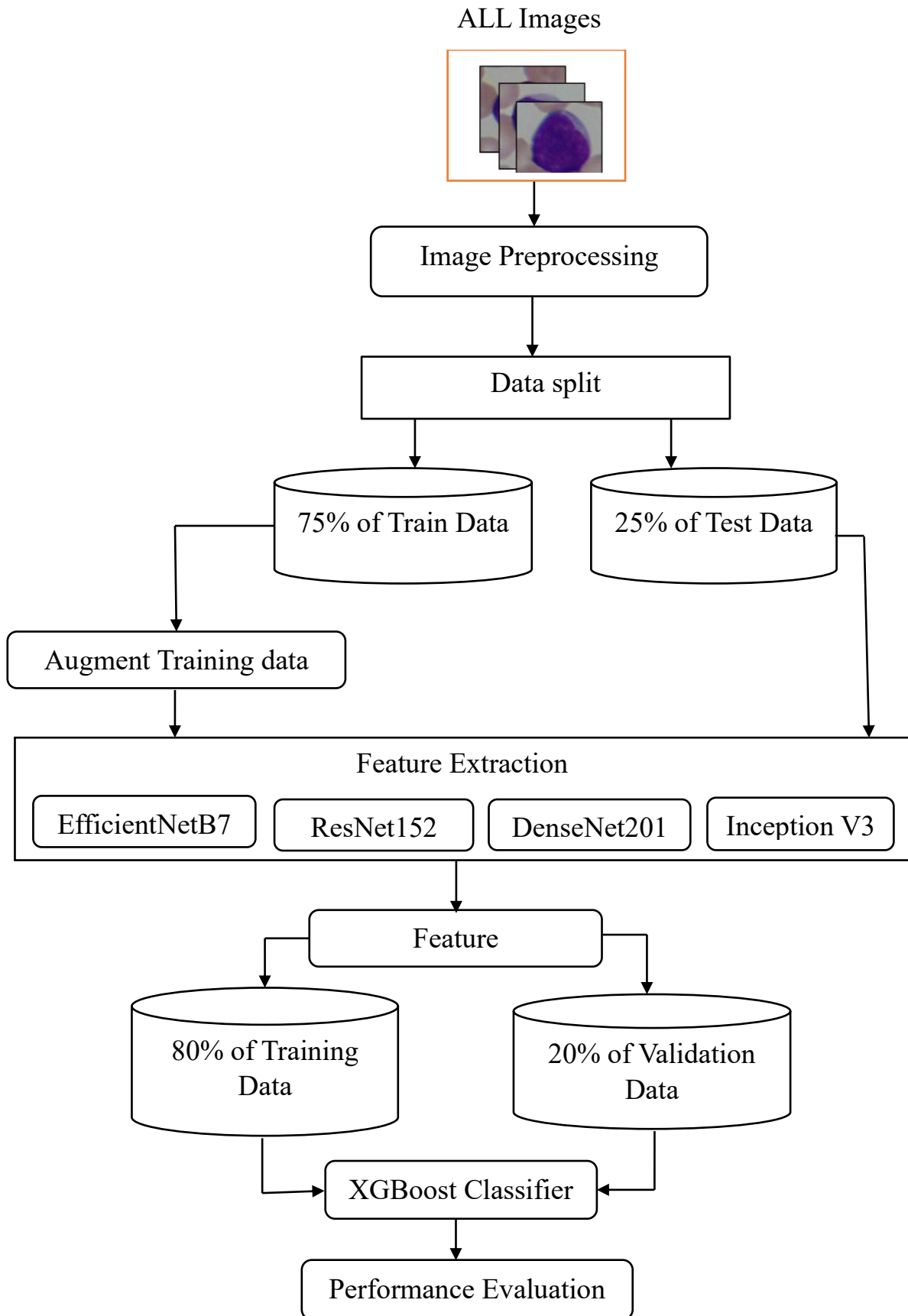


Figure 4.6. Proposed Work Architecture

4.3 ADVANTAGES OF PROPOSED WORK

The proposed blood cancer classification system incorporates advanced deep learning and ensemble methodologies, offering several key advantages over traditional single-model approaches:

- 1. Enhanced Generalization via Ensemble Feature Fusion:** By extracting and integrating features from multiple high-performing CNN architectures (EfficientNetB7, ResNet152V2, DenseNet201, and InceptionV3), the system captures a broader spectrum of discriminative patterns. This architectural ensemble significantly improves model generalization and robustness to variations in cell morphology across different classes.
- 2. Optimized Transfer Learning for Medical Imaging:** Leveraging pre-trained models fine-tuned on natural images enables effective knowledge transfer, which is particularly valuable given the limited size and diversity of labeled medical datasets. This approach reduces the need for large-scale annotated data and accelerates convergence during training.
- 3. High Classification Accuracy through XGBoost Meta-Learning:** The integration of XGBoost as a meta-classifier allows the system to learn complex, non-linear relationships between extracted deep features. Known for its strong performance on structured data, XGBoost enhances classification precision and supports multi-class discrimination with high fidelity.
- 4. Reduced Risk of Overfitting:** The combination of feature-level ensemble learning, data augmentation (e.g., rotation, contrast adjustment), and the decoupling of feature extraction from classification contributes to a lower risk of overfitting. This design ensures that the model maintains high performance even on unseen test samples.

- 5. Modular, Scalable Architecture:** The system's pipeline is modular, with clear separations between data preprocessing, feature extraction, and classification stages. This modularity facilitates future upgrades such as the addition of new feature extractors or classifiers without significant reengineering of the system.
- 6. Balanced and Reliable Training Strategy:** A rigorous training-validation-testing split ensures reliable model evaluation. The use of data augmentation further balances the class distribution and increases variability, strengthening the model's ability to generalize across diverse inputs.
- 7. Clinical Relevance and Practical Deployment Potential:** Designed with a focus on diagnostic utility, the system supports early-stage detection of blood cancer subtypes such as Benign, Pre-leukemic, Pro-leukemic, and Early leukemia stages. Its accuracy, specificity, and ease of integration into digital pathology workflows make it a viable tool for aiding clinical decision-making and supporting pathologists.

CHAPTER 5

IMPLEMENTATION

This chapter outlines the design and implementation details of the proposed system. It describes the system architecture, design methodology, and the steps taken to translate the conceptual model into a working application. The aim is to provide a detailed overview of how the system was developed and the technologies used.

5.1 SYSTEM REQUIREMENTS

A robust infrastructure is essential to support the computational demands of training and deploying deep learning models on clinical and imaging data.

5.1.1 Software Requirements

Operating System: Windows 10 / 11 or Ubuntu 20.04+ or macOS

Programming Language: Python 3.8 or above

Development Environment: Jupyter Notebook / Google Colab

Frameworks: TensorFlow 2.x, Keras

Libraries: OpenCV, NumPy, Pandas, Matplotlib, Seaborn, Scikit-learn, Albumentation

IDE / Notebook Environment: Google Colab or Jupyter notebook

Additional Tools:

- Google Drive (for dataset storage and loading)
- Git for version control

5.1.2 Hardware Requirements

CPU Processor: Intel i7+ or AMD Ryzen 7+

RAM: 16 GB or more

Storage: SSD with 256 GB+ free space

GPU: NVIDIA Tesla T4 or V100 with ≥ 16 GB VRAM

Internet Access: Required for using cloud-based tools like Google Colab and downloading pre-trained models

5.2 SOFTWARE SPECIFICATION

The software specification outlines the tools, frameworks, libraries, and other technologies used in the development and deployment of the proposed Alzheimer’s disease classification system. This section provides a detailed description of the software environment, ensuring reproducibility and clarity in the implementation process.

5.2.1 Google Colab

Google Colab is a cloud-based platform offering free access to GPUs and TPUs, making it ideal for rapid prototyping and experimentation with deep learning models. It provides high-performance computing capabilities for training complex models such as CNNs and ANNs on imaging and clinical data.

Colab also supports collaborative notebook sharing and editing, making it an excellent tool for joint research and experimentation. However, due to session timeout limitations, integrating periodic checkpointing (e.g., saving model weights with ModelCheckpoint) is crucial to avoid data loss and ensure continuity.

However, there are some limitations to be aware of. Colab sessions have timeouts, meaning that if a session is idle for too long or exceeds a certain runtime, it will automatically disconnect. This can lead to potential data loss if the work is not saved or checkpointed regularly. Therefore, it's essential to integrate checkpointing into the code to save the model and training progress at regular intervals. This ensures that in case the session disconnects, the work can be resumed from the last saved checkpoint, minimizing the impact of session timeouts

5.2.2 JupyterLab

JupyterLab is an open-source web-based interactive development environment (IDE) for data science and scientific computing. It serves as an enhanced version of the original Jupyter Notebook, providing a more feature-rich and flexible interface for working with code, data, and visualizations. JupyterLab is particularly favored for local development and experimentation, as it allows integration with a variety of programming languages and tools, including Python, R, and Julia.

One of the key features of JupyterLab is its integration with VSCode, allowing users to access the powerful debugging and code-editing capabilities of Visual Studio Code within the JupyterLab environment. This seamless integration enables more effective debugging, code navigation, and even version control support, providing a comprehensive development environment.

Another standout feature is its side-by-side view functionality, where users can work with multiple panels simultaneously. For example, you can have the code editor, output console, and visualization panels open side by side. This makes it easier to run and debug code while simultaneously visualizing results, enhancing the overall workflow efficiency. JupyterLab's flexible and extensible

nature also allows users to install additional extensions to tailor the environment to their specific needs, making it an adaptable platform for a wide range of tasks.

In summary, JupyterLab is an excellent choice for local experimentation, debugging, and visualization, providing a powerful environment for data analysis and machine learning model development.

5.2.3 Python

Python is a high-level programming language widely used in data science and deep learning due to its simplicity and vast ecosystem of libraries. In this project, Python was the main language used for all components, including data preprocessing, image augmentation, model integration, and performance evaluation. Libraries such as NumPy, Pandas, OpenCV, and Matplotlib enabled efficient handling of data, visualization, and image transformations. Its compatibility with frameworks like TensorFlow, Keras, and XGBoost made it ideal for building and managing the ensemble learning pipeline. Python's flexibility and ease of use were instrumental in implementing the complete classification system efficiently.

5.2.4 Supporting Libraries

A variety of Python libraries were used to support different stages of the project, including data handling, image processing, augmentation, visualization, and evaluation. These libraries played a crucial role in streamlining the workflow and enhancing model performance.

NumPy and SciPy

NumPy and SciPy are fundamental libraries for scientific computing in Python. NumPy provides powerful array structures and operations that enable

efficient numerical computation, which was essential for handling image data and intermediate feature arrays. SciPy builds on NumPy and offers additional tools for mathematical operations, such as optimization, interpolation, and statistical analysis. Together, these libraries formed the core of data manipulation and mathematical processing in the project.

Pandas

Pandas is a highly efficient library for data manipulation and analysis, particularly with tabular data. In this project, Pandas was used to manage metadata, image labels, and to structure data splits for training, validation, and testing. Its dataframes allowed for easy indexing, filtering, and merging of data, which helped streamline the preparation of input labels and ensured consistency throughout the modeling pipeline.

OpenCV

OpenCV (Open Source Computer Vision Library) is widely used for real-time image processing. It was utilized in this project to read, resize, convert, and manipulate medical image data. OpenCV made it simple to apply transformations such as grayscale conversion and image normalization, which were necessary to standardize the dataset before feeding it into deep learning models for feature extraction.

Albumentations

Albumentations is a fast and flexible image augmentation library that was used to increase dataset diversity and reduce overfitting. It provided advanced augmentation techniques such as horizontal and vertical flipping, brightness and contrast adjustments, rotations, and CLAHE (Contrast Limited

Adaptive Histogram Equalization). These transformations helped improve the robustness and generalization of the model by simulating variations in the training data.

Scikit-learn

Scikit-learn is a comprehensive library for classical machine learning and utility functions. In this project, it was used for encoding class labels, splitting the dataset into training, validation, and test sets, and evaluating model performance through metrics like accuracy, confusion matrix, and classification report. Its integration with other libraries like XGBoost also supported the implementation of the meta-classifier.

Matplotlib and Seaborn

Matplotlib and Seaborn are employed to create visual representations of performance metrics. These include plotting training and validation accuracy/loss curves, drawing confusion matrices as annotated heatmaps, and generating multi-class ROC curves with area-under-the-curve (AUC) scores for each class. These visualizations aid in evaluating both the convergence behavior of the model and its classification effectiveness.

5.3 DATA FLOW DIAGRAM

The proposed blood cancer classification system follows a structured data pipeline, starting with the ingestion of grayscale blood smear images resized to 224×224 pixels and categorized into four classes: Benign, Pre, Pro, and Early. During preprocessing, data augmentation techniques such as random rotations, horizontal flipping, CLAHE (Contrast Limited Adaptive Histogram

Equalization), and brightness/contrast adjustments are applied to enhance model generalization and address class imbalance. The dataset is split using a stratified approach into training, validation, and test sets, where 75% of the data is used for training and 25% for testing. The training set is further divided into 80% training and 20% validation subsets to ensure balanced class distribution.

Feature extraction is carried out by passing the images through four pre-trained CNN architectures: EfficientNetB7, ResNet152V2, DenseNet201, and InceptionV3, with their top classification layers removed. Global average pooling converts the convolutional features into fixed-length vectors, which are concatenated to form a comprehensive feature representation combining diverse learned patterns. Labels are encoded into numerical form to prepare for classification.

The classification module employs an XGBoost classifier trained on these fused feature vectors. The model uses carefully tuned hyperparameters such as learning rate, tree depth, and subsampling to effectively perform multi-class classification across the four blood cancer stages.

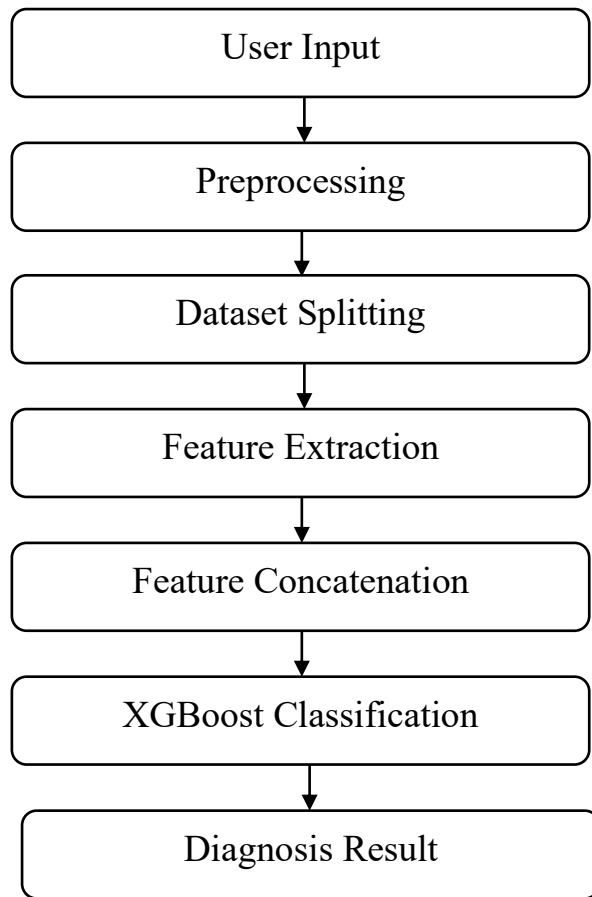


Figure 5.1. Data Flow Diagram

5.4 SYSTEM MODULES

5.4.1 Data Ingestion Module

Purpose: Load and organize images into a format usable for deep learning.




Implementation Details:

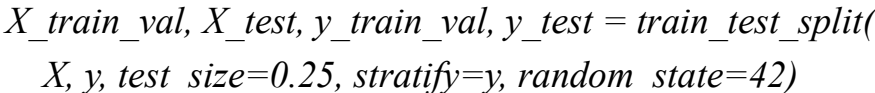
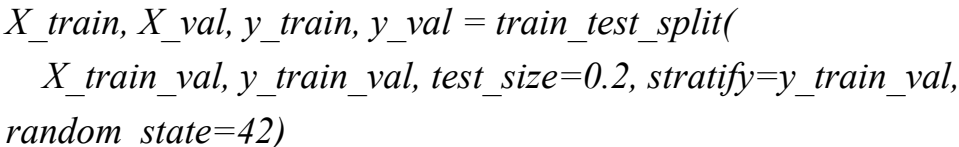
- Images are stored in class-specific folders: Benign, Pre, Pro, and Early.
- OpenCV (cv2) is used to load each image in RGB format (cv2.cvtColor(img,cv2.COLOR_BGR2RGB)), ensuring color consistency.

- Images are resized uniformly to 224×224 pixels using `cv2.resize()` to match CNN input requirements.
- Class labels are derived from folder names and mapped to numeric labels (e.g., via a Python dictionary).
- After loading, Scikit-learn's `train_test_split` function is applied twice with the `stratify` parameter to maintain class proportions:
 - Stage 1: 75% training, 25% testing split
 - Stage 2: Further split training data into 80% train and 20% validation, resulting in final splits of 60% training, 15% validation, and 25% testing.
- Dataset and labels are typically stored as NumPy arrays (`numpy`) for efficient manipulation and optionally saved using `np.save()` for reuse.

Python Code:

```
from sklearn.model_selection import train_test_split
import cv2
import numpy as np

# Read and resize images




# Stratified splitting example


```

5.4.2 Preprocessing Module

Purpose: Prepare image data for robust learning by applying transformations and normalization.

Implementation Details:

- All images are resized to 224×224 and converted to RGB (if necessary).
- Pixel intensities are normalized to the range [0, 1] (e.g., dividing by 255) to stabilize training.
- Albumentations library is used for fast, flexible, and GPU-accelerated augmentations, applied only to training data to improve generalization. Augmentations include:
 - Random rotations and flips
 - CLAHE (Contrast Limited Adaptive Histogram Equalization) for local contrast enhancement
 - Brightness and contrast adjustments
- Labels are encoded numerically using Scikit-learn's LabelEncoder for compatibility with machine learning models.

5.4.3 CNN Feature Extraction Module

Purpose: Extract deep features from images using pre-trained CNNs.

Implementation Details:

- Pre-trained models are loaded from TensorFlow Keras Applications without top classification layers (include_top=False).

- A GlobalAveragePooling2D layer is appended to convert spatial maps into fixed-length vectors.
- Models used: EfficientNetB7 (2560 features), ResNet152V2 (2048), DenseNet201 (1920), InceptionV3 (2048).
- Images are fed through each model separately to generate feature vectors, leveraging transfer learning from ImageNet weights.

Python Code:

```
from tensorflow.keras.applications import EfficientNetB7, ResNet152V2,
DenseNet201, InceptionV3
from tensorflow.keras.layers import GlobalAveragePooling2D
from tensorflow.keras.models import Model

base_model = EfficientNetB7(weights='imagenet', include_top=False,
input_shape=(224,224,3))
x = GlobalAveragePooling2D()(base_model.output)
model = Model(inputs=base_model.input, outputs=x)
features = model.predict(preprocessed_image)
```

5.4.4 Feature Fusion Module

Purpose: Combine features from multiple CNNs into a single feature vector.

Implementation Details:

- Feature vectors from each CNN are concatenated horizontally using NumPy (np.concatenate) along the feature axis.

- This produces a comprehensive 8576-dimensional feature vector, enriching the representation by leveraging the complementary strengths of different CNN architectures.
- The fused vector serves as the input for the final classifier.

Python Code:

```
import numpy as np

fused_features = np.concatenate([feat_efficientnet, feat_resnet,
feat_densenet, feat_inception], axis=1)
```

5.4.5 XGBoost Classification Module

Purpose: Classify fused features into one of the four cancer stages.

Implementation Details:

- XGBoost (xgboost Python package) is employed for its efficiency and ability to handle high-dimensional data.
- Model parameters include:
 - `n_estimators=1600` (number of trees)
 - `learning_rate=0.05`
 - `max_depth=8`
 - `subsample=0.8` and `colsample_bytree=0.8` for better generalization
- Multi-class soft probability (multi:softprob) objective outputs class probabilities, from which the highest is selected as the predicted class.

5.4.6 Training and Validation Module

Purpose: Monitor and optimize model performance.

Implementation Details:

- Training is conducted on the training set, with validation data used for hyperparameter tuning and overfitting control.
- Early stopping monitors validation loss to halt training if no improvement is seen over a predefined number of rounds.
- Model evaluation metrics include accuracy, precision, recall, F1-score, and confusion matrices, calculated with Scikit-learn's metrics module.

5.4.7 Deployment Module

Purpose: Enable real-time use of the trained model for predictions.

Implementation Details:

- The trained XGBoost model is saved using joblib or pickle (.pkl files).
- CNN feature extractors are saved as TensorFlow SavedModel format for reloading.
- The prediction pipeline includes: loading and preprocessing images, extracting features from CNNs, fusing features, and applying the XGBoost classifier to predict classes.
- This pipeline can be wrapped into a web service using frameworks like Flask or Streamlit for user-friendly interfaces.

5.4.8 Monitoring and Maintenance Module

Purpose: Ensure continued reliability and improvement of the deployed system.

Implementation Details:

- Real-time monitoring tracks accuracy, precision, recall, and inference latency.
- Error logs and user feedback identify misclassified cases for review and potential retraining.
- Scheduled retraining updates the model with new data patterns.
- System resource usage is monitored to maintain scalability.
- Version control manages model updates and rollback capability.
- Data privacy and security compliance are enforced, especially for clinical environments.

CHAPTER 6

RESULT AND ANALYSIS

6.1 PERFORMANCE METRICS

To evaluate the classification performance of the CNN model, several statistical metrics were used. These include Sensitivity (Recall), Precision, Specificity, Accuracy, and F1 Score. These metrics are critical in medical diagnosis applications where both false negatives and false positives can have significant consequences.

Sensitivity (Recall)

Sensitivity, also known as recall, measures the proportion of actual positive cases correctly identified by the model. It evaluates the model's ability to detect positive instances.

Equation:

$$Recall = \frac{TP}{TP+FN}$$

Precision

Precision quantifies the proportion of correctly predicted positive observations among all predicted positive observations. It is especially useful in scenarios where false positives are costly.

Equation:

$$Precision = \frac{TP}{TP+FP}$$

Specificity

Specificity evaluates the model's ability to correctly identify negative cases, focusing on true negatives. This is especially useful in distinguishing between affected and unaffected cases.

Equation:

$$Specificity = \frac{TN}{TN+FP}$$

Accuracy

Accuracy is the overall correctness of the model and is defined as the ratio of correctly predicted instances (both positives and negatives) to the total instances.

Equation:

$$Accuracy = \frac{TP + TN}{TP + TN + FP + FN}$$

F1 Score

The F1 Score is the harmonic mean of precision and recall. It balances the two, making it a useful metric when there's class imbalance.

Equation:

$$F1 = 2 \times \frac{Precision \times Recall}{Precision + Recall}$$

Confusion Matrix

The confusion matrix below summarizes the performance of the trained model across four diagnostic categories: Benign, Pre, Pro, Early. Each cell

represents the count of predictions for a given actual vs. predicted class combination.

6.2 MODEL EVALUATION

- **Test Accuracy:** The model achieved a final accuracy of 98.65%, demonstrating strong predictive performance on unseen data.
- **Classification Metrics:** A detailed classification report and confusion matrix were generated, showing high precision, recall, and F1-scores across all four classes (Benign, Pre, Pro, Early).
- **ROC-AUC Performance:**
 - Macro-Averaged AUC: 0.9996
 - Weighted-Averaged AUC: 0.9996
- **Specificity:**
 - Macro Average Specificity: 0.9954
 - Weighted Average Specificity: 0.9952

These evaluation metrics highlight the model's excellent generalization ability and robust discriminative power, with consistent and reliable performance across all blood cancer stages.

6.3 TRAINING DETAILS

- **Device Used:** CPU/GPU (depending on Google Colab environment; XGBoost supports GPU acceleration when available)

- **Input Features:** Concatenated deep features extracted from EfficientNetB7, DenseNet201, ResNet152V2, and InceptionV3
- **Training-Validation Split:** 80% training and 20% validation from the training portion (stratified to maintain class balance)
- **Model:** XGBoost Classifier using the multi:softprob objective for multi-class classification
- **Hyperparameters:**
 - `n_estimators = 1600`
 - `learning_rate = 0.05`
 - `max_depth = 8`
 - `subsample = 0.8`
 - `colsample_bytree = 0.8`
- **Evaluation Metric:** Accuracy, precision, recall, F1-score, and ROC-AUC evaluated post-training

6.4 EVALUATION METRICS

Evaluation on the test set (2560 samples) yielded the following metrics:

Classification Report Summary:

- Precision, Recall, and F1-score all exceeded 0.97 for all classes.
- Macro Average Specificity: 0.9954
- Weighted Average Specificity: 0.9952

Table 6.1. Classification Metrics of Proposed Work

Class	Precision	Recall	F1-Score
Benign	0.98	0.97	0.97
Pre	1.00	0.99	0.99
Pro	0.99	0.99	0.99
Early	0.98	0.99	0.98

- Overall Test Accuracy: **98.65%**

6.5 CONFUSION MATRIX

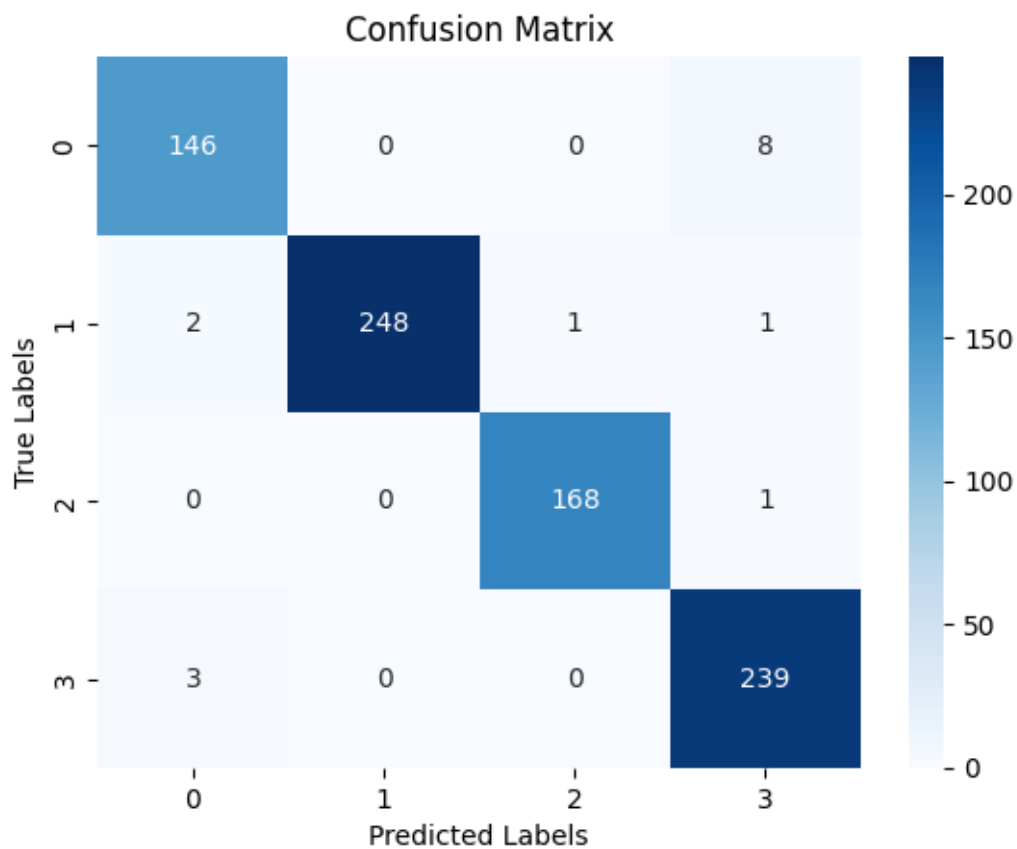


Figure 6.1. Confusion Matrix of Proposed Work

This confusion matrix demonstrates very low misclassification rates, with only a few confusions mainly occurring between the Benign and Pre stages. Such overlaps are understandable given the subtle visual differences in these early disease stages, highlighting the model's strong discriminative capability across all classes.

6.6 ROC CURVE AND AUC ANALYSIS

To evaluate the discriminative power of the proposed ensemble CNN-XGBoost model beyond traditional accuracy, Receiver Operating Characteristic (ROC) curves and Area Under the Curve (AUC) scores were computed for each class, along with macro and weighted averages.

ROC Curve

- ROC curves plot the True Positive Rate (TPR) against the False Positive Rate (FPR) at various classification thresholds.
- An ideal model generates a ROC curve that arcs toward the top-left corner, indicating high sensitivity and low false positives.

In this study:

- A One-vs-Rest (OvR) strategy was employed for each of the four classes: Benign, Pre, Pro, and Early stages of blood cancer.
- The predicted class probabilities from the XGBoost classifier were used to construct the ROC curves.
- The ROC curves were visualized using matplotlib, with a separate curve for each class.

AUC (Area Under the Curve)

- AUC quantifies the overall ability of the model to distinguish between classes.
- A value closer to 1.0 implies outstanding classification capability.

Results:

- **Macro-Averaged AUC: 0.9996**
 - Gives equal importance to all classes regardless of their frequency.
- **Weighted-Averaged AUC: 0.9996**
 - Takes into account class distribution, giving more weight to frequent classes.

ROC Curve Visualization

The ROC visualization included:

- Separate ROC curves for each class (Benign, Pre, Pro, Early)
- A diagonal dashed line to represent random classification (AUC = 0.5 baseline)
- A legend displaying AUC values for each class individually
- Curves plotted in distinct colors to enhance clarity

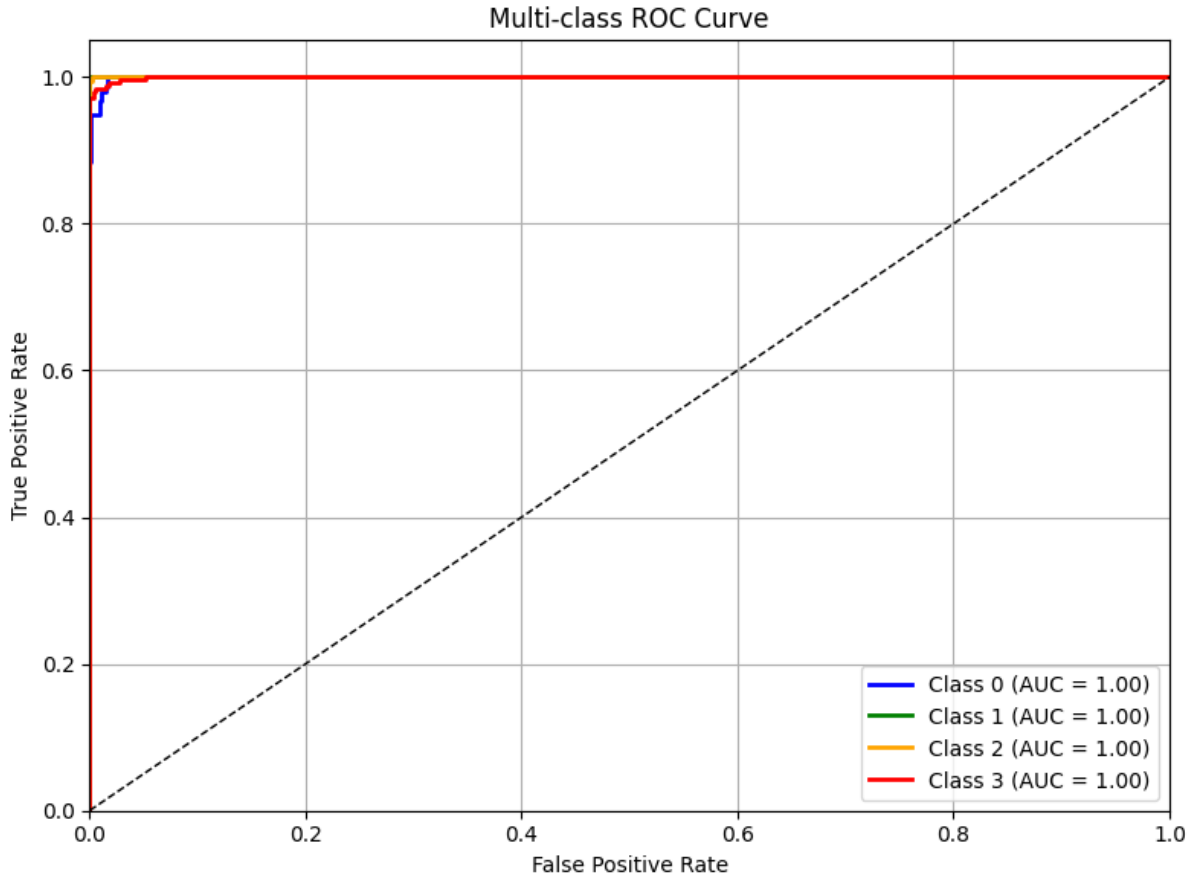


Figure 6.2. Multi-Class ROC Curve of Proposed Work

6.7 PERFORMANCE COMPARISON

Table 6.2 presents a succinct comparison of the overall performance between the DL4ALL architecture and proposed model.

Table 6.2. Performance Comparison Across Existing and Proposed model

Metric	DL4ALL	Proposed CNN–XGBoost
Accuracy	0.98	0.99
Precision	0.99	0.99
Recall	0.96	0.99
F1 Score	0.98	0.99

Across all performance metrics, the proposed model outperforms DL4ALL, demonstrating its superiority in classifying different stages of blood cancer. Notable improvements include:

- **Accuracy:** A 1% increase, indicating more correct predictions on the test set.
- **Sensitivity (Recall):** A 3% gain, suggesting better identification of cancerous cases and reducing false negatives.
- **Specificity:** A marginal yet important improvement from 0.99 to 0.995, enhancing the model's ability to correctly identify non-cancerous samples.

These enhancements are primarily attributed to:

- The integration of features from four powerful CNN architectures: EfficientNetB7, ResNet152V2, DenseNet201, and InceptionV3.
- The use of Albumentations for effective data augmentation, which improves generalization.
- The XGBoost classifier, known for its robustness in handling high-dimensional, tabular feature sets and managing class imbalance.
- Rigorous tuning and validation, ensuring optimized model performance across diverse samples.

Thus, the proposed approach provides a more accurate and reliable tool for aiding pathologists in the early detection and classification of blood cancer.

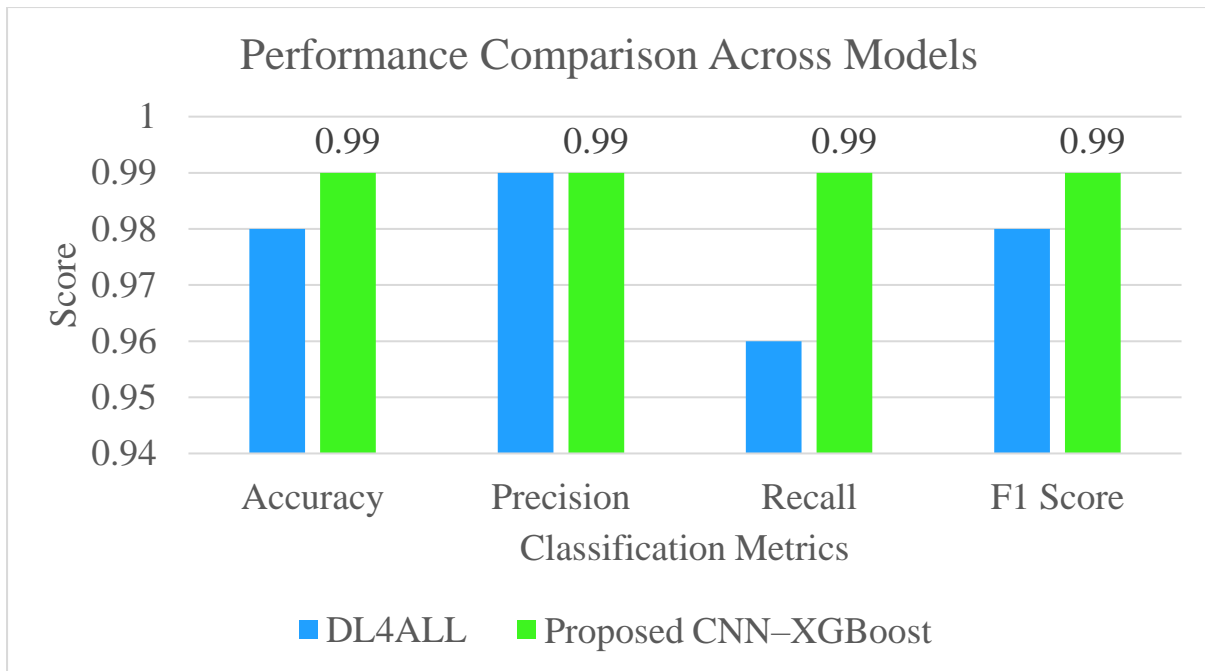


Figure 6.3. Performance Comparison Across Existing and Proposed model

The bar chart compares the classification performance of two models—DL4ALL and the Proposed CNN-XGBoost—across four key evaluation metrics: accuracy, precision, recall, and F1 score. The Proposed CNN-XGBoost consistently scores 0.99 on all four metrics, while DL4ALL shows slightly lower values, achieving 0.98 for accuracy and F1 score, and 0.96 for recall, although precision remains equal at 0.99 for both models.

This consistent performance advantage indicates that the Proposed CNN-XGBoost not only excels in accurately identifying the majority of samples but also achieves a better balance between false positives and false negatives. The higher recall (0.99 vs. 0.96) especially suggests that CNN-XGBoost is more effective at detecting true positive cases, which is critical in medical diagnostics such as blood cancer detection. Overall, the results highlight the robustness and reliability of the CNN-XGBoost framework over DL4ALL.

CHAPTER 7

CONCLUSION AND FUTURE ENHANCEMENT

7.1 CONCLUSION

This study presents a high-performance ensemble deep learning framework for the automated detection of Acute Lymphoblastic Leukemia (ALL) using microscopic blood smear images. The proposed system effectively combines four state-of-the-art pre-trained Convolutional Neural Networks (CNNs): EfficientNetB7, ResNet152V2, DenseNet201, and InceptionV3. Each network contributes distinct capabilities in capturing complex spatial, morphological, and textural characteristics from the input images. These diverse feature representations are concatenated to form a unified high-dimensional feature vector that is further refined to reduce redundancy and enhance discriminative capability. This optimized feature vector is classified using an XGBoost classifier, which is fine-tuned through grid search and regularization techniques to achieve high generalization and robustness.

The proposed ensemble model demonstrated outstanding performance in the classification of ALL. It achieved an overall accuracy of 98.65 percent, precision of 98.65 percent, recall of 98.54 percent, and F1 score of 98.59 percent. The macro-averaged ROC AUC score of 0.9996 further indicates the model's high discriminative power. Additionally, the model attained remarkable specificity values for each class: 99.55 percent for Benign, 99.82 percent for Pre-leukemia, 99.85 percent for Pro-leukemia, and 98.96 percent for Early leukemia. This resulted in a macro average specificity of 99.54 percent and a weighted average of 99.52 percent, underscoring the model's balanced performance in both sensitivity and specificity — crucial factors in clinical diagnostics to minimize missed cases and false positives.

When compared to the existing DL4ALL model, which reported 98 percent accuracy, 96 percent sensitivity, and 99 percent specificity, the proposed system showed consistent improvements across all key performance indicators. These results validate the effectiveness of the CNN-XGBoost ensemble architecture. Its high accuracy, balanced diagnostic metrics, and robustness position it as a highly reliable tool for clinical decision support in hematological malignancy diagnosis.

7.2 FUTURE ENHANCEMENT

While the proposed ensemble model for leukemia detection has demonstrated exceptional performance, there remain several opportunities to extend and enhance its capabilities. One major area for future work involves expanding the dataset to include additional subtypes of leukemia and more diverse demographic and clinical characteristics. A more comprehensive dataset would improve the model's ability to generalize across various manifestations of the disease and enhance its real-world applicability in broader patient populations.

Another important direction is the incorporation of temporal data to analyze disease progression over time. By integrating sequential medical imaging or clinical history, the system could transition from static classification to dynamic monitoring, thereby offering insights into disease stages and treatment efficacy. Such functionality would be invaluable in clinical settings where continuous patient monitoring is critical for effective management of leukemia.

Improving model interpretability is also a key consideration. Although the ensemble architecture offers high accuracy, its black-box nature may hinder clinical adoption. Techniques such as SHAP (SHapley Additive exPlanations) and Grad-CAM (Gradient-weighted Class Activation Mapping) can be employed to visualize and explain the decision-making process of the model. Enhancing

interpretability can build trust among healthcare professionals and support regulatory compliance for AI-driven medical tools.

Moreover, deploying the model in accessible, user-friendly platforms such as mobile or web-based interfaces could democratize expert-level diagnostics, particularly in remote or low-resource environments. Such deployment would make it possible for non-specialist clinicians or technicians to leverage advanced AI tools without the need for extensive infrastructure.

Lastly, efforts could be directed toward optimizing the model for deployment on edge devices through techniques like model pruning, quantization, or knowledge distillation. These improvements would ensure the system remains computationally efficient while maintaining its diagnostic precision, paving the way for scalable, real-time leukemia detection in diverse clinical settings.

APPENDIX

SOURCE CODE

```
import os

import numpy as np

import cv2

import tensorflow as tf

from sklearn.model_selection import train_test_split

from tensorflow.keras.applications import EfficientNetB7, ResNet152V2,
DenseNet201, InceptionV3

from tensorflow.keras.layers import GlobalAveragePooling2D

from tensorflow.keras.models import Model

from sklearn.metrics import accuracy_score, precision_score, recall_score,
f1_score, classification_report, confusion_matrix, roc_curve, auc,
roc_auc_score

from sklearn.preprocessing import label_binarize

from xgboost import XGBClassifier

from albumentations import Compose, RandomRotate90, HorizontalFlip,
CLAHE, RandomBrightnessContrast

from tqdm import tqdm

import matplotlib.pyplot as plt

import seaborn as sns
```

```

IMG_SIZE = 224

datadir = r'/content/drive/MyDrive/bloodcancer/Original'

categories = ['Benign', 'Pre', 'Pro', 'Early']

# Load images

images = []

labels = []

def create_training_data():

    for category in categories:

        path = os.path.join(datadir, category)

        class_num = categories.index(category)

        for img in os.listdir(path):

            try:

                img_array = cv2.imread(os.path.join(path, img)) # Load in RGB

                if img_array is None:

                    print(f'Warning: Failed to load image {img}')

                    continue

                new_array = cv2.resize(img_array, (IMG_SIZE, IMG_SIZE))

                images.append(new_array)

                labels.append(class_num)

            except Exception as e:

                print(f'Error processing image {img}: {e}')

    return

```

```

create_training_data()

x = np.array(images)

y = np.array(labels)

# Print counts before split

print(f"Total images before split: {len(x)}")

# Train-test split

X_train, X_test, y_train, y_test = train_test_split(x, y, test_size=0.25,
random_state=42)

print(f"Training set size: {X_train.shape[0]}")

print(f"Testing set size: {X_test.shape[0]}")

# Albumentations augmentation

augment = Compose([

    RandomRotate90(),

    HorizontalFlip(),

    CLAHE(clip_limit=2.0),

    RandomBrightnessContrast(p=0.2)])

def augment_data(images):

    return np.array([augment(image=img)['image'] for img in images])

# Apply augmentation

X_train = augment_data(X_train)

X_test = augment_data(X_test)

# Normalize

```

```

X_train = X_train / 255.0

X_test = X_test / 255.0

# Build feature extractor

def build_feature_extractor(base_model):

    x = base_model.output

    x = GlobalAveragePooling2D()(x)

    return Model(inputs=base_model.input, outputs=x)

# Initialize pre-trained models

efficientnet = build_feature_extractor(EfficientNetB7(weights='imagenet',
include_top=False, input_shape=(IMG_SIZE, IMG_SIZE, 3)))

resnet = build_feature_extractor(ResNet152V2(weights='imagenet',
include_top=False, input_shape=(IMG_SIZE, IMG_SIZE, 3)))

densenet = build_feature_extractor(DenseNet201(weights='imagenet',
include_top=False, input_shape=(IMG_SIZE, IMG_SIZE, 3)))

inception = build_feature_extractor(InceptionV3(weights='imagenet',
include_top=False, input_shape=(IMG_SIZE, IMG_SIZE, 3)))

# Feature extraction

def extract_features(model, data, name='Model'):

    features = []

    for i in tqdm(range(0, len(data), 32), desc=f"Extracting with {name}"):

        batch = data[i:i+32]

        features.append(model.predict(batch, verbose=0))

    return np.concatenate(features)

```



```

features = [
    extract_features(model, X_train, name=name)
    for model, name in zip([efficientnet, resnet, densenet, inception],
                           ['EfficientNetB7', 'ResNet152V2', 'DenseNet201',
                           'InceptionV3'])]

X_train_combined = np.concatenate(features, axis=1)

# Meta-learner train-validation split

X_train_meta, X_val_meta, y_train_meta, y_val_meta = train_test_split(
    X_train_combined, y_train, test_size=0.2, random_state=42)

print(f'Meta-training set size: {X_train_meta.shape[0]}')

print(f'Validation set size: {X_val_meta.shape[0]}')

# Train XGBoost meta-classifier

xgb_model = XGBClassifier(
    n_estimators=1600,
    learning_rate=0.05,
    max_depth=8,
    subsample=0.8,
    colsample_bytree=0.8,
    objective='multi:softprob',
    num_class=len(np.unique(y_train)),
    verbosity=1)

xgb_model.fit(X_train_meta, y_train_meta)

```

```

# Evaluate on meta-validation set

val_pred = xgb_model.predict(X_val_meta)

print("Validation Accuracy:", accuracy_score(y_val_meta, val_pred))

# Extract test features

test_features = [

    extract_features(model, X_test, name=name)

    for model, name in zip([efficientnet, resnet, densenet, inception],

                           ['EfficientNetB7', 'ResNet152V2', 'DenseNet201',

                             'InceptionV3'])]

X_test_combined = np.concatenate(test_features, axis=1)

# Final predictions

test_pred = xgb_model.predict(X_test_combined)

print("Test Accuracy:", accuracy_score(y_test, test_pred))

# Metrics

precision = precision_score(y_test, test_pred, average='macro')

recall = recall_score(y_test, test_pred, average='macro')

f1 = f1_score(y_test, test_pred, average='macro')

print(f"Precision: {precision:.4f}, Recall: {recall:.4f}, F1-Score: {f1:.4f}")

print("\nClassification Report:\n", classification_report(y_test, test_pred))

# Confusion Matrix

cm = confusion_matrix(y_test, test_pred)

sns.heatmap(cm, annot=True, cmap='Blues', fmt='d')

```

```

plt.title('Confusion Matrix')

plt.xlabel('Predicted Labels')

plt.ylabel('True Labels')

plt.show()

# ROC Curve

test_pred_proba = xgb_model.predict_proba(X_test_combined)

y_test_bin = label_binarize(y_test, classes=[0, 1, 2, 3])

n_classes = y_test_bin.shape[1]

fpr = dict()

tpr = dict()

roc_auc = dict()

for i in range(n_classes):

    fpr[i], tpr[i], _ = roc_curve(y_test_bin[:, i], test_pred_proba[:, i])

    roc_auc[i] = auc(fpr[i], tpr[i])

plt.figure(figsize=(8, 6))

colors = ['blue', 'green', 'orange', 'red']

for i in range(n_classes):

    plt.plot(fpr[i], tpr[i], color=colors[i], lw=2, label=f'Class {i} (AUC = {roc_auc[i]:.2f})')

plt.plot([0, 1], [0, 1], 'k--', lw=1)

plt.xlim([0.0, 1.0])

plt.ylim([0.0, 1.05])

```

```

plt.xlabel('False Positive Rate')

plt.ylabel('True Positive Rate')

plt.title('Multi-class ROC Curve')

plt.legend(loc="lower right")

plt.grid(True)

plt.tight_layout()

plt.show()

# Macro and weighted ROC-AUC

macro_roc_auc = roc_auc_score(y_test_bin, test_pred_proba, average='macro',
multi_class='ovr')

weighted_roc_auc = roc_auc_score(y_test_bin, test_pred_proba,
average='weighted', multi_class='ovr')

print(f'Macro-Averaged ROC-AUC: {macro_roc_auc:.4f}')

print(f'Weighted-Averaged ROC-AUC: {weighted_roc_auc:.4f}')

def compute_specificity(y_true, y_pred, class_names=None):

    cm = confusion_matrix(y_true, y_pred)

    num_classes = cm.shape[0]

    specificities = []

    supports = []

    for i in range(num_classes):

        TP = cm[i, i]

        FP = cm[:, i].sum() - TP

```

```

FN = cm[i, :].sum() - TP
TN = cm.sum() - (TP + FP + FN)
specificity = TN / (TN + FP) if (TN + FP) > 0 else 0
specificities.append(specificity)
supports.append(cm[i, :].sum())

macro_specificity = np.mean(specificities)
weighted_specificity = np.average(specificities, weights=supports)

print("Per-class Specificity:")
for i, spec in enumerate(specificities):
    label = class_names[i] if class_names else str(i)
    print(f" Class {label}: {spec:.4f}")

print(f"\nMacro Average Specificity: {macro_specificity:.4f}")
print(f"Weighted Average Specificity: {weighted_specificity:.4f}")

return specificities, macro_specificity, weighted_specificity

```

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