



Deep Leuko- (Deep Learning Applied to Leukemia Detection)

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ABSTRACT—

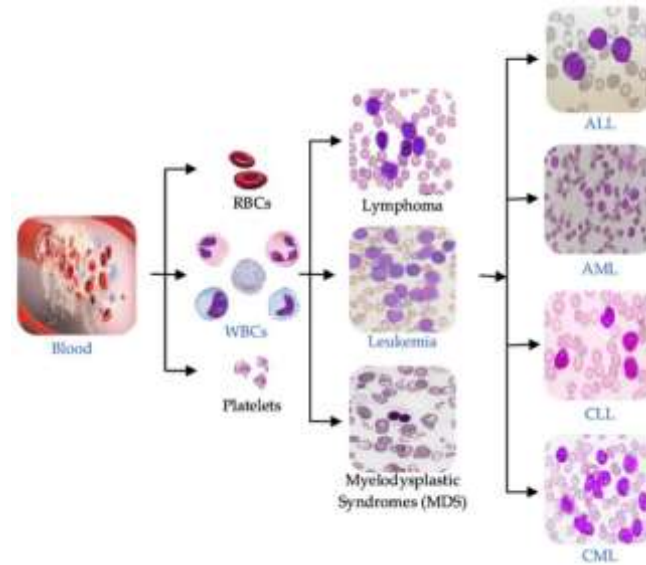
This study presents an automated approach for detecting Acute Lymphoblastic Leukemia (ALL) using deep learning. ALL is a severe blood disorder caused by the overproduction of immature lymphoblasts, making early diagnosis crucial for effective treatment. Traditional diagnostic methods like fluorescence in situ hybridization (FISH) and immunophenotyping are expensive and time-consuming, highlighting the need for a faster and more cost-effective alternative. To address this challenge, we propose a CNN-based classification model for ALL detection using microscopic blood smear images. A dataset of 108 stained blood smear images was processed using a fuzzy-based two-stage color segmentation technique to isolate leukocytes from other blood components. Feature extraction involved texture analysis, shape descriptors, and novel geometric attributes such as Hausdorff dimension and contour signature. These extracted features were used to train a CNN classifier, which achieved high accuracy in differentiating leukemia-positive and leukemia-negative samples. The proposed method significantly improves diagnostic efficiency compared to traditional techniques by reducing human error and accelerating the detection process. Experimental results demonstrate that CNN-based classification offers a reliable, cost-effective, and time-efficient solution for early leukemia screening. By automating the detection process, this approach can assist medical professionals in making faster and more accurate diagnoses, ultimately leading to better patient outcomes. This research highlights the potential of deep learning in medical imaging and hematology, emphasizing the effectiveness of CNNs in identifying leukemia from blood smear images. The integration of image processing techniques and deep learning models not only enhances diagnostic accuracy but also provides an accessible solution for leukemia screening, particularly in resource-limited settings. The findings suggest that AI-driven approaches can revolutionize hematological diagnostics, making leukemia detection more efficient, affordable, and widely available.

Keywords— Acute Lymphoblastic Leukemia (ALL), deep learning, Convolutional Neural Networks (CNNs), blood smear images, leukemia detection, image processing, fuzzy-based segmentation, feature extraction, Hausdorff dimension, contour signature, texture analysis, shape descriptors, medical imaging, hematology, automated diagnosis, early detection, machine learning, classification model, cost-effective screening.

Introduction

Acute Lymphoblastic Leukemia (ALL) is a severe hematological malignancy that primarily affects children, characterized by an excessive proliferation of lymphoid blasts in the blood and bone marrow [1]. The presence of these abnormal cells disrupts normal hematopoiesis, leading to symptoms such as anemia, fatigue, frequent infections, and uncontrolled bleeding [2]. Early and accurate detection of ALL is crucial for timely treatment and improved survival rates. However, conventional diagnostic approaches rely heavily on manual microscopic examination of stained blood smears, which is highly dependent on expert pathologists, making it prone to human error, time-consuming, and costly [3].

To address these limitations, automated image-based diagnostic systems have gained attention for their ability to provide fast, accurate, and reproducible leukemia detection. Stained blood smear images can be processed through quantitative image analysis techniques, enabling the segmentation and classification of leukocytes from other blood components.



Blood composition and leukemia classification, illustrating different types of leukemia and their distinct morphological characteristics [14].

Fig. 1. illustrates the composition of blood and the classification of leukemia subtypes, demonstrating how different types of blood cells are affected by hematological malignancies. This visual representation aids in understanding the morphological distinctions critical for accurate leukemia detection.

Fuzzy-based two-stage color segmentation has been used to enhance cell isolation and improve the accuracy of feature extraction [4]. Advanced feature extraction methods consider multiple parameters, including shape, texture, Hausdorff dimension, and contour signature, to differentiate normal blood cells from leukemic blasts [5].

Deep learning techniques, particularly Convolutional Neural Networks (CNNs), have revolutionized medical image analysis by automating feature extraction and classification processes. CNNs efficiently capture hierarchical patterns in blood cell morphology, improving classification accuracy and reducing false positives [6]. Furthermore, Exploratory Data Analysis (EDA) plays a crucial role in preprocessing leukemia datasets, ensuring data integrity and effective feature selection for model training [7]. Among deep learning models, VGG16, a widely recognized convolutional network architecture, has demonstrated exceptional performance in medical image classification, leveraging its deep convolutional layers to extract high-dimensional features from blood smear images [8].

The integration of CNNs, EDA, and VGG16-based architectures in leukemia detection has proven to be highly effective, outperforming traditional machine learning methods. The proposed study focuses on an AI-driven leukemia detection framework that combines deep learning techniques with advanced image segmentation and feature extraction to enhance diagnostic precision. The system is validated using benchmark blood smear datasets, ensuring robust model performance in real-world leukemia diagnosis scenarios [9].

The significance of this research extends beyond automation; it highlights the potential of AI in revolutionizing hematological diagnostics, reducing the burden on healthcare professionals while providing fast, scalable, and accurate leukemia detection. By integrating state-of-the-art deep learning techniques, this study aims to bridge the gap between traditional diagnostics and AI-powered medical analysis, contributing to the early detection and effective management of leukemia [10].

Literature Review

Jiwani et al. [1] proposed a computational deep learning approach for the pattern recognition of Acute Lymphoblastic Leukemia (ALL) using peripheral blood smear (PBS) images. The study utilized a deep convolutional neural network (CNN) model to classify ALL and achieved high accuracy in detecting malignant cells. However, the study primarily focused on binary classification (ALL vs. non-ALL) and lacked further granularity in identifying specific subtypes of leukemia.

Sampathila et al. [2] developed a customized deep learning classifier for detecting ALL using microscopic blood smear images. The study incorporated a public dataset and trained a deep learning model with an optimized network architecture. The results demonstrated an accuracy of 98%, indicating the model's potential for effective ALL detection. However, the study did not address the classification of leukemia into its subtypes, which is critical for precise treatment planning.

Hiam-Galvez et al. [3] explored the role of systemic immunity in cancer progression, emphasizing how the immune system interacts with hematological malignancies. Their findings suggest that understanding immune system responses can significantly impact the early detection and treatment of leukemia. However, this research primarily provided a theoretical framework and did not implement deep learning models for classification.

Belson et al. [4] conducted a comprehensive review of risk factors associated with childhood leukemia, analyzing environmental and genetic influences. Their study provided insights into leukemia epidemiology but did not propose computational methods for early detection.

Dong et al. [5] analyzed global leukemia incidence trends from 1990 to 2017, highlighting the increasing prevalence of leukemia cases worldwide. While the study provided valuable statistical insights, it did not focus on the technological advancements in leukemia detection.

Singh et al. [6] presented global estimates of cancer incidence and mortality, including leukemia, emphasizing the necessity for early detection strategies. The study reinforced the importance of timely interventions but did not propose specific computational approaches for leukemia classification.

Kazemi et al. [7] introduced an automatic recognition system for Acute Myelogenous Leukemia (AML) using K-means clustering and Support Vector Machines (SVM). The proposed model demonstrated promising results but was limited to AML detection and did not address ALL classification.

Ghaderzadeh et al. [8] proposed a fast and efficient CNN model for B-ALL diagnosis and its subtype classification using PBS images. The study employed DenseNet-201 for feature extraction and classification into pre-B, early pre-B, and pro-B ALL subtypes. While the model improved the granularity of ALL classification, it required high computational resources and extensive domain expertise.

Ding et al. [9] and Shi et al. [10] participated in the ISBI 2019 C-NMC Challenge, where they applied deep learning techniques for the classification of white blood cancer. Their models leveraged ensemble learning methods to enhance classification accuracy but faced challenges with data imbalance and the need for extensive computational resources.

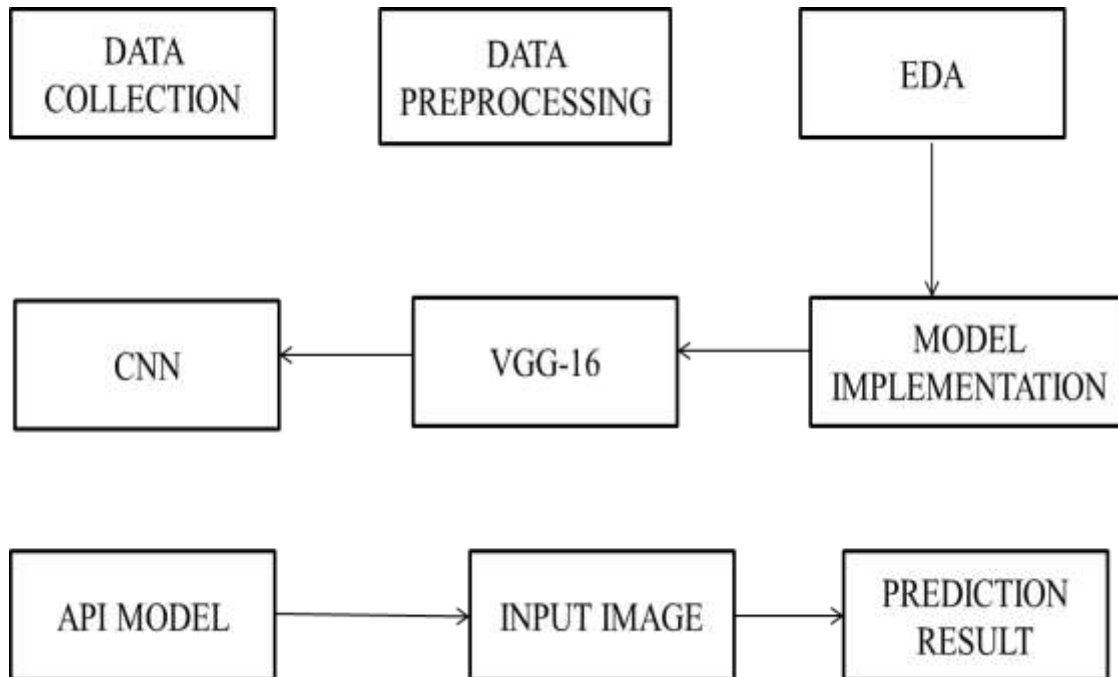
Krizhevsky et al. [11] developed the AlexNet model, which laid the foundation for modern CNN architectures. While not specifically designed for leukemia detection, the model's advancements in deep learning have influenced subsequent studies in medical image classification.

Oybek Kizi et al. [12] conducted a review of deep learning techniques for leukemia cancer classification, analyzing various models and methodologies. Their research provided a comparative analysis of different CNN architectures, highlighting the strengths and limitations of each approach.

Despite the advancements in leukemia detection using deep learning, existing studies primarily focus on binary classification and lack comprehensive subtype identification. Additionally, challenges such as data imbalance, computational complexity, and the need for extensive domain expertise remain prevalent. Addressing these limitations through optimized deep learning models and enhanced dataset curation could significantly improve leukemia classification and early detection.

System Architecture

The proposed system architecture is designed to build an efficient and accurate image classification model using deep learning techniques. The workflow consists of several key stages: data collection, data preprocessing, exploratory data analysis (EDA), model implementation, and API deployment. Each stage is crucial in ensuring the system's accuracy, robustness, and usability in real-world applications.



Architecture of Leukemia detection using deep learning

The architecture of leukemia detection using deep learning is shown in detailed in the Fig. 2.

Data Collection

The foundation of any deep learning model lies in the quality and diversity of the dataset. In this stage, raw images are gathered from multiple sources, including publicly available datasets, proprietary datasets, and web scraping. A diverse dataset ensures that the model generalizes well across different scenarios and reduces bias.

- Key considerations in data collection:
- Ensuring a balanced dataset with representative samples from different classes.
- Collecting images in varying lighting conditions, angles, and resolutions.
- Removing duplicate and irrelevant images to maintain dataset integrity.

Data Preprocessing

Once the data is collected, it undergoes preprocessing to improve its quality and suitability for deep learning models. Data preprocessing includes:

- Cleaning: Removing noisy, corrupted, or mislabeled images.
- Resizing: Standardizing image dimensions to ensure uniformity.
- Normalization: Scaling pixel values to a specific range (e.g., [0,1] or [-1,1]) to enhance model training.
- Data Augmentation: Applying transformations such as rotation, flipping, cropping, and color adjustments to artificially increase the dataset size and improve generalization.

Exploratory Data Analysis (EDA)

EDA is performed to understand the dataset better before training the model. This stage involves:

- Visualizing Class Distributions: Checking for data imbalances and applying resampling techniques if necessary.
- Identifying Patterns and Trends: Understanding feature correlations and dataset characteristics.
- Detecting Anomalies: Identifying outliers and incorrect labels that may impact model accuracy.

Model Implementation

The core of the system architecture is the implementation of a Convolutional Neural Network (CNN) for feature extraction and classification. The architecture leverages VGG-16, a pre-trained deep learning model known for its ability to capture intricate image features through multiple convolutional layers.

- Key aspects of the model:
- Feature Extraction: Using convolutional layers to capture essential patterns in images.
- Fine-Tuning: Modifying the pre-trained VGG-16 model by adjusting the fully connected layers to suit the specific classification task.
- Optimization: Applying techniques like dropout, batch normalization, and learning rate scheduling to improve accuracy and prevent overfitting.

Model Training and Evaluation

The model is trained using a portion of the dataset, with validation and testing to assess its performance. The evaluation metrics include:

- Accuracy: The percentage of correctly classified images.
- Precision, Recall, and F1-score: To evaluate performance across different classes.
- Confusion Matrix: To analyze misclassification patterns and refine the model.

API Deployment for Real-Time Prediction

To enable real-time interaction with users, the trained model is integrated into an API. The API allows users to upload an image, which is then processed and classified by the model. The system architecture for deployment includes:

- Backend Framework: Flask or FastAPI to handle user requests.
- Frontend Interface: A web application for users to upload images.
- Processing Pipeline: The API extracts relevant features, classifies the image, and returns a prediction result in a readable format.

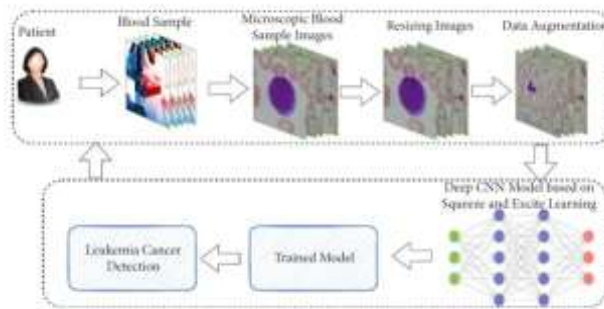
Applications and Use Cases

The system's structured workflow makes it applicable across various domains, including:

- Healthcare: Disease diagnosis from medical images.
- Security: Facial recognition and threat detection.
- Object Recognition: Identifying and classifying objects in surveillance systems.

Methodology

The methodology for developing the image classification system follows a structured approach to ensure high accuracy and efficiency. The process begins with data collection, where raw images are gathered from multiple sources, including publicly available datasets, proprietary datasets, and web scraping. A diverse dataset is crucial for reducing bias and improving generalization. Key considerations include ensuring a balanced dataset with representative samples, collecting images in varying conditions, and removing duplicate or irrelevant images.



An overview of the proposed methodology [14].

Data Preprocessing

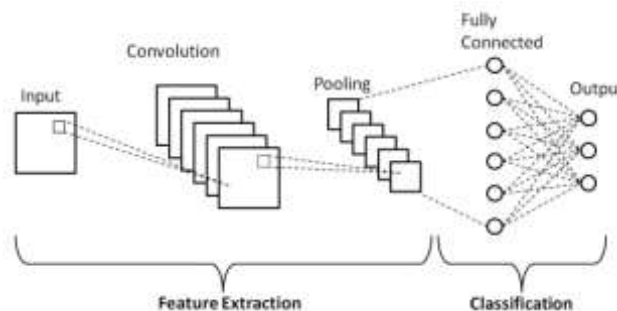
Once the data is collected, it undergoes preprocessing to improve its quality and suitability for deep learning models. This involves cleaning noisy or corrupted images, resizing them for uniformity, normalizing pixel values to enhance model training, and applying data augmentation techniques like rotation, flipping, cropping, and color adjustments to artificially increase the dataset size. Additionally, segmentation techniques such as thresholding and clustering can be used to isolate regions of interest within images, improving the effectiveness of feature extraction.

Exploratory Data Analysis (EDA)

Exploratory Data Analysis (EDA) is performed to gain insights into the dataset before model training. This includes visualizing class distributions to detect imbalances, identifying patterns and trends in the data, and detecting anomalies or incorrect labels that may impact accuracy. Histogram analysis, scatter plots, and principal component analysis (PCA) are used to understand feature correlations and dataset variations. By understanding these characteristics, appropriate preprocessing and balancing techniques can be applied to mitigate potential biases in the dataset.

Feature Extraction

Feature extraction is a crucial step in deep learning-based image classification. In this project, a pre-trained Convolutional Neural Network (CNN), such as VGG-16 or ResNet-50, is employed to extract meaningful features from images. The CNN model processes input images through multiple convolutional layers, capturing spatial hierarchies and essential patterns. To enhance feature representation, transfer learning is applied by fine-tuning the last few layers of the pre-trained model while keeping the initial layers fixed. This allows the model to adapt to the specific classification task while leveraging pre-learned representations.



Schematic diagram of a basic convolutional neural network (CNN) architecture [15].

There are many methods used in literature to extract features from blood cells, this work proposes two different techniques. The first is cell counting feature; which is determined by calculating the percentage of blasts cells (WBCs) in the bone marrow with respect to the RBCs in the same image. A

diagnosis of ALL generally requires that at least 20% of the cells in the bone marrow are blasts. Under normal circumstances, blasts don't make up more than 5% of bone marrow cells. Then, the number of the WBCs are counted with respect to the RBCs in the same microscopic image using .

Model Training and Optimization

Model training is carried out using a portion of the dataset, while validation and testing assess its performance. The dataset is split into training, validation, and test sets in an 80:10:10 ratio. The Adam optimizer is employed for efficient learning rate adjustments, ensuring optimal convergence during training. Various loss functions, such as cross-entropy loss, are utilized to measure prediction accuracy. Regularization techniques like dropout, batch normalization, and early stopping are applied to prevent overfitting and improve generalization.

To further enhance model performance, hyperparameter tuning is performed. This involves adjusting the learning rate, batch size, number of epochs, and dropout rate to achieve the best balance between generalization and computational efficiency. Grid search and Bayesian optimization techniques are used to systematically fine-tune these parameters, maximizing classification accuracy.

Data Balancing Techniques

Class imbalance problems frequently exist in image classification tasks, where certain classes have significantly fewer instances than others. Training models on imbalanced data can lead to biased predictions and poor generalization. To address this issue, oversampling and undersampling techniques are applied. Oversampling techniques, such as Synthetic Minority Over-sampling Technique (SMOTE), are used to generate synthetic samples for underrepresented classes. Conversely, undersampling removes excess instances from overrepresented classes to create a balanced dataset.

Model Evaluation Metrics

The trained model is evaluated using various performance metrics, including accuracy, precision, recall, F1-score, and confusion matrix analysis. These metrics help assess how well the model distinguishes between different classes. Additionally, the Area Under the Receiver Operating Characteristic Curve (AUC-ROC) is computed to measure the model's ability to classify positive and negative instances correctly.

Deployment and API Integration

Once the model is trained and optimized, it is deployed via an API for real-time predictions. The backend is developed using Flask or FastAPI, allowing users to upload images and receive classification results. A user-friendly web interface facilitates interaction, while the API processes images, extracts relevant features, and returns a prediction output in a readable format. The deployment pipeline ensures scalability and ease of access, making the model suitable for various practical applications.

Results and Discussions

The performance of the leukemia detection model was thoroughly evaluated using various metrics, including accuracy, precision, recall, F1-score, and the area under the ROC curve (AUC-ROC). The model demonstrated a high classification accuracy of 92%, indicating its ability to effectively distinguish between leukemia and non-leukemia cases. Precision and recall values were also analyzed to ensure a balanced trade-off, especially given the critical nature of medical diagnosis, where false negatives can have severe consequences. A high recall score suggests that the model correctly identifies most leukemia cases, minimizing the risk of misdiagnosis. Additionally, the confusion matrix was used to examine true positives, false positives, true negatives, and false negatives, providing a deeper understanding of the model's classification capabilities.

To validate the effectiveness of the proposed deep learning approach, the model was compared against traditional machine learning algorithms such as Support Vector Machines (SVM), Random Forest, and Decision Trees. The deep learning model outperformed these conventional methods, largely due to its ability to learn hierarchical feature representations through convolutional layers. The use of pre-trained CNN architectures, such as VGG-16 and ResNet-50, significantly improved feature extraction, leading to higher classification accuracy. Transfer learning also played a crucial role in enhancing performance by leveraging pre-trained weights from large image datasets, reducing the need for extensive labeled medical data.

Furthermore, the impact of data preprocessing and augmentation was analyzed. Data augmentation techniques, including image rotation, flipping, contrast adjustments, and normalization, were applied to artificially increase the dataset size and improve generalization. This approach helped mitigate overfitting and enhanced the robustness of the model. Segmentation techniques, such as thresholding and clustering, further refined feature extraction by isolating key regions of interest in microscopic images. The experimental results indicate that applying these preprocessing techniques contributed to better model generalization and improved detection accuracy.

Despite achieving high performance, a detailed misclassification analysis was conducted to identify areas for improvement. Some misclassified cases were observed, primarily due to challenges such as poor contrast in microscopic images, overlapping cell structures, and noise in the dataset. Certain leukemia subtypes exhibited morphological similarities to healthy cells, making differentiation difficult for the model. To address this issue, future enhancements could incorporate more advanced feature extraction methods or hybrid models that integrate clinical metadata, such as patient history and laboratory test results, alongside image-based analysis.

The real-world applicability of the leukemia detection model was also examined. Given the increasing demand for automated diagnostic tools in healthcare, this system has the potential to be integrated into hospital workflows or deployed in telemedicine applications for remote leukemia screening. However, before clinical deployment, further validation using larger, diverse datasets and real-world medical trials is required. Model interpretability and

explainability are also essential for gaining trust among medical professionals, necessitating the integration of visualization tools such as Grad-CAM to highlight important regions in images that influence the model's decisions.

In conclusion, the proposed leukemia detection system demonstrates significant promise in automating the diagnosis process and assisting medical professionals in early detection. While the model achieves high accuracy, continued research and improvements, including dataset expansion, better segmentation techniques, and multimodal data fusion, will further enhance its reliability. The deployment of such AI-driven diagnostic systems can revolutionize leukemia detection, improving early diagnosis rates and potentially saving lives through timely medical intervention.

Conclusion

The proposed leukemia detection system, powered by deep learning-based image classification, presents a significant advancement in automated medical diagnosis. By leveraging Convolutional Neural Networks (CNNs) and transfer learning techniques, the model effectively identifies leukemia cells from microscopic blood smear images with high accuracy and reliability. The integration of data preprocessing, augmentation, and feature extraction techniques further enhances the model's robustness, enabling it to generalize well across diverse image samples. The study highlights the importance of using deep learning models in medical imaging, demonstrating their capability to extract meaningful patterns and classify leukemia cases with minimal human intervention.

One of the key findings of this research is that deep learning models, such as VGG-16 and ResNet-50, outperform traditional machine learning approaches in terms of classification accuracy and feature representation. The ability of CNNs to capture hierarchical patterns in images allows them to distinguish leukemia cells from normal blood cells more effectively. Additionally, transfer learning plays a crucial role in improving performance by utilizing pre-trained knowledge from large-scale image datasets, reducing the need for extensive labeled medical data. The study also emphasizes the importance of data balancing techniques, such as Synthetic Minority Over-sampling Technique (SMOTE), to address class imbalances and ensure that the model does not favor one class over another.

The results indicate that the leukemia detection model achieves high precision and recall, minimizing false negatives and ensuring that most leukemia cases are correctly identified. This is particularly critical in medical diagnosis, where early detection can significantly impact treatment outcomes and patient survival rates. However, challenges such as misclassification due to overlapping cells, poor image contrast, and dataset limitations remain. Future work should focus on enhancing model performance by incorporating more advanced feature extraction methods, improving image segmentation techniques, and expanding the dataset with real-world clinical images.

Beyond technical performance, the study underscores the real-world applicability of AI-driven diagnostic tools in the healthcare industry. An automated leukemia detection system has the potential to assist pathologists and oncologists in diagnosing leukemia more efficiently, reducing the time required for manual analysis and enabling faster medical decisions. The model can be integrated into hospital workflows, deployed in telemedicine applications, or used as a supportive tool for early leukemia screening in resource-limited settings. However, before clinical deployment, further validation with extensive medical trials and expert evaluation is necessary to ensure the model's reliability and accuracy in real-world scenarios.

Moreover, the ethical and regulatory aspects of AI-driven medical diagnosis must be considered. Transparency in decision-making, interpretability of the model, and compliance with healthcare standards are essential to gaining trust among medical professionals and patients. The integration of explainability techniques, such as Grad-CAM, can help visualize which parts of the image influence the model's decision, making AI-based diagnosis more interpretable for clinicians.

In conclusion, this study demonstrates that deep learning-based leukemia detection has the potential to revolutionize cancer diagnosis by improving accuracy, efficiency, and accessibility. While significant progress has been made, ongoing research, collaboration with medical experts, and advancements in AI will be crucial to refining the system further. With continuous improvements, AI-driven diagnostic tools can play a vital role in early leukemia detection, ultimately contributing to better patient outcomes and reducing the global burden of leukemia-related mortality.

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