An Optimized Deep Learning Framework for Classification and Detection of Acute Lymphoblastic Leukemia (ALL)

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DEDICATION

“In the name of Allah, the most Beneficent, the most Merciful"

Glory be to **Allah Almighty**, the Creator and Sustainer of the universe. His divine guidance and blessings have been the cornerstone of this endeavor. I dedicate this thesis to my family, friends, and teachers who supported me each step of the way, especially **my parents**.

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Abstract

Keywords: Leukemia, CNN, feature fusion, accuracy, classification.

Acute Lymphoblastic Leukemia (ALL) a medical threat which principally affects the pediatric population, demands early diagnosis for fruitful treatment results. Deep learning models have set a really high standard in medical imaging by providing extensive applications for the identification and categorization of ALL. Over time, convolutional neural networks (CNN) have made significant stature in medical image analysis, especially when it comes to detection and categorization of ALL. The proposed study presents a pioneering classification model, XIncept-ALL, which benefits from the transfer learning technique. Furthermore, by improving generalization with incorporation of valuable traits extracted a diverse dataset, the projected model mitigates the concerns of overfitting with the help of two pre-trained models, Inception and Xception, both of which are trained on the widespread ImageNet dataset. Additionally, through merger of distinctive features extracted from both models, the proposed system is expected to refine feature representation and overall performance by using feature fusion. Nevertheless, the anticipated model proves itself as a unique and remarkable framework with not only an exceptional accuracy of 99.0% on the ALL dataset, but also the capability to classify various ALL subtypes (Benign, Earl, Pre-Acute and Pro-Acute) with unequalled correctness within a single classifier. Our results show the superior performance of XIncept-ALL for accurate and rapid effective classification of acute lymphocytes images, thereby highlighting its competence as an efficient diagnostic tool. Furthermore, this model has the potential to be employed in diverse medical imaging contexts, beyond leukemia.

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List of Abbreviations and Acronyms

Acute Lymphoblastic Leukemia	ALL
Acute Myelogenous Leukemia	AML
Chronic Lymphoblastic Leukemia	CLL
Chronic Myelogenous Leukemia	CML
Acute Lymphoblastic Leukemia International Database	ALL-IDB
Convolutional Neural Network	CNN
Artificial Neural Network	ANN
Machine Learning	ML
Deep Learning	DL
Disseminated Intravascular Coagulation	DIC
Hue Saturation Value	HSV
Gaussian Blurring	GB
Computer Aided Design	CAD
Efficient Channel Attention	ECA
Analysis of Variance	ANOVA
Adaptive Network-Based Fuzzy Inference Systems	ANFIS
Global Average Pooling	GAP
Support Vector Machine	SVM
Long Short-Term Memory	LSTM
Rectified Linear Unit	ReLU
Gaussian Error Linear Unit	GELU
Peripheral Blood Smear	PBS
Neural Search Architecture Network	NASNet

Chapter 1

Introduction

Cancer is the considered to be one of the foremost causes of death worldwide. One of the deadliest types of cancer is Acute Lymphoblastic Leukemia (ALL). ALL is a blood cell cancer that begins from the bone marrow and is characterized by an uncontrolled, accelerated growth of immature blood cells that affects both children and adults. The three primary components of blood have varying weights: red blood cells, plasma, and white blood cells (WBC). One WBC for every 100 red blood cells, or approximately 1% of the blood, are WBCS cells [1]. WBCs consists of five different types and there is a standard count of each type of these from the total WBC count. Any change in the percentage of each type is considered an abnormality that can lead to immune disorders. These include basophils, eosinophils, neutrophils, lymphocytes, and monocytes. According to the total WBC count, the standard counts for these cells are 60%, 30%, 5%, 4%, and less than 1%, correspondingly [2]. Any abnormalities in these counts can be considered as a probable sign of cancer. The abnormality in the WBC count can be related to the production of other unwanted cells. The overproduction of cells, sometimes referred to as blasts or leukemic cells, causes them to hinder normal hematopoiesis and push out healthy leukocytes in the bone marrow. This makes it more difficult for the body to fight infections and control bleeding [3].

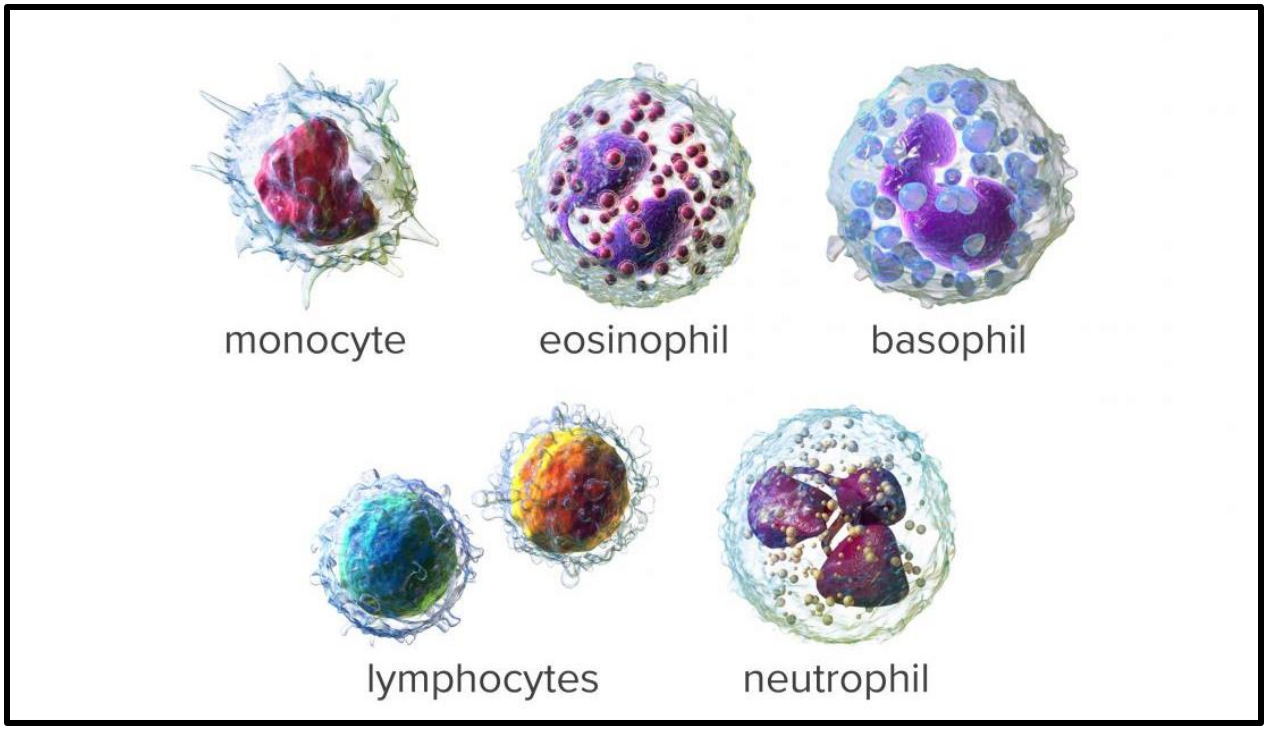

Figure 1.1: Different Types in White Blood Cell (WBC)

In ALL the malignant WBC are produced. These malignant cells attack normal blood cells which may cause death as a worst-case scenario. Malignant WBC also causes other types of deadly illnesses by travelling through the circulation thus harming the liver, spleen, kidneys, brain, and other organs. Leukemia is a deadly disease and the most common one disease between children and adults. It is linked to cancer that primarily arises from the production of immature white blood cells by the bone, which subsequently compromises the immune system [4]. It can be divided into four types: chronic myelogenous leukemia (CML), acute lymphoblastic leukemia (ALL), acute myelogenous leukemia (AML), and chronic lymphocytic leukemia (CLL). ALL being one of the most prevalent cancers affecting children has a decent chance of being cured. However, adults may also experience this, but the prospects of a recovery are minimal if discovered at a later stage. Direct blood infusions into veins, chemotherapy, and any type of transplant that involves moving organs or tissues inside the body or from one person to another are all forms of treatment for acute lymphocytic leukemia. For doctors to detect this kind of disease. stained blood smear microscopy

pictures are manually evaluated to provide the first diagnosis of ALL. This method can cause an error in diagnosing the disease and requires an expert eye to detect the disease. This method is also quite time consuming.

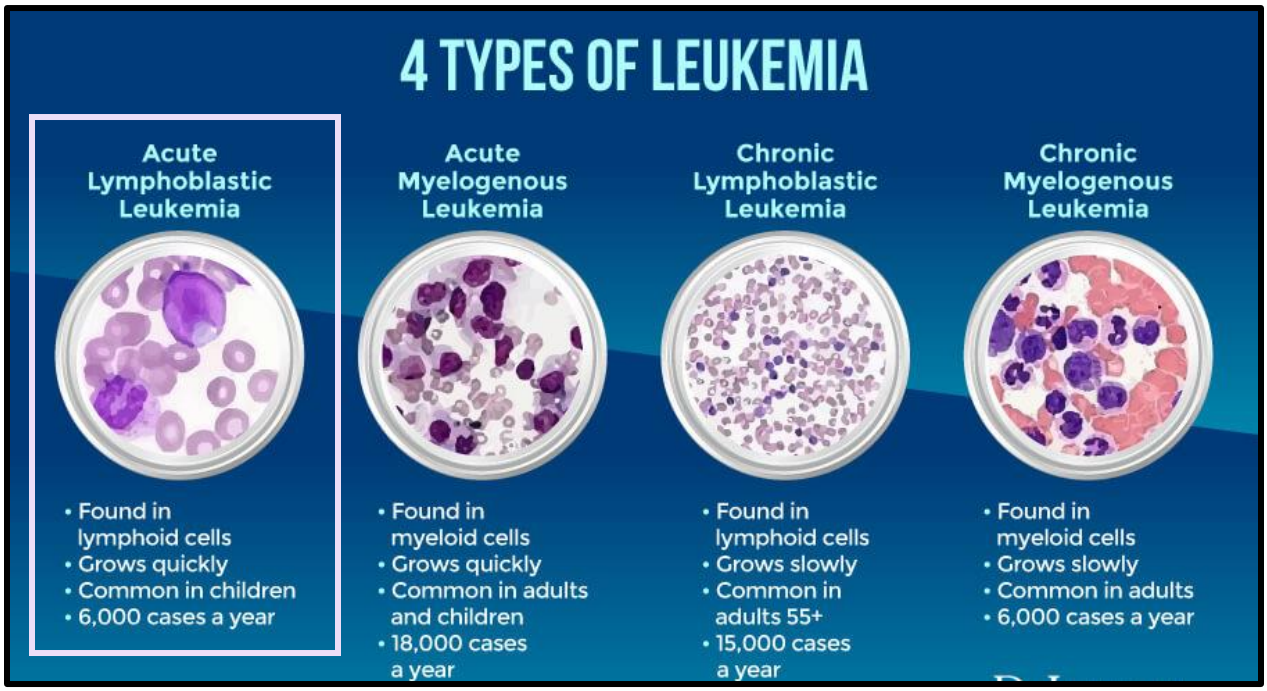

Figure 1.2: Types of Leukemia

It is imperative to develop a model capable of effectively handling images acquired under various environmental conditions. This is to ensure that the limitations of existing techniques and systems are addressed. To solve this issue computer aided design tools are usually proposed. Automated analysis is provided by computer vision techniques, which can aid in the diagnosis of this illness by professionals. These tools help doctors diagnose the disease at early stage and hence increase the patient's survival rate. There are many tools in literature that provide an automated system for diagnose of this disease. These systems rely on deep learning models to classify images.

1.1 Medical Background Information about Acute Lymphoblastic Leukemia

The malignancy known as acute lymphoblastic leukemia (ALL) affects B or T lymphoblasts and is typified by the unchecked growth of aberrant, immature lymphocytes and their progenitors. This finally leads to the replacement of additional lymphoid organs and parts of the bone marrow, resulting in a distinctive pattern of illness.

The following are some of the medical information about ALL:

1. Signs and symptoms: Bone marrow infiltration and/or extramedullary illness are frequently observed in patients with ALL. Anemia, thrombocytopenia, and neutropenia are symptoms of bone marrow failure that individuals experience when leukemic blasts replace their bone marrow. Additionally, people may exhibit fever, bleeding, blood clots, disseminated intravascular coagulation (DIC) and anemia symptoms such tiredness, pallor, palpitations, heart murmur, and dyspnea even with little exercise.

2. Treatment: The subtype of ALL, the patient's age, and the existence of certain genetic abnormalities are some of the variables that affect how an individual with ALL is treated. Utilizing risk-adapted treatment methods has reduced medication toxicity while increasing cure rates. Treatment options for pediatric ALL include chemotherapy, stem cell transplantation, and radiation treatment.

3. Prognosis: Various factors, including the patient's age, subtype of ALL and presence of specific genetic anomalies contribute significantly to the prognosis of ALL. Enhanced diagnostic techniques and therapeutic interventions have led to significant advancements, resulting in a remarkable 90% overall cure rate among pediatric patients diagnosed with acute lymphoblastic leukemia [5]. Different classes of ALL are shown in **Figure 1.3**.

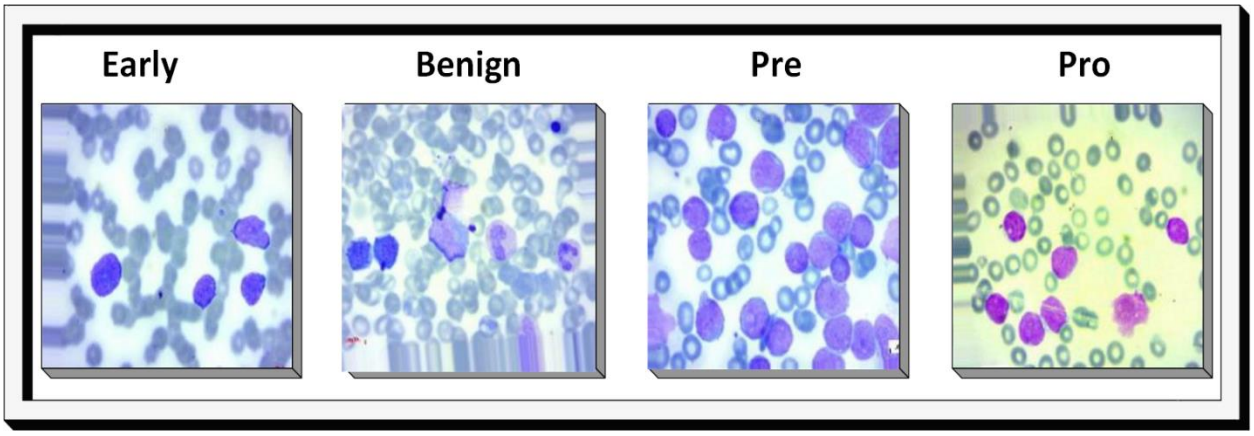

Figure 1.3: A Visual Diagram of Benign, Early Lymphoblastic Leukemia, Pre-Acute and Pro-Acute Lymphoblastic Leukemia via Diagnosis by Images

Understanding the medical information behind ALL is crucial for healthcare professionals and patients to develop effective treatment plans and manage the physical and emotional challenges associated with this disease.

1.2 Background

Numerous studies on the subject of white blood cell classification can be found in the literature. Earlier methods classify the blood picture data by combining a machine learning model with an image processing technique. In [6] a traditional approach of ALL classification is proposed which involves using a handcrafted image features extraction method along with support vector machine classifier. The authors of [7] offer yet another technique for using SVM classifiers to identify acute lymphoblastic leukemia (ALL), in which the classifier is trained using the geometrical and statistical characteristics of nuclei. In [8] the authors present a proposal using handcrafted quantitative features to build a system for automatic cell image recognition. For the purpose of detecting pediatric ALL, tests with a variety of models are presented in [9]. Based on the results

of these experiments, it is determined that the CART model was the most appropriate model for the dataset used in the study.

In [10] an automatic approach for classifying ALL from blood smear images using ML algorithms combined with digital image processing techniques is presented. The method makes use of a three-phase filtration algorithm and thorough preparation. From the picture, sixteen manually created features are extracted out and fed into SVM and ANN classifiers. Recent papers have effectively applied deep learning-based approaches to ALL classification. Numerous cell categorization tasks have seen successful training and testing of pretrained CNNs. In [11] the authors use pretrained Deep learning models (GoogleNet, AlexNet, and ResNet-101) to build a system for white blood cells (WBCs) classification. The authors compare between the models in terms of classification accuracies. In [12] the authors propose a comparison between conventional digital image processing approaches and deep learning architectures for the task of classifying WBCs. The results prove the superior performance of deep learning architectures over traditional methods. A customized CNN architecture for classifying WBCs cells is presented in [13]; High accuracy scores are obtained by this design in multiclass and binary classification scenarios.

In [14] a novel system that combines ResNet and Inception networks for WBCs classification is proposed. In the preprocessing phase, the suggested method additionally makes use of a number of augmentation strategies. CNNs use hierarchical topological feature extraction to classify WBCs. A model that uses the most important features of a color picture to detect ALL is provided in [15]. The suggested technique consists of four basic stages: accuracy measurement, feature extraction, segmentation, and improvement. The ALL-IDB dataset's highest accuracy was archived using the suggested approach. The authors of [16] suggest a comparison study of several approaches for the early identification of ALL. This study compares and analyses the various phases of the diagnostic process. A methodology for recognizing ALL using WBC microscopic pictures is presented in [17]. For classification, four distinct ML models are used, and the results are compared. The

authors find that the SVM model provided the best accuracy for the used dataset based on the experimental results.

The work in [18] provides a unique method for segmenting the WBC's cytoplasm and nucleus. The work evaluates several approaches utilized in the literature to segment WBCs. The microscopic images are then classified into the four classes of ALL using supervised classification models constructed to extract characteristics. The authors of [19] suggest using an aggregated pretrained CNN algorithm to identify ALL in microscopic WBC images. The authors prevent overfitting by employing a number of data augmentation strategies. The VGG19 and NASNetLarge collectively make up the grid, which is applied for classification. As a result, the overall accuracy achieved by the final collaborative models was calculated to be higher as compared to the individual networks. An in-depth synopsis of the trends and techniques used to identify Leukemia from microscopic images have been described in [20–22].

1.3 Research Motivation

Despite advancements in varied methodologies for diagnosing ALL considerable challenges still persist. Even with the application of sophisticated image processing technologies during and after image acquisition, accurately delineating distinctive abnormal features in images related to normal cases pose a significant challenge. The intricacies involved in precisely identifying and extracting relevant features associated with ALL contribute to the complexity of this task. Publicly available datasets encompass a diverse range of images. Therefore, feature extraction of pertinent and valuable traits is crucial. Consequently, computerized systems encounter difficulties in precisely diagnosing the symptoms associated with ALL. This research has a dual objective. Firstly, it aims to construct a comprehensive dataset for the classification of benign, early, pre-acute and pro-acute lymphoblastic leukemia. Secondly, the study seeks to develop feature fusion model deep learning (DL) model capable of autonomously interpreting images relevant to ALL. To achieve this, a

hybrid model called XIncept is proposed, engaging two pre-trained models from the ImageNet dataset: Inception and Xception. This work is significant as it proposes an innovative classification system for ALL, potentially offering real-world implications in medical diagnosis and treatment.

1.4 Research Contribution

In this research, a novel system (XIncept-ALL) is premeditated to address the challenging task of ALL classification. This research focuses not only on enhancing the robustness of machine learning-based classification of ALL images but also to increase the generalizability. In order to complete this aim, a diverse dataset has been used. Additionally, a machine learning model, though highly complex but capable of efficiently processing such varied data has been developed. This tedious task is achieved by classifying available data into Benign, Early, Pre-Acute and Pro-Acute using the proposed architecture. The combination formed by using this diverse dataset along with a robust model is intended to improve the performance and significantly alleviate the reliability classification system for ALL images. The following points are the XIncept-ALL system's important contributions points.

1. Integration of Inception and Xception blocks was used to formulate a multilayer architecture of the XIncept-ALL system. To identify any illness affiliated with ALL, Inception blocks were added to the multifaceted formation of the XIncept-ALL model. This approach led to the development of a multi-layered architecture that proved adept at effectively addressing the classification challenge.
2. The classification approach proposed in this study for ALL relies on deep features and color space phases, constituting the core of the methodology. An intricate color scheme and various deep features were made the foundations of the classification technique employed in the projected model. To the best of the author's knowledge there is no work in literature that works more efficiently than the proposed systems.

3. Our system has exhibited superior performance compared to other state-of-the-art methods proposed in the current literature, achieving a significantly higher accuracy rate since the proposed model (XIncept-ALL) is trained with a large dataset of ALL images. The significance of this extensive dataset is crucial in empowering the trained model to attain exceptionally high classification accuracy.

1.5 Paper Organization

This thesis is divided into seven chapters:

1. **Chapter 1**: This chapter includes the basic introduction, background, research motivation and research contribution.
2. **Chapter 2**: This chapter provides an overview of relevant literature, encompassing articles pertinent to the scope of this study.
3. **Chapter 3**: This chapter presents the material and methods.
4. **Chapter 4**: This chapter delivers the experimental results.
5. **Chapter 5**: This chapter describes the discussion.
6. **Chapter 6**: This chapter presents a comparative analysis between our research and the latest advancements in the field.
7. **Chapter 7**: This chapter concludes the report and highlights the direction for future work.

Chapter 2

Literature Review

Plentiful research studies have explored the identification of ALL, employing various methodologies and technologies critical for enhancing the precision and efficiency of disease diagnosis. This section summarizes papers from literature that apply deep learning models on the (ALL) classification problem.

2.1 Advanced Techniques in ALL Diagnosis using CNNs

In [23] a novel automated system for diagnosis of acute lymphoblastic leukemia (ALL) using CNN is proposed. The fundamental layer of a CNN architecture is the convolutional layer, tasked with extracting image features from input images. To generate diverse image feature outcomes, a convolution layer generally employs multiple convolution kernel filters. Next comes the layer that plays a role in reducing the dimensionality of extracted features and compressing data to avoid overfitting. The pooling layer, also referred to as the down-sampling layer, plays a role in reducing the dimensionality of extracted features and compressing data to prevent overfitting, enhancing the model's fault tolerance. We utilize max-pooling, and the final results of the object classification function are generated by the fully connected dense layer. Image classification occurs in this layer by amalgamating the feature data from each neuron in the top layer. With the exception of the final weighted layer, the layers of the CNN architecture are set to a not-trainable mode to ensure optimal performance. Typically, a CNN architecture comprises three main layers. The convolutional layer, serving the purpose of extracting image features from input images, employs multiple convolution kernel filters to produce diverse image feature results. However, the use of DL comes with its own set of concerns, including aspects related to clinical implementation as well as technically ensuring

that everything runs smoothly. Other similar challenges include conveying the findings of algorithm, considerations related to legality of processes and finally difficulties in convincing people to adopt artificially intelligent algorithms. These individuals range from doctors and physicians to patients. Researchers have found applications of deep learning in several fields such as speech recognition and natural language processing. Similarly, image recognition in another area impacted by it however, the healthcare industry has only recently started to witness its impacts.

The model was made capable to work on labelled microscopic blood images to recognize malignant leukemic cells obtained from a database called ALL-IDB. In this model, in order to quantity the obtained data from said dataset, the authors perform multiple data augmentation procedures which also helps in reducing the issue of over-training the model. Through a five-fold validation process, the model was trained on 515 photos, achieving 95.54% accuracy rate. The model has been tested on the remaining 221 photos, obtaining nearly 100% accuracy during the majority of the trials, retaining an average of 99.5% accuracy. The approach effectively uses unprocessed data without the requirement for pre-processing or segmentation. Thus, using this technique can help pathologists accurately diagnose ALL. In [24] a novel system for ALL classification is proposed. The initial step of the system is preprocessing of image. The authors use Gaussian Blurring (GB) method for enhancing the image before classification. The Gaussian Blur technique is employed to lessen the noise/ irrelevant fragments in an image. The picture is then subjected to a segmentation phase employing the Hue Saturation Value (HSV) technique and morphological stage. The HSV method works in three steps representing colors that matches with how human eye perceives a color. Starting off with Hue, a channel which performs color encoding when translated from RGB. As a second step, saturation codes the purity and intensity of the color. Lastly, value encrypts the brightness, gloss and shading features of a color. Grouping of two datasets with real-time is used by authors to evaluate their proposed model. A total of 190 images (89 cancerous images and 101 non-cancerous images) are taken for experimentation. In order to

improve and enhance the quality of dataset images, various pre-processing techniques including edge smoothing, noise removal and contrast enhancement are used. Overall, the system achieved an accuracy of 96.30% on author' dataset, while achieving 95.41% accuracy on ALL-IDB1 dataset.

In [25] a novel diagnostic model based on CNN is projected. The suggested approach is built on deep learning processing of medical images. The authors have used C-NMC 2019 for training their model which is a publicly available dataset. The main goal of this research is to create a computer-aided design (CAD) which would facilitate in differentiation of leukemic cells in images pf blood clotting from normal cells. In this study, a non-invasive diagnostic method based on CNN is presented which consists of a CNN-based model, uses the visual geometry group from Oxford (VGG16) and an attention module called Efficient Channel Attention (ECA) to extract better quality deep features from the image dataset, improving feature representation and classification outcomes. The attention module used by the authors forces the system to learn the high-level features. The proposed technique shows how the ECA module helps in minimizing morphological similarities between photos of healthy and cancerous cells. Using a range of augmentation techniques also increases the quantity and quality of training data. As for the performance evaluation, five metrics including accuracy, sensitivity, precision, specificity and F1 score are used by the authors. In [26] a novel algorithm for classification of leukemic cells to healthy and non-healthy blood cells is proposed. The algorithm is implemented with CNN to predict the disease from microscopic images. The trained system reached maximum accuracy of 95.54% on a dataset procured from "ALL Challenge Dataset of ISBI, 2019"' which contains cell images belonging to both healthy individuals and patients diagnosed with ALL. Imbalance in images of dataset was removed using various augmentation techniques namely vertical horizontal flipping, clockwise and anti-clockwise rotation, random brightness adjustments and Gaussian blur. Moreover, auto-orientation and resizing were used to remove bias from images. For this research, segmented while blood cell regions are used for CNN categorization of leukemia. Advantage of this work is that it

is capable to operate on all available data while reducing the error rate and computational time during the screening process. In summary, these studies collectively showcase diverse approaches and technologies in the field of oncology for detecting and diagnosing a wide spectrum of cancers. They underscore the potential of artificial intelligence, deep learning, and automated diagnostic systems in enhancing accuracy, objectivity, and efficiency in disease diagnosis, ultimately benefiting patients and healthcare practitioners alike.

2.2 Progressive Ensemble and ML Practices for ALL Identification

In [27] an ensemble automated prediction model is proposed. C-NMC leukemia dataset publicly available in Kaggle repository is employed by authors to evaluate the performance of their model for detection of leukemia. The system is first built using a data preprocessing step in which the image is cropped in order to exclude the noisy data which adversely affects the performance of the model. Generally, all useful information obtained from raw data is acquired using machine learning (ML) models on the dataset. After data preprocessing step, feature extraction is performed using pre-trained convolutional neural network architectures (VGG19, ResNet50 or ResNet101). The MinMaxScaler normalization technique is used to scale the data. For feature selection methods, the authors employed random forest, recursive feature removal, and analysis of variance (ANOVA). Selected features must exhibit relevant traits that helps classify data into classes or groups ultimately facilitating decision-making to attain high accuracy. Ensemble voting of the classifications machine learning algorithms is applied which shows that SVM can reach 90% accuracy.

Manual examination and dependence on experience of medical specialists for detection of ALL are time-consuming conventional methods. Automated detection systems are introduced to minimize human intervention and provide more accurate clinical outcomes. In order to automatically identify ALL, a novel method based on ML algorithms and digital image processing

techniques is presented in [28]. In order to get the best segmentation results, a pre-processing step using three phase filtering algorithms is suggested following a segmentation step to tackle this issue. Moreover, to increase the capability of classifiers to better recognize leukemic cells in images, 16 robust features were extracted from available images. For classification of images two machine learning classifiers (ANN, SVM) are proposed which utilize the whole range of samples from dataset to find the optimal characteristics possessed by both classifiers. The authors used a local dataset for training and testing of their procured from University Hospital Ostrava. Native experts performed manual examination on blood smear images using multiple morphological methods to differentiate between normal and leukemic cells. Standard arithmetic operations are employed as pre-processing steps to enhance the quality of images in dataset. The system achieved 98.25% and 100% accuracies respectively. Afterwards, the authors also carried out a reverse analysis to determine the primary failures encountered in the classification process. In [29] novel modifications to conventional neural network architectures are implemented. In this study, two datasets namely ALL-IDB1 and ALL-IDB2 containing blood smear images of normal individuals and leukemic patients along with cropped images featuring relevant parts of an image are used to evaluate the performance and efficiency of the proposed model. As far as the training of the model is concerned, authors employed another dataset called C-NMC 2019 which consists of images of both healthy and leukemic cells. Various data augmentation methods and image transformation practices including mirroring, rotation and Gaussian blurring are used to balance dataset images for proper training and validation of the model. The modifications suggested by authors result in good performance in classification of malignant leukocyte. Some of the image processing steps applied to images are spinning, fading, shearing, and inserting salt-and-pepper noise. The testing model used for testing are VGG16, VGG19, and Xception. Moreover, the proposed model uses achieves f1-score of 92.6 using data augmentation.

2.3 Innovative DL Models for Enhanced ALL Classification

In [30] the authors propose a new hybrid model for the classification of ALL disease. In this model, the residual convolutional neural network (CNN), ResNet-50V2 is trained with the GA method to determine the optimal hyperparameters that maximize accuracy. The reason for using GA is to ensure accurate predication which would lead to highest accuracy rate. This method of using optimization algorithms is normally used instead of tuning values obtained manually which is a time-consuming task and does not always result in best accuracies. A striking accuracy of 98.4% is achieved by the authors by employing GA optimization for enhancing the accuracy of the classifier. In [31] an explainable system for ALL classification is applied. This study proposes novel deep learning model for ALL classification that is extremely accurate and understandable due to the visual aids added to the model. The proposed model is trained and tested on digitalized images of blood/ bone marrow from 6 diverse databases. Images available in each database have distinct characteristics such as saturation, color of image, size of image, number of images, illumination etc. The authors employed 7 of the most widely used performance metrics to evaluate the efficiency of their model which include accuracy, precision, recall, specificity, dice similarity coefficient and intersection over union. The study suggests a leveraging robust segmentation of White Blood Cell (WBC) nuclei as a stringent attention mechanism within an Explainable AI (XAI) framework for leukemia classification, aiming to address this challenge effectively. Achieving WBC segmentation is facilitated by integrating image processing and U-Net methodologies, thereby bolstering the system's overall efficacy.

This study [32] proposes a variant of deep neural networks called (ALNett) model that uses depth-wise convolution with different dilation rates to categorize images of tiny white blood cells. Convolution, max-pooling, and normalization are the specific cluster layers that are used to accurately predict ALL by taking powerful local and global information from the microscopic blood images. These layers also give richer structural and contextual data. When compared with

other models including VGG16, ResNet-50, GoogleNet and AlexNet, the model's performance was impressive. Based on metrics such as precision, recall, accuracy, F1 score, loss accuracy, and receiver operating characteristic (ROC) curves, the suggested ALNett model produced the maximum classification accuracy of 91.13% and an F1 score of 0.96 with reduced computational complexity, according to experimental data. ALNett outperformed the other training networks and showed promising ALL classification.

2.4 Latest Advancements in ALL Detection and Categorizations

In [33] a new deep learning model system is executed to classify the images of C-NMC 2019 and ALL-IDB2 datasets with high efficiency and accuracy. In the proposed system blood micrographs were enhanced and the WBC-only areas were then extracted using the active contour approach and sent to three different CNN models (ResNet50, DenseNet121, and MobileNet) for additional analysis. In this study, a novel hybrid model was developed by integrating CNN-RF and CNN-XGBoost techniques, marking the inaugural attempt at analyzing ALL images within the two datasets. Deep feature maps are extracted in this hybrid model using the DenseNet121, ResNet50, and MobileNet models. With redundant and insignificant features, these CNN models generate large feature counts. To ensure the selection of highly representative features, deep feature maps extracted by CNN were subjected to Principal Component Analysis (PCA). From there, the features were given to the classifiers (RF,XGBoost) for classification.

In [34] the advancement of cutting-edge medical technology, especially when it comes to the crucial area of leukemia research; its detection and diagnosis. The convolution technique, which is frequently applied in this field, might result in human mistake. In order to diagnose and categorize leukemia cases, instruments such as the Adaptive Network-Based Fuzzy Inference Systems (ANFIS) are used to handle this problem. ANFIS is a useful tool because of its reputation for function approximation. Nevertheless, its accuracy could be improved. An enhanced ANFIS (I

ANFIS) model is suggested in order to get over this restriction. By comparing training and test feature data, it makes use of Euclidean distance to predict leukemia data. Noteworthy in our findings is the demonstrated efficacy and utility of our study, emphasizing that features obtained through deep learning. Our overarching objective is to enhance the prospects for timely intervention and improved outcomes by advancing the early detection of ALL through the fusion of computer science and medical imaging. For a detailed overview of research findings related to the identification and classification of ALL, refer to **Table 2.1**.

Table 2.1. Contributions and Outcomes of Different Articles for the Classification of ALL Images

Authors	**Publication Year**	**Contribution**	**Results**
Vaghela, Himali P [1]	2020	Used CNN for classification of ALL disease	99.5% in average of all trials
Alexandrea Bodzas [28]	2020	Used neural network and support vector machine as a classifier for their own dataset	The neural network model achieved 97.5% which is better than the SVM model
Zakir Ullah [25]	2021	Performed attention enhancement of VGG6	91.1% on C-NMC 2019
de Oliveira [29]	2021	Made small modifications to different neural network models (VGG16, VGG19, Xception) and used image augmentation methods to balance the training and validation sets	Accuracy is not reported however the model achieves f1-score of 92.6

Larissa Ferreira Rodrigues [30]	2022	Used genetic algorithm to optimize deep residual neural network	98.46%
Ghada Atteia [35]	2022	Tuned the hyperparameters of CNN using Bayesian optimization algorithm	100% accuracy on ALL-IDB dataset
Ahmad Almadhor [27]	2022	Contrasted several machine learning algorithms such as RF, SVM, KNN, and NB, as well as ensemble voting classifiers using predefined CNN architectures (VGG16, ResNet50, or ResNet101) for feature extraction methods	Superior performance of the SVM model over other techniques reaching 90% on C-NMC 2019 is reported.
Ibrahim Abdulrab Ahmed [33]	2023	After merging DenseNet121-ResNet50-MobileNet's deep features map, RF or XGBoost were used to classify the data	Accuracy 98.8% on C-NMC 2019 Accuracy 100% on ALL-IDB2
Tulasi Gayatri Devi [24]	2023	Proposed a novel GBHSV-Leuk to detect an classify ALL disease The method consists of two stages Gaussian blurring	Using the ALL-IDB1 public dataset, the accuracy was 95.41%.

		technique and Hue Saturation Value (HSV) technique	
Jose Luis Diaz Resendiz [31]	2023	Implemented an explainable model to solve the problem of black-box and used novel image segmentation technique combining image processing and U-net techniques	Accuracy 98.51 % on ALL-IB2
M.Anline Rejula, [34]	2023	Classification of ALL using improved ANFIS	Accuracy 97.4% on ALL image dataset

Chapter 3

Materials and Methods

The proposed architecture of this work is illustrated in **Figure 3.1.** To improve picture visualization, a pretreatment procedure is applied once the image is first obtained using appropriate image processing techniques. Subsequently, the deep learning model under discussion is deployed to detect features within the images and identify the most relevant features for Acute lymphoblastic leukemia (ALL) classification. Finally, a XGBoost classifier is utilized to categorize the image into distinct ALL-related categories. This paper introduces the XIncept-ALL system for the categorization of blood related illnesses, specifically ALL. The XIncept-ALL system leverages the InceptionV3 model and Xception model. Deep learning is instrumental in extracting meaningful characteristics from the computer-Aided Diagnosis (CAD) system. In order to retain an already learned model on ALL dataset, transformation learning is employed. The XIncept-ALL architecture, designed for extracting relevant ALL characteristics from images, comprises six major phases as depicted in **Figure 3.1**. The properties derived from both the InceptionV3 model and Xception model are synergistically combined. Notably, the proportions of the thick blocks continuously evolve during the training process. The classifier layer, is incorporated as the final step to detect the image as Benign, Early Lymphoblastic Leukemia, Pre-Acute and Pro-Acute. The XGBoost classification process, thereby enhances overall classification outcomes.

An outstanding feature of the innovative model under study, which combines Inception and Xception architectures, lies in its extensive empirical validation. Through a multitude of comprehensive studies spanning diverse datasets and real-world applications, the combined model consistently exhibits superior performance compared to conventional methods. The robust empirical evidence holds particular significance in the domains of deep learning and computer

vision. Moreover, this hybrid model demonstrates high resource efficiency, rendering it well-suited for deployment in resource-constrained environments, such as edge devices, where computational and memory constraints are critical considerations. In addition to its enhanced efficiency, the model stands out for improved interpretability, a crucial aspect in industries like healthcare and autonomous driving. The elucidation of the decision-making process, achieved through the integration of blocks from Inception and Xception components, proves pivotal for applications where trust and safety are paramount concerns.

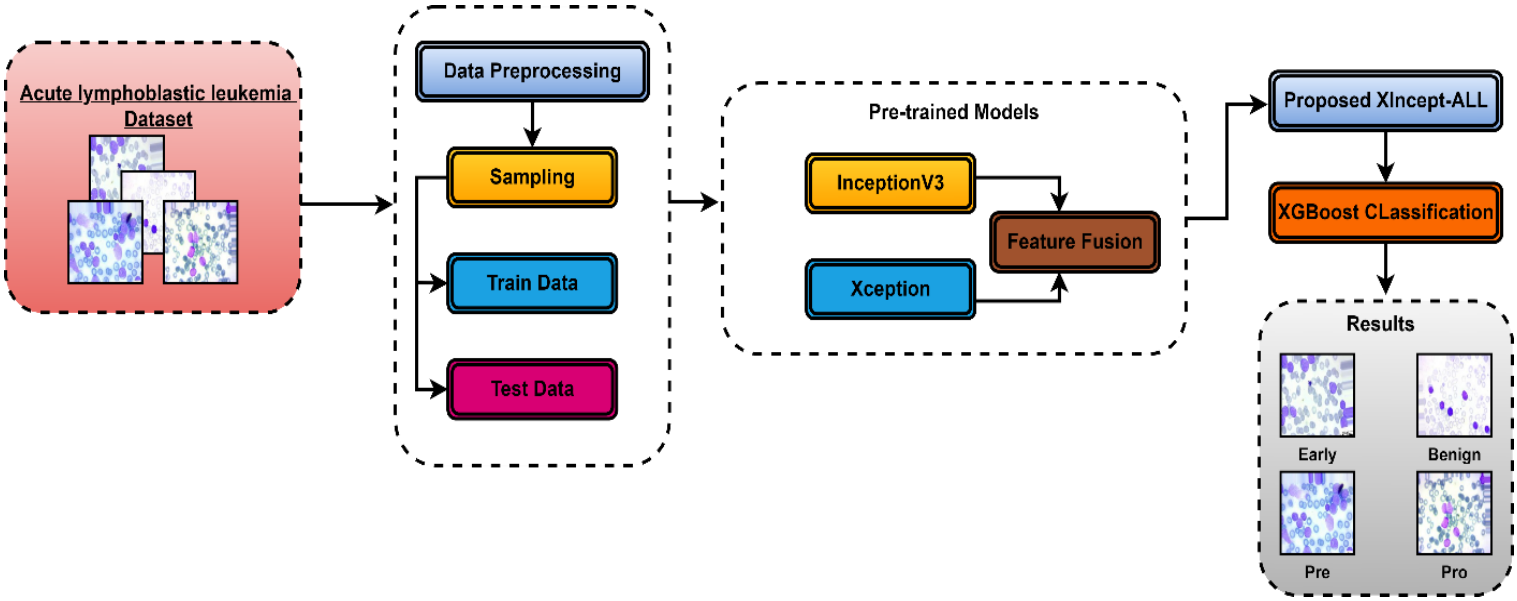

Figure 3.1: Block Diagram of a Proposed XIncept-ALL Model

3.1 Dataset

The dataset under consideration was meticulously curated within the bone marrow laboratory of Taleghani Hospital in Tehran, Iran. Comprising 3256 PBS images derived from 89 subjects suspected of ALL, these images were prepared and stained by adept laboratory professionals. The dataset has four classes Benign, Early Lymphoblastic Leukemia, Pre-Acute, and Pro-Acute. All images were captured with a Zeiss camera under a microscope at 100x magnification and saved in

JPG format. Definitive cell type and subtype determinations were made by a specialist employing the flow cytometry tool. Additionally, to enhance analysis, segmented images were generated through HSV color space image segmentation (using thresholding), providing a valuable resource for further investigation and interpretation. Samples from dataset are shown in **Figure 3.2**. **Table 3.1** shows the details numbers of each class in ALL.

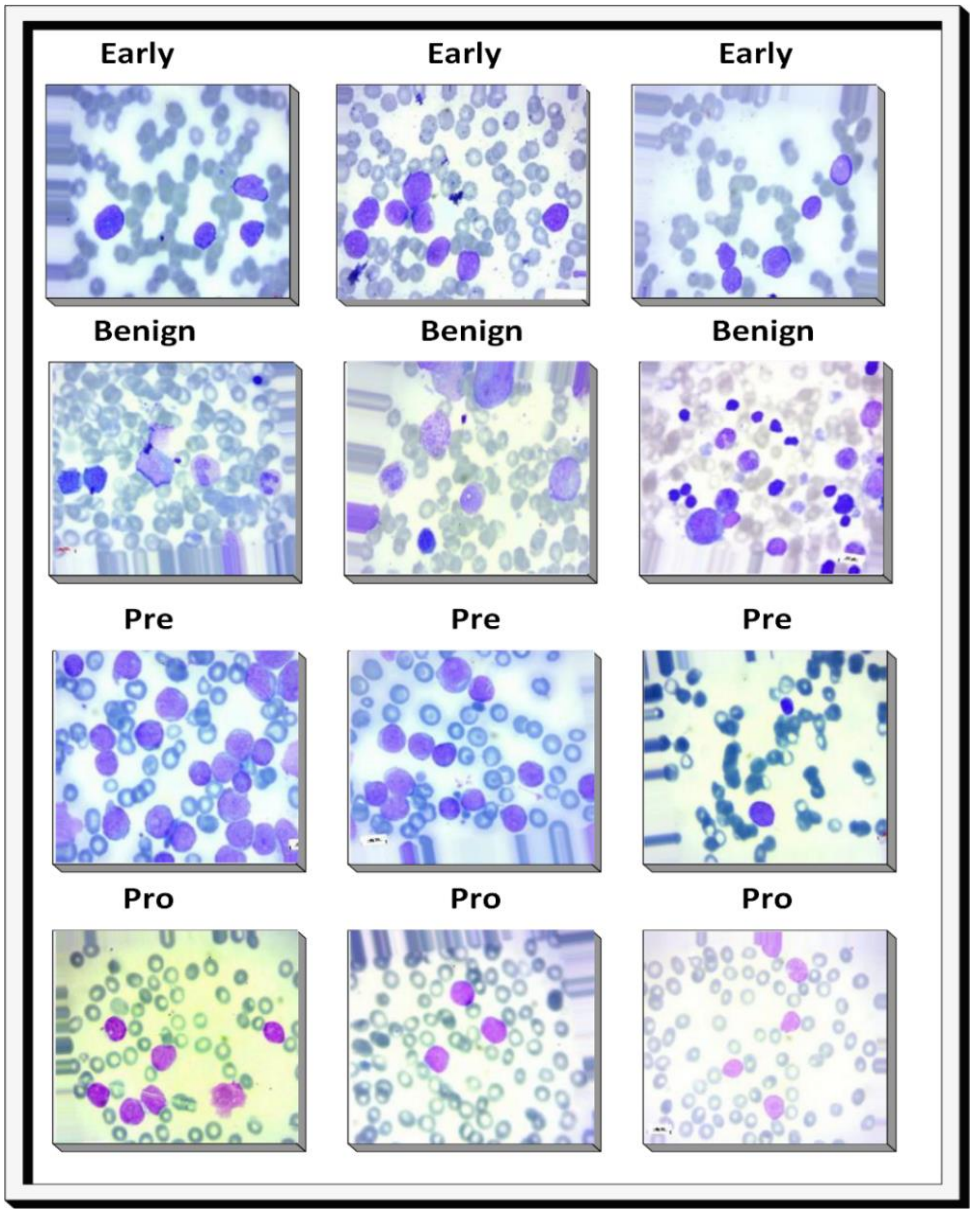

Figure 3.2: The First, Second, Third and Fourth Rows represent Benign, Early Lymphoblastic Leukemia, Pre-Acute and Pro-Acute stage of ALL

Table 3.1. Data Division Detail of ALL Datasets for Benign, Early, Pre and Pro Classes

Stages	**Number of Images**	**Size of Images**
Benign	504	224x224
Early	985	224x224
Pre	963	224x224
Pro	804	224x224
Total	3,256	

3.2 Preprocessing and Augmentation

The preprocessing of ALL photos entails a multifaceted series of procedures aimed at refining the raw data. Initially, the raw data of the photos was extracted, followed by a careful cleaning process utilizing a flip-flop procedure and an array of procedures to ensure their suitability for subsequent processing. The comprehensive approach encompassed addressing missing or inaccurate pixel values and eliminating outliers within the dataset. Additionally, two distinct preprocessing techniques were employed: CAMSR and Gradient-weighted Class Activation Mapping (Grad-Cam). It is pertinent to highlight that the preprocessing stage featured extensive feature engineering endeavors. This involved the normalization of data and the deliberate selection or generation of additional characteristics designed to enhance the efficacy of the algorithms employed. Each of these measures was strategically implemented to optimize algorithmic performance on the dataset. **Table 3.2** presents multiple preparatory approaches used in our model, hence giving an inclusive illustration of the meticulousness intrinsic in the preprocessing stage.

Table 3.2. Preprocessing Steps applied on the Dataset Images

Preprocessing step	Parameters used
Zoom Range	0.2
Crop	True
Width shift range	0.2
Rotation range	15
Vertical Flip	False
Horizontal Flip	True

Furthermore, data augmentation stands out as a widely used and effective strategy for solving class imbalance problem, owing to various reasons. First off, data augmentation is a simple procedure that doesn't require a lot of changes to the hyperparameters or model architecture. It entails applying different transformations, including rotation, flipping, cropping, or noise introduction, to existing data in order to create new training samples. This creates an artificially larger minority class, which helps to achieve a more even distribution of classes. Secondly, data augmentation is a data-driven technique that requires no external knowledge about the data distribution. It uses existing data to create new instances that can aid the model for generalizing. This strategy is essential for enhancing and maintaining the model's functionality while preventing overfitting. The dataset photos underwent various processing operations such as cropping, contrast correction, horizontal flipping, spinning, panning, and boosting during the preparatory phase using the CAMSR approach. The outcomes of the preprocessing steps applied on images prior to being inserted in the proposed model are demonstrated in **Figure 3.3**. In order preserve the desired portions of the image, the undesirable ones had to be cropped out. Images brightness levels were adjusted with the help of contrast filter. Moreover, image was reoriented to respective axes using horizontal and vertical flips. Furthermore, to provide depth and texture to a picture, pixels were

moved up or down using the embossing process. The combined impact of these procedures enhanced both image quality and classification accuracy.

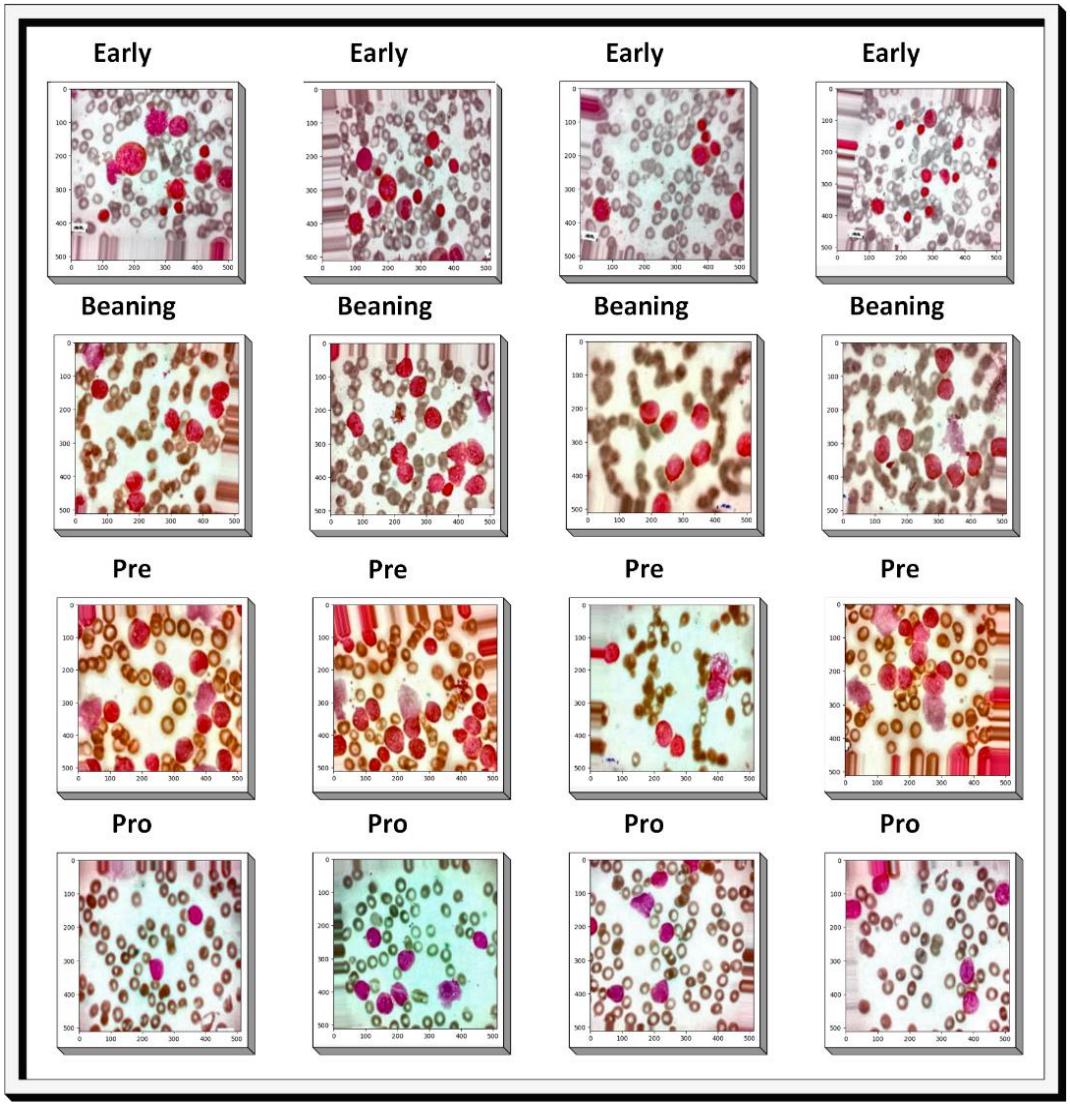

Figure 3.3: Results of Image Preprocessing Steps to Enhance, Contrast and Adjust Noise

Training a DL model on a dataset that has been customized, involves making use of augmented photos. This is done to enhance performance and generalization. While recognizing the challenge of imbalanced class is important and highlights a persistent issue in machine learning, it does not offer a comprehensive solution beyond the use of data augmentation strategies. Exploring better and more efficient approaches for dealing with this issue is crucial in order to achieve more

effective, robust and consistent outcomes. Grad-CAM serves as a methodology for visualizing the distinctive features extracted by a Deep Learning (DL) architecture pertaining to a specific class or category. In our endeavor to assess the severity of ALL, we have utilized Grad-CAM to highlight the features extracted from a proposed XIncept-ALL model, as illustrated in **Figure 3.4**. To analyze these patterns, a pretrained XIncept-ALL model is employed, requiring prior training on a dataset consisting of ALL images labeled with varying degrees of severity. The resulting Grad-CAM heatmap is normalized to values ranging from 0 to 1. Subsequently, this heatmap is superimposed onto the original image, thereby visually indicating the specific regions within the image upon which the model focuses to determine the severity level.

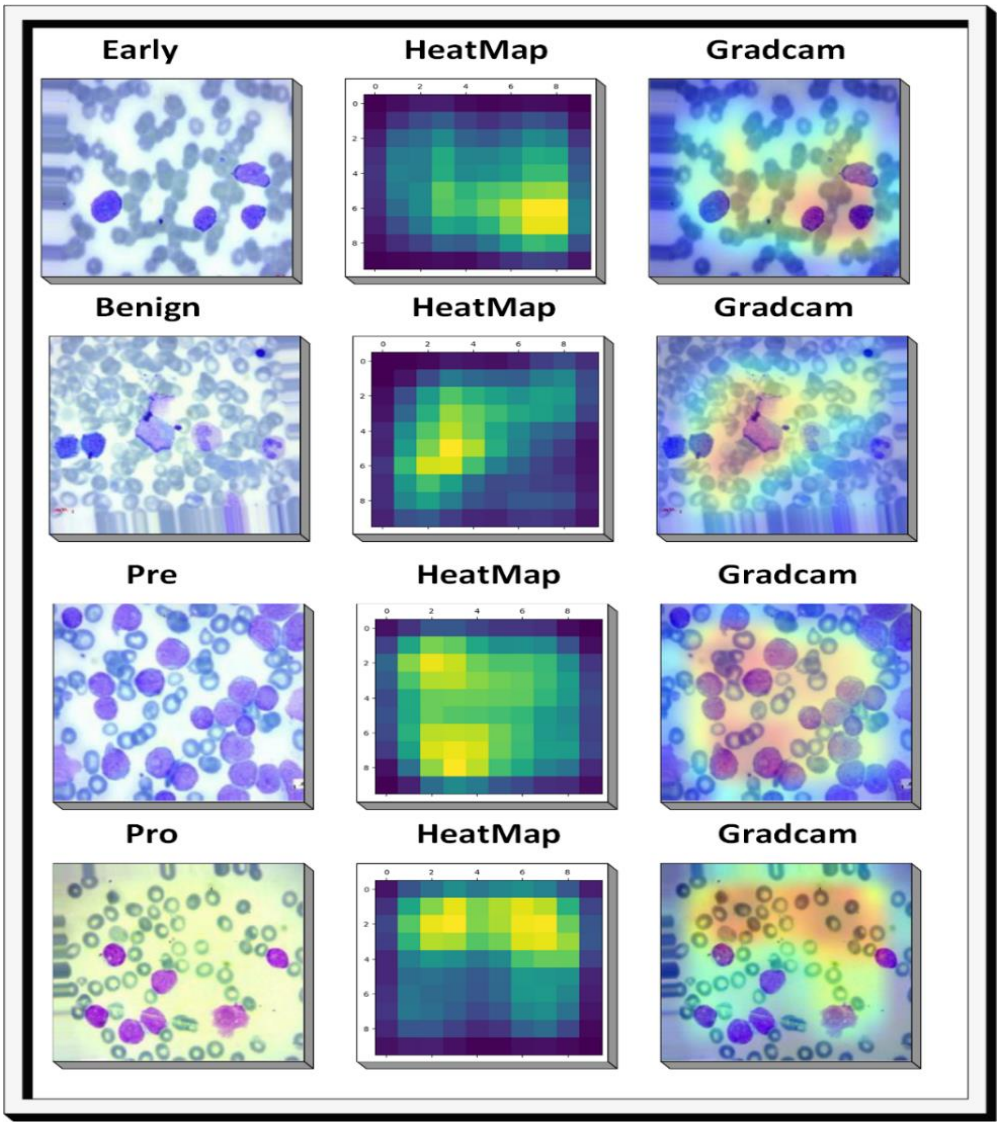

Figure 3.4: HeatMap and Gradcam Patterns identified Proposed XIncept-ALL System when Diagnosed by ALL Images

Chapter 4

Proposed Architecture

Deep learning algorithms can handle huge volumes of data. This allows DL algorithms to have excellent processing skills and effective classification of ALL images. The utilization of these algorithms enables the comprehensive management of each phase within the modeling process, encompassing tasks like data preparation, architectural design, hyperparameter optimization and the selection and refinement of architectural parameters. In this study, two models, InceptionV3 and Xception, are presented to build a model for ALL classification. These two models offer multiple noteworthy benefits, including remarkable outcome, well thought-out feature extraction architecture along with capability to capture both large and small-scale features because of their variable filter size (within range "1 × 1 to 7 × 7"). Furthermore, these models enhance the quality of feature representation, and mitigate the existing problem of gradient vanishing by addressing issues such as residual connections and linear units. To lower the chance of overfitting, they additionally use dropout layers and global average pooling (GAP). Identification of ALL images is made further efficient and effective by adding Batch Normalization layers which also expedite the training process.

The fusion methodology, facilitated by global average pooling and concatenation, strategically captures and harmonizes spatial information from both architectures. Subsequent dense layers further refine the feature space, extracting nuanced relationships. The final architectural element introduces an XGBoost classifier, extending the model's versatility beyond the neural network domain. This hybrid architecture, combining deep learning with gradient boosting, offers a sophisticated ensemble approach for image classification tasks, leveraging the strengths of both paradigms to achieve enhanced predictive performance. The model is poised not only to benefit

from the hierarchical feature extraction capabilities of deep neural networks but also to capitalize on the interpretability and ensemble learning process of XGBoost, ensuring robust and accurate classification outcomes. A brief description of the sophisticated models used in this work will be provided in the paragraphs that follow.

4.1 InceptionV3 Architecture

The InceptionV3 architecture represents an advanced deep CNN designed to extract features across various scales [36]. The three primary structural components of this design are the final layers, initiation blocks, and stem. The stem block reduces the computational complexity in the model following layers. The inception block consists of convolutional layers and inception modules. Deepening the network is the main focus of inception blocks. Within this framework, convolutional layers contribute to the network's depth, while the inception modules play a crucial role in capturing features at multiple scales. The last layer minimizes the spatial resolution of the feature maps and generates the model's output, consisting of many convolutional layers and a GAP layer. The final classification is produced by a completely linked layer, which receives the output from the previous layers. **Figure 4.1** shows the structure of the InceptionV3 model.

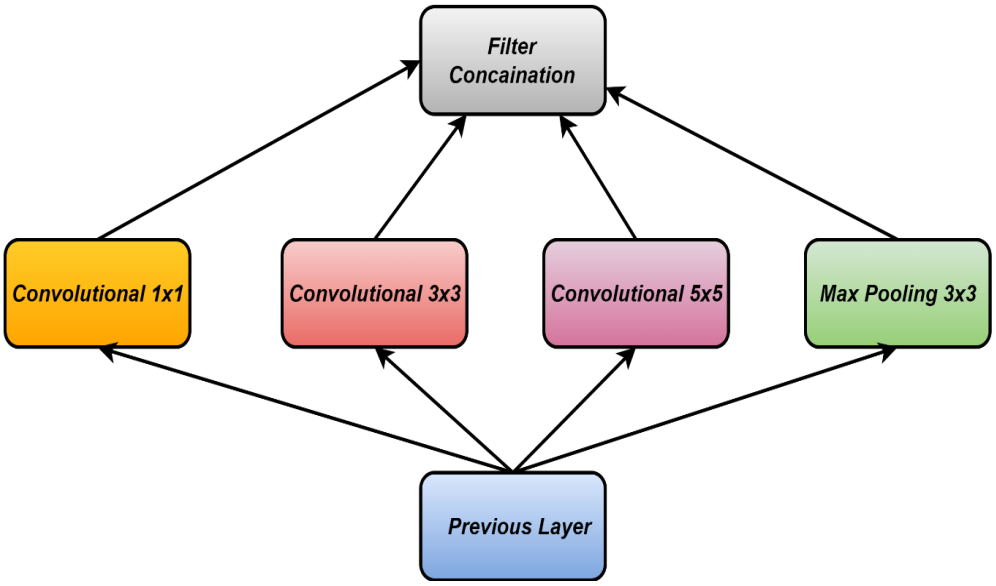

Figure 4.1: the InceptionV3 architecture

4.2 Xception Architecture

The Xception model is another erudite deep CNN model [37] that makes advantage of depth wise separable convolution, a more efficient convolutional procedure. The convolution process is divided into two stages: a pointwise convolution that combines the output of the depth-wise convolution and a depth-wise convolution that deals with application of one filter to each input channel. This reduces the number of parameters in the network and speeds up processing. The architecture reduces the spatial dimensions of the feature map and inhibits overfitting by incorporating fully connected layers, a GAP layer, and an optionally included dropout layer [38]. Structure of the Xception model is illustrated in **Figure 4.2**.

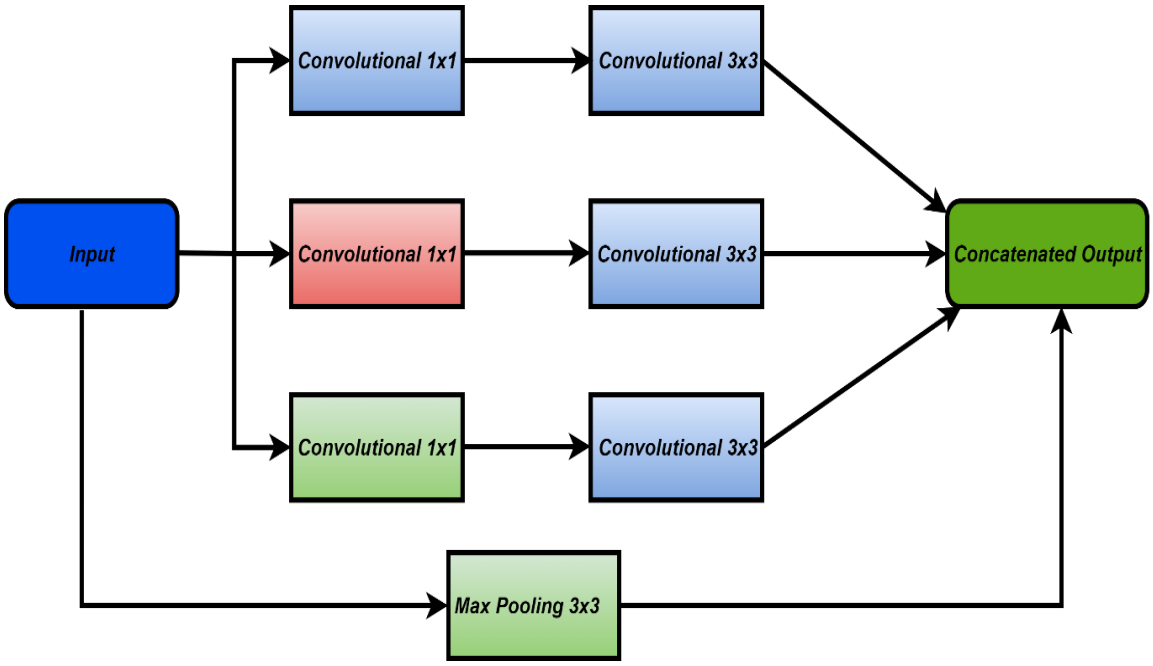

Figure 4.2: Flow Diagram of Xception Model

4.3 The Proposed Fusion Model

Three essential modules make up the structure of the proposed Fusion model, each contributing to its comprehensive functionality: a cooperative Convolutional Neural Network module, a feature fusion module, and a feature classification module. The visual representation of the Fusion model is encapsulated in **Figure 4.3**. Starting with the collaborative CNN module, the model carefully extracts significant features by utilizing the strengths of two pre-trained CNN models, Xception and InceptionV3. These CNN models, initially trained on the ImageNet dataset, undergoes fine-tuning through Transfer Learning (TL) to extract pertinent features from images. Following the extraction of features from collaborative CNN, the feature fusion module merges them into a cohesive feature pool, which acts as the input for the subsequent feature classification phase. This module employs a range of machine learning classifiers such as Support Vector Machine, K-Nearest Neighbor, AdaBoost, Logistic Regression, Random Forest, XGBoost, and LightGBM. This module ascribes class probabilities and distinguishes between four distinct classes: Benign,

Early Lymphoblastic Leukemia, Pro-Acute and Pro-Acute. Notably, the classification process dynamically trains the weights of the features. The Fusion model is intentionally crafted to provide multiple beneficial features, making it a robust and versatile tool for behavior classification and detection. To avoid the arduous process of repeatedly training the models, an adaptable methodology for integration of multiple Convolutional Neural Network (CNN) has been presented. The models are trained independently on relevant dataset, thereby making the proposed approach effectual. As a result, existing feature pool is populated with extracted features extracted from the individually trained models. In terms of time and resource efficiency, this approach bears notable advantages. A considerable reduction in time and computational resources is attained by eliminating the need to retrain pre-existing models and allowing for the independent training of new models. Thus, a practical solution for prompt integration and adaptability is formulated which not only enhances efficiency but also removes the requirement for redundant training efforts on pre-existing models.

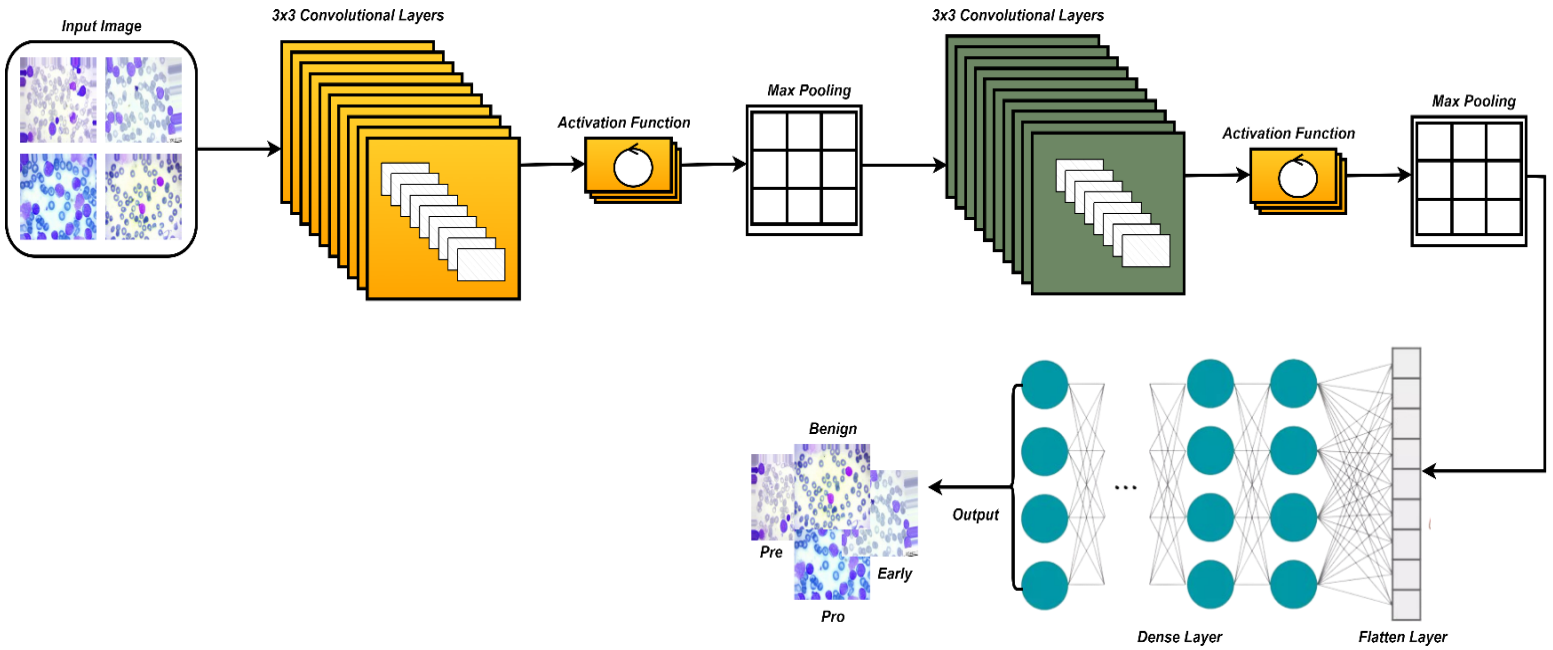

Figure 4.3: Schematic Diagram of the Proposed Architecture highlighting each Layer from Preprocessing Steps to Final Output

Feature extraction from diverse models proposed by this approach, contributes to an enhanced feature representation which exceeds the results achieved by a singular model. It is pertinent to highpoint that various models have their own capability with varying degrees of effectiveness when it comes to identifying particular features or patterns in data. A wider range of inherent data patterns and relationships is acquired with the help of these models' integration which provides an inclusive and varied feature representation. Moreover, the risk of overfitting can be reduced subject to combination of multiple models with addition to enhancement of the model's ability to generalize effectively. In a nutshell, an adaptable and resilient predictive framework is fostered with the above described synergistic integration which minimizes the impact peculiarities in disparate models, augments its capacity to extrapolate patterns to unseen data and bolster the model's robustness. **Algorithm 1** presents the steps of the proposed XIncept-ALL model.

Algorithm 1*: Detailed Steps of XIncept-ALL Model for Feature Extraction*

Input	Image dataset with labeled classes: $\{(x1, y1), (x2, y2), \ldots, (xN, yN)\}$
Output	Trained combined model for image classification
$Step\ 1$	Initialize Xception and InceptionV3 base models: $MXcep \leftarrow Xcep(weights = "imagenet", include\_top = False, input\_tensor = Input(shape = (224,224,3)))$ $and\ MIncep \leftarrow Incep(weights = "imagenet", include\_top = False, input\_tensor = Input(shape = (224,224,3)))$.
$Step\ 2$	$FXcep \leftarrow Xcep\_last\_layer(Xtrain)$ Get features from the desired layer in Xception.

$Step$ 3 $FIncep \leftarrow Incep\_last\_layer(Xtrain)$ Get features from the desired layer in InceptionV3.

$Step$ 4 $DXcep \leftarrow Dense(FXcep, units = 64, activation = "relu")$ Dense layer for Xception features.

$Step$ 5

- $OXcep \leftarrow Dense(DXcep, units = 2, kernel_{regularizer} = l2(0.01), activation =$ linear) Linear output layer for Xception features.
- $OIncep \leftarrow Dense(DIncep, units = 2, kernel\_regularizer = l2(0.01), activation = "linear")$ Linear output layer for InceptionV3 features.

$Step$ 6

- $MXcep \leftarrow Model\big(inputs = Xcep_{input}, outputs = OXcep\big)$ Create model for Xception.
- $MIncep \leftarrow Model(inputs = Incep\_input, outputs = OIncep)$ Create model for InceptionV3

$Step$ 7 Set all layers in $MXcep$ and $MIncep$ as non-trainable.

$Step$ 8 $Ffusion \leftarrow Concat([OXcep, OIncep])$ Concatenate the output features from Xception and InceptionV3 models.

$Step$ 9

- $Ffusion \leftarrow Dense(Ffusion, units = 128, activation = "relu")$ Additional dense layer.
- $Ffusion \leftarrow Dense(Ffusion, units = 64, activation = "relu")$ Additional dense layer.

$Step$ 10 $Ofinal \leftarrow Dense(Ffusion, units = 2, kernel\_regularizer = l2(0.01), activation = "linear")$ Final output layer.

$Step\ 11$ $Mcombined \leftarrow Model(inputs = [Xcep\_input, Incep\_input], outputs = Ofinal)$ Build the combined model.

$Step\ 12$ Print the summary of $Mcombined$.

$Step\ 13$ Compile $Mcombined$ with appropriate loss, optimizer.

$Step\ 14$ Train $Mcombined$ on the training dataset $Xtrain$.

$Step\ 15$ Evaluate $Mcombined$ on validation and testing datasets $Xval$ and $Xtest$.

$Step\ 16$ Fine-tune $Mcombined$ based on evaluation results.

$Step\ 17$ Visualize learned features for model interpretability.

$Step\ 18$ The trained combined model $Mcombined$ is ready for image classification tasks.

The efficacy of the XGBoost algorithm for recognizing features associated with ALL was also discovered in our research. Using decision trees as base learners, a gradient boosting framework is employed as outlined in Algorithm 1. Binary classification tasks are better handled with XGBoost, and therefore we configured it with hyperparameters such as the learning rate (η), regularization term (λ), and the number of trees (T).

A Depth-wise Conv2D was adopted for the task of feature extraction for provision of a more specialized convolutional operation. Iterative construction of decision trees leading to update in model based on the calculated gradients (gi) and Hessians (hi) for each training sample is all part of the training process.

Optimization of an objective function and that balances a loss and regularization term is part of XGBoost model training.

$$\text{Objective} = \sum i = 1m[L(ai, \hat{a}i) + \lambda \cdot \Omega(f)] \quad (4.1)$$

where m is the number of training samples, ai is the true label, $\hat{a}i$ is the predicted output, λ is the regularization term, and $\Omega(f)$ is the regularization term for the function f.

The calculation of the $t - th$ tree is sequentially merged into the ensemble during the training of the XGBoost model:

$$\hat{a}i(t) = \hat{a}i(t-1) + \eta \cdot ft(xi) \quad (4.2)$$

Sum of predictions from all trees in the ensemble is the final prediction for a testing sample:

$$\hat{a}test = \sum t = 1T\eta \cdot ft(xtest) \quad (4.3)$$

Algorithm 2 presents a detailed account of the operational principles of our recommended classifier.

***Algorithm 2**: XGBoost Classifier to Recognize ALL Extracted Features*

Input	Initialize XGBoost model with hyperparameters such as learning rate (η), regularization term (λ), and the number of trees (T).
$Step\ 1$	Train the XGBoost model with the extracted features $x = (a1, a2, \ldots, an)$ and annotations $a = 0,1$.

$Step$ 2 Replace $Conv2D$ with $Depthwise\ Conv2D$ in the feature extraction process.

$Step$ 3 Computing gradients (gi) and Hessians (hi) for each sample in the training set, constructing decision trees, and updating the model iteratively combined make up the training process. Refer to the $XGBoost$ algorithm steps for details.

$Step$ 4 The final model is an $ensemble$ of decision trees, each contributing to the overall prediction.

$Step$ 5 Use the XGBoost model to allocate class labels for testing samples. The prediction can be calculated as $A_{test} = \sum_{t=1}^{T} n.w_t.h(xi)$, where wt is the weight of tree t and $h(xi)$ is the prediction of the tree for the input xi

$Step$ 6 The output is the recognition result based on the $XGBoost$ model.

Chapter 5

Experimental Results

A dataset of 3256 Acute Lymphoblastic Leukemia (ALL) pictures acquired from Kaggle was used to train the XIncept-ALL. All 3256 photos were resized to 700 × 600 pixels in order to perform the feature extraction and categorization tasks. The proposed XIncept-ALL system is a combination of InceptionV3 and Xception models.

The most optimal F1-score of 0.99 was achieved during 20^{th} epoch after training the XIncept-ALL model over 100 epochs. Based on the statistical methods, the effectiveness of the proposed XIncept model was evaluated by calculating the values of performance metrics including accuracy (ACC), specificity (SP), and sensitivity (SE). System performance of the projected model was then compared with the existing or similar systems present in literature based on the computed values of these metrics. To construct and enhane the XIncept-ALL system, a PC equipped with an HP-i7 CPU, boasting 8 cores, 16 GB of RAM, and a 2 GB NIVIDA GPU were employed. The computer had Windows 11 Professional 64-bit operating system.

Following equations facilitate the calculation of above-mentioned statistical indicators:

$$Accuracy = (TP + TN)/(TP + TN + FP + FN) \times 100 \quad (5.1)$$

$$Recall = TP/(TP + FN) \times 100 \quad (5.2)$$

$$Specificity = TN/(TN + FP) \times 100 \quad (5.3)$$

$$F1 - Score = 2 \times (precision \times recall)/(precision + recall) \quad (5.4)$$

Concept of true positive (TP) and true negative (TN) values was used to compute these metrics which indicate how well the model predicts whether the data is real or fake or the data prediction was accurate or false. The other two values required in the calculations are false positive (FP) and false negative (FN). These values show whether the false classification is accurate or not.

The tabulated data reveals a distinctive feature of the model when compared with conventional generic CNN. Notably, the model avoids channel-wise convolution, resulting in a reduction in the number of connections. This deliberate design choice imparts a lightweight characteristic to the model, facilitating the attainment of exceptional accuracy with a scant number of epochs. Evidently, the training accuracy of 99.0% is achieved within a mere 10 epochs, underscoring the efficacy of the proposed XIncept-ALL architecture.

Furthermore, a comparative analysis presented in **Table 5.1 and Figure 5.1** delves into the contrasting performance of the original CNN+LSTM, ResNet, GoogleNet, VGGNet, InceptionV3 and Xception architectures and the proposed XIncept-ALL architecture. In this context, the XIncept-ALL architecture emerges as the frontrunner, exhibiting the highest level of accuracy. This notable achievement can be attributed to the strategic fusion of the InceptionV3 and Xception architectures. The incorporation of these architectures proves instrumental in elevating the overall performance of the XIncept-ALL model, as validated by the comparative results outlined in the table.

Table 5.1. Results of Typical DL Algorithms' Classification in terms of Several Metrics in Comparison to the Suggested Approach

Ser No	Architectures	Sensitivity	Specificity	Accuracy	Precision	F1-Score
1	CNN+LSTM	0.838	0.840	0.860	0.849	0.845
2	ResNet	0.843	0.840	0.824	0.818	0.807
3	GoogLeNet	0.880	0.884	0.845	0.885	0.867
4	VGGNet	0.734	0.843	0.840	0.807	0.818
5	InceptionV3	0.840	0.838	0.860	0.837	0.849
6	Xception	0.858	0.850	0.880	0.855	0.847
7	XIncept-ALL	0.990	0.988	0.990	0.989	0.990

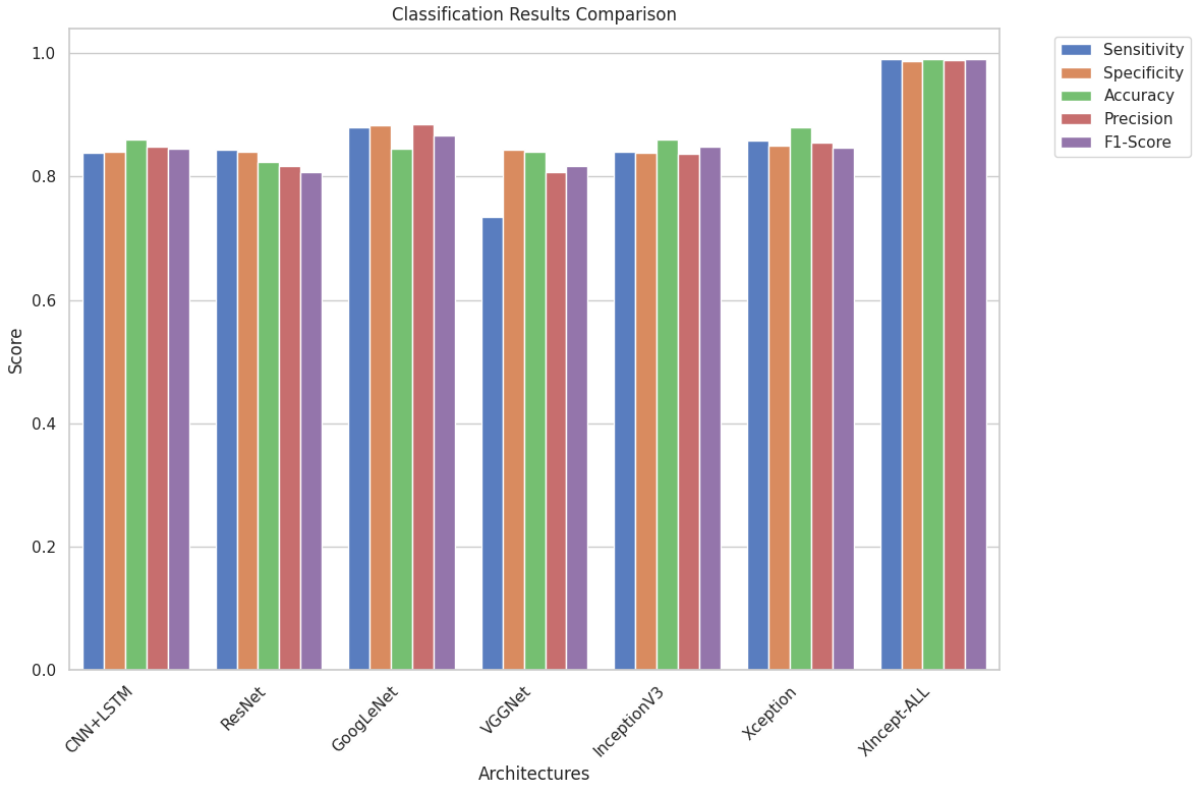

Figure 5.1: Comparative Analysis of Various Deep Learning Models

5.1 Computational Cost

A comprehensive evaluation of computational complexity was conducted to compare deep learning models with the proposed XIncept-ALL system. As delineated in **Table 5.2**, a total processing time of approximately 184.5 seconds was exhibited by the suggested DL architecture. In contrast, the total processing times for prominent models such as VGGNet, InceptionV3, ResNet, GoogleNet, CNN+LSTM and Xception were recorded at 211.8 s, 207.5 s, 230.1 s, 217.4 s, 246.2 s, and 194.4 seconds respectively.

This comparison proves the efficiency of our suggested XIncept-ALL technique, which needs less processing time for the identification of various severity levels of ALL. The expeditious processing time is particularly pivotal in settings where computational performance is of paramount importance. This not only underscores the efficacy of the proposed approach but also highlights its relevance in the current paradigm.

Furthermore, in-depth experiments were meticulously conducted as elaborated in subsequent paragraphs, augmenting the robustness of the findings. Additionally, **Table 5.2** and **Figure 5.2** illuminates the enhanced computational speed of the XIncept-ALL model when compared with the original architecture of the InceptionV3 and Xception models, further substantiating the advancements introduced in our proposed methodology.

Table 5.2. DL Algorithms Average Processing Time Comparison

Model	Preprocessing (seconds)	Feature Extraction (seconds)	Training Time (seconds)	Prediction Time (seconds)	Overall Result (seconds)
CNN+LSTM	19.5	15.4	250.5	11.8	250.2
ResNet	17.6	13.2	200.5	9.8	240.1
GoogLeNet	15.3	15.8	198.5	8.8	227.4
VGGNet	16.2	18.3	180.5	7.8	221.8
InceptionV3	17.1	14.1	175.5	9.8	217.5
Xception	7.8	8.3	195.5	4.8	198.4
XIncept-ALL	1.7	1.9	160.5	1.8	187.5

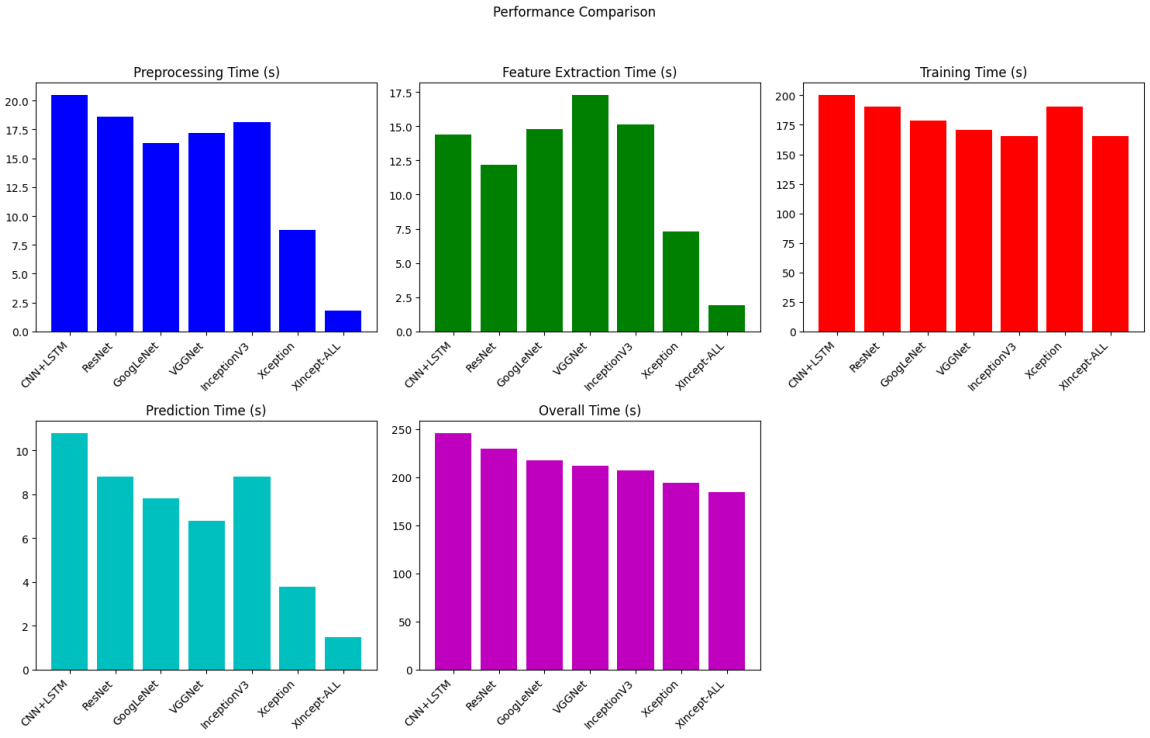

Figure 5.2: Enhanced Computational Speed of the XIncept-ALL Model

5.2 Experiment 1

A thorough 10-fold cross-validation approach is used to evaluate the effectiveness of our proposed model in the first experiment. As a principal metric for the assessment of categorization performance, Area under the curve (AUC) was employed. **Table 5.3** presents the outcomes of the quantitative evaluation, defining the efficacy of the XIncept-ALL system. With a training error as low as 0.1, the developed XIncept-ALL model exhibited a commendable performance. Moreover, the model's exceptional ability to detect and classify cases symbolic of ALL was demonstrated with a high AUC of 99%. The effectiveness of the XIncept-ALL system is characterized by these quantitative indicators which reflect a judicious balance between training error minimization and robust discriminatory capacity, as indicated by the high AUC. In the context of ALL disease detection, our findings contribute to a wholesome understanding of the model's proficiency.

Table 5.3. Performance Metrics of the XIncept-ALL

ALL Types	SE	SP	ACC	AUC	Error
Benign	0.99	0.99	0.99	0.99	0.1
Early	0.99	0.99	0.99	0.99	0.1
Pre-Acute	0.99	0.99	0.99	0.99	0.1
Pro-Acute	1.0	1.0	1.0	1.0	0
Average Results	0.99	0.99	0.99	0.99	0.1

5.3 Experiment 2

Our second experiment involves the application of binary classification techniques, specifically our novel XIncept-ALL model to analyze the ALL-image dataset. Keeping in mind analysis of both training and validation aspects along with a careful examination of loss functions, model's effectiveness was assessed. **Figure 5.3** visually depicts the commendable performance, notable training and validation accuracy of 100% within a concise ten-epoch training period in XIncept-ALL model that we put forth. A loss function of under 0.1 for both the training and validation datasets, the model demonstrated exceptional performance. The efficacy of our proposed model in the realm of binary classification on the ALL-image dataset can be underscored with these compelling results. Factors such as model generalization, overfitting, and the need for robust performance across various datasets are required to be kept into consideration while acknowledging the significance of these findings. The aptitude of XIncept-ALL model for classification can be represented through attainment of high accuracy and low loss. In addition to these achievements, it is imperative to note that, a thorough assessment of the model's suitability for unseen data and its ability to withstand variations is indispensable for comprehension of its practical value. Moreover, credibility and completeness of the experimental findings can be improved by incorporating insights from a separate test dataset, not explicitly mentioned in the provided excerpt would.

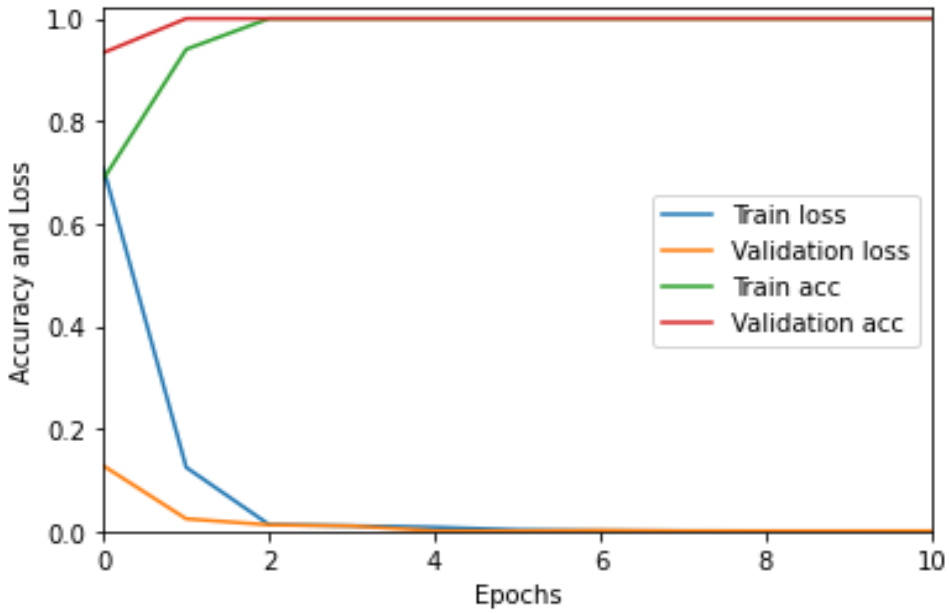

Figure 5.3: XIncept-ALL Accuracy and Loss Using the Binary Classification with Acute Lymphoblastic Leukemia (ALL) Image Dataset

5.4 Experiment 3

In our third experiment, we used another Acute Lymphoblastic Leukemia (ALL) image dataset acquired from Kaggle. The dataset used in this research was selected from the Taleghani Hospital's bone marrow laboratory in Tehran, Iran which encompasses 3256 Peripheral Blood Smear (PBS) images derived from 89 subjects suspected of Acute Lymphoblastic Leukemia (ALL). These images were prepared and stained by highly skilled laboratory professionals. The dataset is organized into four distinct classes: Benign, Early Lymphoblastic Leukemia, Pre-Acute, and Pro-Acute. A Zeiss camera mounted on a microscope employed with 100x magnification was used to capture these images. The images were saved in JPG format. A specialist with the help of flow cytometry tool conducted the distinctive determination of cell types and subtypes. Segmented images were produced using color thresholding-based segmentation within the HSV color space

for in-depth examination which enhances the dataset's utility, thus providing valuable resources for subsequent investigation and interpretation.

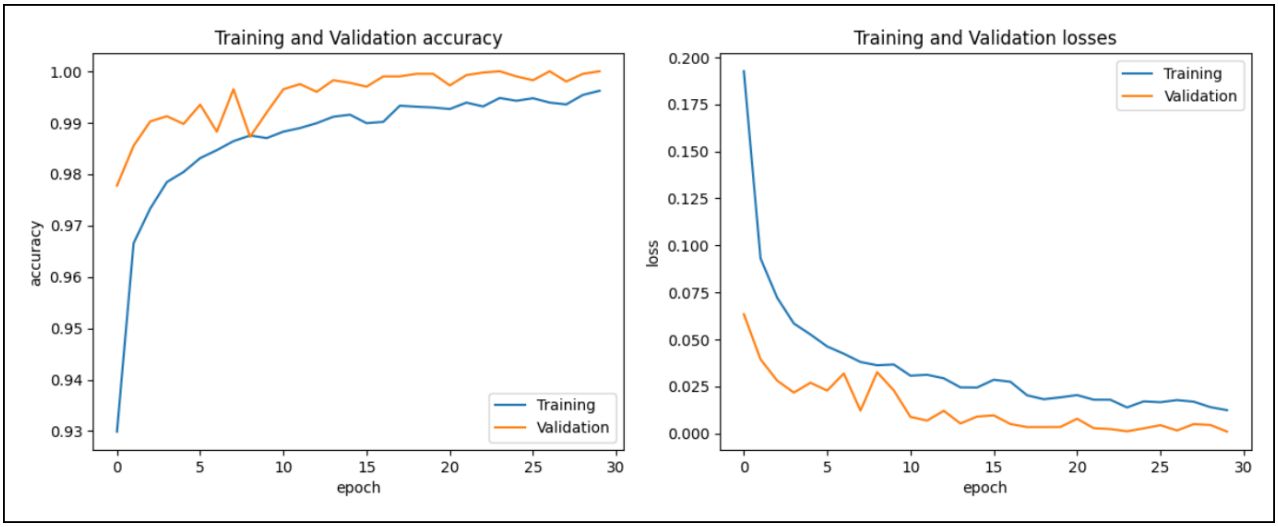

Figure 5.4: Accuracy and Loss versus Epochs for Training and Validation of the Proposed Model

5.5 Experiment 4

An alternative dataset consisting of 150 professionally labelled images by expert oncologists (with each class containing 50 images) procured from Kaggle is used in our fourth experiment to assess the efficiency of the proposed model. According to French-American-British (FAB) classification, these images are divided into three classes.

L1 - Blasts that are small, homogeneous with regular nuclei but a little clefted and inconspicuous nucleoli. Cytoplasm is scanty and usually without vacuoles.

L2- Blasts that are large, heterogeneous with irregular nuclei and often clefted. Usually, one large nucleolus is present. The volume of cytoplasm is variable, but often abundant and may contain vacuoles.

L3- Blasts are moderate-large in size and homogeneous. The nuclei are regular and round-oval in shape. One or more prominent nucleoli are present. The volume of cytoplasm is moderate and contains prominent vacuoles.

The confusion matrix show that the proposed model was able to classify the first two classes with 100% accuracy while the third class was classified with 97.5% accuracy.

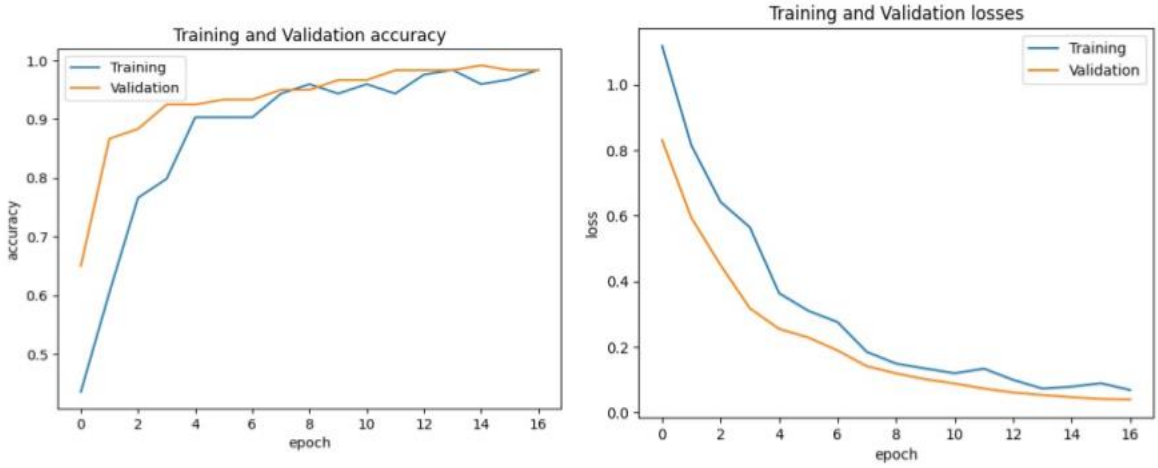

Figure 5.5: Accuracy and Loss versus Epochs for Training and Validation of Proposed Model

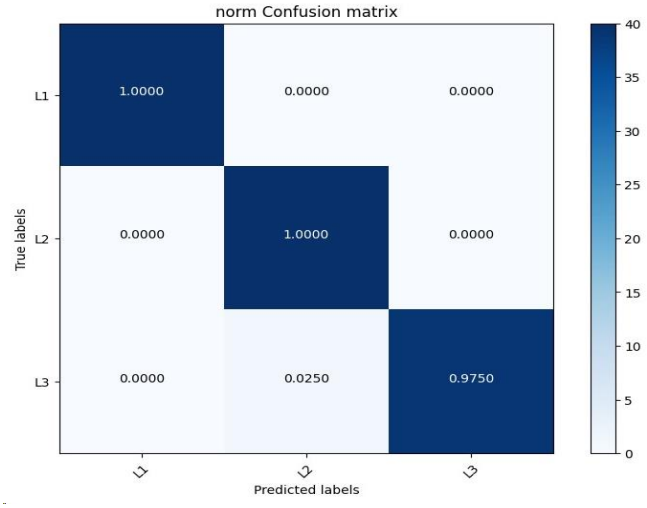

Figure 5.6. Confusion Matrix L1, L2, L3 are the Class Labels

Chapter 6

State-of-the-Art Comparison

In this section, a state-of-the-art comparison between the proposed work and previous work from literature is introduced. First, it can be seen that the proposed model is compared with advanced models (CNN+LSTM, ResNet, GoogleNet, VGGNet, InceptionV3, Xception). The data presented in **Table 5.2** and **Table 5.3** illustrates that the suggested model attains the highest level of accuracy while requiring the least amount of computational time. Our proposed model accomplishes higher accuracy over other deep learning models by over 10% increase in accuracy. This shows the superior performance of the proposed architecture over other architectures. In [34] the authors propose an Improved ANFIS model for solving the same problem. The authors use the same dataset of Experiment 1. The maximum achieved accuracy is 97.4%. Our model on the other hand shows 99.0% accuracy on same dataset that proves the improved performance of our model. The proposed system was also experimented on ALL dataset with small number of samples (150) in which the system was able to achieve more than 99% on average on the three classes. This again signifies the enhanced performance of the model while achieving high classification accuracy on a small dataset without using data augmentation techniques.

Table 6.1. State-of-the-Art Comparison

	Iranian Dataset	**ALLBD1 Kaggle**
Proposed XIncept-ALL model	99.0%	99.0%
Adaptive Network-Based Fuzzy Inference System (ANFIS)	97.4%	

Chapter 7

Summary of Research Work

Ensuring accurate results in the classification of ALL necessitates addressing the challenge of data imbalance. While deep learning (DL) methods leverage multiple artificial neuron layers for effective image recognition, the issue of class imbalance is mitigated through the implementation of a data augmentation approach with image dimensions set at (700 × 600, 3) pixels. The correction of class imbalance through dataset augmentation proves pivotal, circumventing the need for additional processing power and memory. Our commitment is directed towards streamlining structures and expediting computations. To this end, we introduce the XIncept-ALL design featuring a balanced layer architecture, aimed at offering a less intricate framework.

In our quest for faster computations, we integrated different blocks with kernel regularizations ranging from 0.001 into the framework. Kernel regularization plays a central role in mitigating overfitting concerns associated with the complex architecture. In order to effectively address the issue of noise present in ALL images, an XGBoost classifier is used in our study to identify ALL. With the help of multiple optimizers excluding GELU due to performance considerations, our projected system establishes efficacy. Our proposed XIncept-ALL model consistently outshines existing models when applied on publicly curated datasets, thereby effectively utilizing them. Our research offers following key advantages:

1. Our research centers around a significant innovation that is the formation of a novel Convolutional Neural Network (CNN) model specifically designed for detecting Acute Lymphoblastic Leukemia (ALL). Our proficient and advanced proposed model stands out when compared with existing deep learning (DL) frameworks. It works to improve both

speed and accuracy by simplifying complex network through integration of Inception and Xception architectures. Both InceptionV3 and Xception play a pivotal role when it comes to refining accuracy without impacting the model's complexity or computational rate. An optimization with respect to model's classification capability is achieved with the help of this distinguished approach, while keeping in mind the balance between accuracy, computational efficiency and model complexity. This distinctive characteristic highlights the effectiveness and significance of the XIncept-ALL architecture within the realm of deep learning methodologies for ALL detection.

2. Highlighting its robust and adept nature, XIncept-ALL displays a rather versatile capability without encountering issued of overfitting or underfitting. Use of GELU function as a deliberate alternation was employed in place of RELU while keeping in mind the critical role of the activation function in refining model accuracy. This modification proves to be a remarkable enhancement in the model's overall performance indicated by our research. Proficiency of our proposed model's capability to differentiate between classes of ALL is clearly enhanced with the integration of GELU activation function. This premeditated choice emphasizes the perceptive approach adopted in optimization of the model's architecture to achieve superior outcomes in ALL classification.

Chapter 8

Conclusion and Future Work

A considerable global population contends with the burdens of Acute Lymphoblastic Leukemia (ALL), emphasizing the pressing need for widespread and efficient detection methods. Early identification of the disease is fundamental for effective prevention strategies. To meet this necessity, our work presents a completely automated ALL identification and categorization method that maximizes accuracy by utilizing deep learning models and creative preprocessing steps. The model integrates CAMSR technique to mitigate noise, accentuate lesions and enhance ALL classification performance. A distinctive contribution to this research is the incorporation of the Grad-CAM technique, illuminating crucial locations on ALL-affected images essential for identification. Furthermore, our study introduces a novel deep learning model based on InceptionV3 and Xception, evaluated on the publicly available dataset.

Comparative analyses with up-to-date models in the literature showcase the superior performance of our proposed methodology. The proposed system has been able to achieve accuracies higher than the reported accuracies in literature. An exploration of strengths and limitations reinforces the efficacy of our model against existing benchmarks. It is crucial to clarify that the proposed method serves as a pre-screening and automatic tool for recognizing ALL severity, distinct from a decision support system. Future iterations may incorporate knowledge-based information to extend the XIncept-ALL model's utility in providing insights into uncontrolled blood symptoms among ALL patients. Additionally, future studies will prioritize picture quality sensitivity in order to guarantee the model's dependability and applicability in a variety of clinical contexts. Rigorous evaluation on large and intricate datasets, encompassing a substantial number of prospective ALL instances, remains imperative for validating the robustness and real-world effectiveness of our proposed

approach. In conclusion, the classification approach proposed in this study relies on feature extraction and features fusion as a core of the methodology. This represents a pioneer attempt to establish a computerized technique that surpasses existing methods in the detection of ALL.

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