Damanhour Journal of Intelligent Systems and Informatics
Volume 2 – Issue 1

AI-Driven Innovations in Leukemia Detection: A Systematic Review of Machine Learning, Deep Learning, and Metaheuristic Techniques

M. A. Sayedelahl [1], Aisha A. Elhussiny [2] ,Basmla H. Khalaf [2] ,Hana A. Elfekharany [2] ,Sama S. Makhlof [2] ,Walaa Y. Badawy [2] ,
[1]Departement of computer science, faculty of Computer and Information, Damanhur University, Egypt.
[2]Departement of Bioinformatics, Faculty of Science, Benha University, Egypt.

Abstract— *This systematic review evaluates artificial intelligence (AI) techniques—including machine learning (ML) , deep learning (DL) , and metaheuristic optimization—in advancing leukemia detection and classification . A PRISMA (Preferred Reporting Items for Systematic Reviews and Meta-Analyses)-compliant search of Scopus, PubMed, and Web of Science (2019–2025) identified 45 high-quality studies analyzing AI applications in leukemia subtypes (e.g., acute lymphoblastic leukemia (ALL) , acute myeloid leukemia (AML) , and multiple myeloma (MM)). Key findings reveal that DL models (e.g., convolutional neural networks (CNNs)) achieved up to 97.2% accuracy in classifying leukemia subtypes using histopathological and flow cytometry data. Hybrid approaches like laser-induced breakdown spectroscopy (LIBS) combined with ML demonstrated 98.34% accuracy in detecting genomic markers, offering cost-effective, non-invasive solutions. Metaheuristic algorithms (e.g., binary brown-bear optimization (BBBO)) improved feature selection, addressing high-dimensional data challenges. Notable advancements include circulating tumor DNA (ctDNA) methylation analysis (95% pre-diagnosis sensitivity) and federated learning for privacy-preserving diagnostics. However, limitations persist, such as small dataset sizes, spectral noise sensitivity in LIBS, and lack of clinical validation. Future directions include multi-center trials, integration of genomics with AI, and explainable AI to enhance clinician trust. This work highlights AI's transformative potential in early detection and precision medicine, with implications for reducing mortality and improving patient outcomes in leukemia management.*

Keywords— ***AI (Artificial Intelligence), ML (Machine Learning), DL (Deep Learning), LIBS (Laser-Induced Breakdown Spectroscopy), PRISMA, leukemia detection, systematic review.***

1.Introduction

Leukemia is a hematological malignancy characterized by the uncontrolled proliferation of abnormal hematopoietic progenitor cells, leading to bone marrow infiltration and impaired blood cell production. According to the World Health Organization (WHO), leukemia is classified into myeloid and lymphoid lineages, encompassing four major subtypes: acute lymphoblastic leukemia (ALL), acute myeloid leukemia (AML), chronic lymphocytic leukemia (CLL), and chronic myeloid leukemia (CML). Globally, leukemia accounts for approximately 2.5% of new cancer cases and 3.1% of cancer-related deaths annually. ALL is the most prevalent form in children under five, while AML remains the most common acute leukemia in both adults and children [1]. Genetic predisposition, environmental exposures (e.g., benzene, radiation), and lifestyle factors (e.g., obesity, smoking) contribute to its etiology [1]. Chronic myeloid leukemia (CML) is strongly associated with the Philadelphia chromosome, which encodes the BCR-ABL fusion gene, while CLL progresses slowly and often requires delayed treatment [2]. Traditional diagnosis relies on manual microscopic evaluation of blood smears and bone marrow biopsies, which are labor-intensive and prone to human error. Recent advancements in artificial intelligence (AI), particularly (ML) and (DL), have revolutionized leukemia detection by automating image analysis. For instance, convolutional neural networks (CNNs) like ALNet achieve 94.2% accuracy in distinguishing APL, AML, ALL, and infections by extracting features from microscopic images [4]. These AI-driven tools reduce diagnostic delays and enhance accuracy, offering clinicians critical decision-support in resource-limited settings [5]. This study explores how AI techniques improve leukemia classification, addressing the limitations of conventional methods.

1.1. Motivation

Despite advancements in treatment, leukemia remains a leading cause of cancer-related mortality in children and adults. Early diagnosis is critical for improving survival rates, yet traditional microscopic analysis is time-consuming and error-prone. AI technologies, including ML and DL, have emerged as

promising tools to address these challenges by automating image analysis and enhancing diagnostic precision [3]. However, current AI models often lack generalizability across diverse datasets and clinical settings. This study is motivated by the urgent need to:

Bridge the gap between AI research and clinical practice by evaluating model performance on real-world datasets. Improve diagnostic reliability through comparative analysis of neural network architectures and hyperparameters Facilitate early detection by integrating AI with routine blood smear analysis, reducing reliance on manual interpretation.

By addressing these challenges, this research aims to refine AI-driven diagnostics and ultimately enhance patient outcomes.

1.2. Main contribution

The paper's primary contribution is a comprehensive collection of recent studies on leukemia blood cancer and the systems that detect them. It presents existing issues and unfulfilled research needs, giving academics a clear picture and a strong starting point for more investigation into the application of AI and metaheuristic to leukemia blood cancer detection and reduction. The research's contributions can be summarized in the following topics:

Systematic Review of AI Techniques : A comprehensive analysis of ML, DL, and hybrid methods (e.g., LIBS combined with ML) applied to leukemia classification, emphasizing their accuracy and clinical applicability.

Critical Evaluation of 30+ Studies : Rigorous assessment of peer-reviewed articles (2018–2025) across methodology, dataset quality, AI techniques, and performance metrics (e.g., accuracy, sensitivity).

Dataset Analysis : Identification of commonly used datasets (e.g., ALL-IDB1, private datasets) and their limitations, such as small sample sizes and class imbalance.

Comparative Tables : Synthesis of key findings into structured tables for easy comparison of model performance, challenges, and future directions.

Future Research Directions : Identification of unresolved issues (e.g., spectral noise in LIBS, lack of clinical validation) and recommendations for multi-center trials and explainable AI. These contributions provide a roadmap for advancing AI applications in leukemia detection and precision medicine.

1.3. Paper structure

The study offers a systematic investigation of AI techniques in leukemia blood cancer and is structured into six main sections and organized as follows:

Section 1: This section outlines the motivation for the study and the contributions made. It emphasizes the importance of exploring this topic and its potential to create a meaningful impact in the field.

Section 2: Traces the historical evolution of leukemia research, including key discoveries in classification and the role of AI in diagnosis and treatment.

Section 3: Reviews recent literature on AI techniques, emphasizing breakthroughs like ALNet and SMOTE-Tomek for addressing class imbalance.

Section 4: Describes the systematic review methodology, including PRISMA compliance, databases (Scopus, PubMed), and inclusion/exclusion criteria.

Section 5: Presents results, including accuracy metrics (e.g., 98.34% for LIBS-ML hybrid models) and critical analysis of limitations.

Section 6: Concludes with implications for clinical practice and future research priorities.

2. Background

Leukemia is a type of cancer that affects blood-forming tissues, including the bone marrow and lymphatic system, leading to abnormal white blood cell production. Historically, it was first described in the early 19th century by physicians like Peter Cullen and Rudolf Virchow, who coined the term leukämie in 1847. Leukemia is classified into acute and chronic types, as well as lymphocytic and myeloid forms, depending on the affected cells and disease progression. While its exact cause remains unclear, risk factors include genetic predisposition, exposure to radiation and chemicals, and certain viral infections. Common symptoms include fatigue, fever, frequent infections, and unexplained bruising. Diagnosis is primarily done through blood tests, bone marrow biopsies, and genetic analysis. Treatment options vary based on the type and severity of leukemia, ranging from chemotherapy and radiation therapy to bone marrow transplants and targeted immunotherapies. Advances in research, particularly in personalized medicine and immunotherapy, have significantly improved patient outcomes over the years [6]. Understanding the risk factors associated with leukemia is crucial for early detection and prevention, as various genetic and environmental influences contribute to its development [7]. Several risk factors contribute to the development of leukemia. Environmental factors such as exposure to ionizing radiation and

toxic chemicals like benzene have been linked to an increased risk of leukemia. Genetic predisposition also plays a role, with chromosomal abnormalities such as the Philadelphia chromosome (Ph+) being associated with CML and some cases of ALL. Additionally, individuals with genetic disorders like Down syndrome have a higher likelihood of developing leukemia. Viral infections, including Epstein-Barr virus (EBV), have also been implicated in the disease's onset. Other contributing factors include age and gender, as leukemia risk tends to increase with age and is more prevalent in males. Moreover, patients who have undergone chemotherapy for other cancers may face an elevated risk of secondary leukemia [7].

Over the past decade, blood cancer has emerged as a growing global health concern, highlighting the need for early and accurate diagnosis to improve patient outcomes. Traditional diagnostic methods rely on a series of laboratory tests and expert medical evaluations, which can be both time-consuming and expensive. As a result, research has increasingly shifted towards developing automated diagnostic systems that leverage machine learning to enhance the accuracy and efficiency of leukemia detection. Despite significant progress, further improvements are needed to optimize diagnostic precision and ensure clinical applicability[8].

Recent advancements in artificial intelligence (AI) have revolutionized leukemia diagnosis, particularly through deep learning techniques like convolutional neural networks (CNNs). These models analyze blood smear images to detect abnormal cells with high accuracy, offering a promising alternative to conventional diagnostic approaches. One notable model, ALNet, has achieved a 94.2% accuracy in distinguishing leukemia subtypes, including acute promyelocytic leukemia (APL), AML, and ALL. Additionally, techniques like SMOTE-Tomek have been employed to address class imbalance issues, further enhancing diagnostic reliability. AI-driven approaches provide a faster, more cost-effective, and highly precise method for leukemia detection compared to traditional techniques, though challenges such as data availability and clinical validation remain key areas for future improvement[9]. With some models achieving nearly 99.9% accuracy, artificial intelligence continues to demonstrate immense potential in transforming leukemia diagnosis and patient care[10].

Significant advancements in leukemia treatment have improved survival rates and patient outcomes in recent years. Targeted therapies, such as tyrosine kinase inhibitors (TKIs) like imatinib, have transformed the management of chronic myelogenous leukemia (CML) by specifically targeting the BCR-ABL fusion protein, thereby inhibiting cancer cell proliferation. Monoclonal antibodies, including rituximab and blinatumomab, have enhanced treatment efficacy by selectively targeting leukemia cells while minimizing harm to normal cells. Immunotherapies, such as chimeric antigen receptor (CAR) T-cell therapy, have demonstrated remarkable success in treating relapsed or refractory ALL by harnessing the patient's immune system to attack cancerous cells. Furthermore, advancements in hematopoietic stem cell transplantation (HSCT) and the development of personalized medicine approaches continue to improve treatment outcomes by tailoring therapies to the genetic profile of individual patients [11].

2.1. Artificial Intelligence

Artificial intelligence-based technologies such as (ML) and (DL) enable doctors to digitize medical images and detect patterns faster and more accurately than traditional methods relying on humaninspection.AI technologies are characterized by their ability to process huge volumes of data such as blood images, genetic testing, and gene expression data. In leukemia, AI models are trained on a huge dataset of medical blood images, such as peripheral blood smears (PBS) and bone marrow images, to recognize abnormal cells such as primitive cells (blasts), which indicate the presence of disease.One of the areas which have been significantly enhanced through the application of artificial intelligence is WBC classification. In traditional procedures, the analysis relies on a visual examination of the cells using the microscope and physically identifying their type, which may be prone to human error. But with artificial intelligence, the computer is able to distinguish more accurately between abnormal and normal cells by examining the pictures, reducing the rate of human error and shortening the diagnosis time.Artificial intelligence also utilizes techniques such as convolutional neural networks (CNNs) which can automatically examine images and detect fine characteristics not discernible by the human eye. This can be utilized to more precisely diagnose many types of leukemia such as acute lymphoid leukemia (ALL) or acute myeloid leukemia (AML).in addition, artificial intelligence mayhasten genetic analysis processes such as multiple gene analysis (PCR) and hybrid fluorography (FISH) by detecting genetic patterns that may be responsible for the disease's onset to aid in the determination of most efficient treatment procedures.Artificial intelligence has become a basic component of computer-aided diagnostic system

development and is crucial to improve the speed and accuracy of diagnosis, leading to improved treatment results and reduced delay in disease detection.

2.2. ML

(TML) techniques have shown great potential in classifying and detecting leukemia by analyzing images of blood smears. These methods usually include several steps such as: pre-image processing, division, feature extraction, and classification. Algorithms such as carrier support machines (SVM), close neighbor (KNN), Navia Bayes, and decision trees have been widely used to classify white blood cells, especially to distinguish between normal and leukemia-infected cells. Research highlights how TML models can help hematologists with early and accurate detection of leukemia, reducing diagnostic time and reducing human errors.

2.3. DL

(DL) and, specifically, bypass neural networks (CNNs) revolutionized medical image analysis by making end-to-end systems that automatically learn high-level features from unprocessed data possible without the need for manual design of features. In leukemia, CNNs were effectively used to differentiate types of white blood cells and detect blood smear abnormalities. DL methods are more robust and precise than traditional methods, and transfer and integration learning approaches have been applied in studies to improve performance in certain studies. The methods are specifically applicable where large amounts of data, where manual analysis is impossible.

3. Literature review

In the last ten years, a growing number of studies have documented the use of artificial intelligence (AI) to classify and detect leukemia. Authors have explored a vast variety of (ML), (DL), and hybrid methods to improve diagnostic accuracy and automate the analysis of blood smears. This section gives a contemporary perspective on recent advances, criticizing the methods employed, their efficacy in different subtypes of leukemia, and the strengths and limitations of each technique.

From 2019 to 2024, several ML and DL approaches have been proposed for leukemia detection and classification from microscopic blood images. Nizar Ahmed et al. [27]used a CNN model on the ALL-IDB and ASH datasets and achieved 88.25% accuracy in binary classification and 81.74% in multi-class classification. Rohit Agrawal et al. [47] enhanced CNN-based classification through preprocessing, segmentation, and texture feature extraction and achieved 97.3% accuracy.

Sara Hosseinzadeh Kassani et al. [48] proposed a hybrid VGG16-MobileNet feature fusion model and attained 96.17% accuracy. Mohamed Loey et al. [49] utilized transfer learning with fine-tuned AlexNet and attained 100% accuracy. Puneet Mathur et al. [50] proposed a Mixup Multi-Attention Multi-Task Learning model and attained an F1-score of 0.9189. Syadia Nabilah Mohd Safuan et al. [51] compared AlexNet, GoogleNet, and VGG16, with AlexNet having the highest accuracy at 97.74%. Shamama Anwar et al. [52] proposed a 10-layer customized CNN that achieved over 99% test accuracy on augmented ALL-IDB datasets.

Lightweight approaches showed promise as well. Md. Alif Rahman Ridoy et al. [53] created a LeNet-derived CNN to classify white blood cells using the BCCD dataset with a result of F1-score equal to 0.97. Nighat Bibi et al. [54] presented an IoMT approach using ResNet-34 and DenseNet-121 that provided 100% accuracy when using samples in ASH as well as ALL-IDB cases.

Transfer learning and attention-based methods were employed to a large extent. Jens Schouten et al. [55] deployed a compact CNN with ROC-AUC of 0.97 ± 0.02 using 200 images for training. Pradeep Kumar Das et al. [56] used ShuffleNet, in combination with resizing and data augmentation, to obtain 96.97% and 96.67% precision for IDB1 and IDB2, respectively. They subsequently suggested hybrid CNNs by combining MobileNetV2 and ResNet18 [56], which had accuracies of 99.39% and 97.18%.

Zhencun Jiang et al. [57] proposed a ViT-CNN ensemble of Vision Transformers and EfficientNet, with 99.03% accuracy on ISBI 2019. De Sant' Anna et al. [58] fused statistical and morphological features with DL to achieve an F1-score of 91.2% on the C-NMC 2019 dataset at minimal computational cost. Azamossadat Hosseini et al. [59] designed a MobileNetV2-based mobile app for real-time detection of B-ALL, achieving 100% accuracy on 3,242 local images.

Other hybrid and ensemble models are Ibrahim Abunadi et al. [60], who compared CNN, ANN, and CNN+SVM with nearly perfect accuracy on ALL-IDB1/2. Maryam Bukhari et al. [61] used squeeze-and-excitation blocks in CNN with 100% and 99.98% accuracy on ALL-IDB1 and ALL-IDB2. Zahra Boreiri et al. [62] introduced a convolutional neuro-fuzzy model with 97.31% accuracy using fuzzy color segmentation.

Tanzilal Mustaqim et al. [63] optimized YOLOv4/v5 with GhostNet to detect ALL subtypes (L1, L2, L3) with a reduction of GFLOPs and parameters by 35–40% without loss of accuracy. Protiva Ahammed et al.

[65] employed a multi-stage transfer learning pipeline of InceptionV3, Xception, and InceptionResNetV2 and U-Net for segmentation with 99.6% accuracy.

Ghaderzadeh et al. [30] proposed a DL approach for ALL subtype classification from PBS images. An optimized CNN architecture was introduced by Atteia et al. [**], while Jha and Dutta [**] proposed a hybrid scheme. Mohammed [67] explored omics data analysis with AI, opportunity and limitation both. Eckardt et al. [64] reviewed the applications of ML in AML diagnosis and therapy, and Anilkumar et al.[66] compared segmentation methods in bone marrow and blood images.

End-to-end pipelines were targeted by Saleem et al. [68] and Aswathy Elma Aby et al. [69], where they used resizing, normalization, enhancement, segmentation, feature extraction, and classification on blood smear, bone marrow, and gene expression data with more than 90% accuracies. CNN-based approaches displayed strong diagnostic performance across the board.

Amogh Ramagiri et al.[70] applied CNNs for the prediction of leukemia. Atteia [**] proposed a hybrid DL model integrating GoogleNet and Inception-v3 on atomic blood smear images. Authors compared seven DL techniques for ALL feature extraction.

Ebtisam Abdullah Alabdulqader et al. [17]employed a number of ML classifiers (KNN, RF, LR, ETC, SVC, ADA, NB, DT) and proposed WVCNN, which showed strong performance for blood cancer prediction. Mustafa Ghaderzadeh et al. [30]reported a systematic review on the use of ML in PBS image-based diagnosis of leukemia.

Mohammad Akter Hossain et al.[38] developed a mobile-based diagnostic system pre-processing image data in servers and applying ML models (DT, RF, KNN, AdaBoost, LR, NB, ANN) to identify leukemia. Wahidur Rahman et al.[25] employed Bayesian-optimized CNN for ALL detection on a hybrid ALL-IDB1/2 dataset with a 100% success rate.

Saroosh Malik et al. [37]criticized manual diagnostic limitations and reviewed historical and current ML applications in leukemia prediction. Kokeb Dese et al.[29] built an automatic ML-based leukemia classifier to replace manual diagnosis. Tulasi Gayatri Devi et al. [46] proposed a color thresholding-based method to detect ALL by detecting WBCs, segmenting lymphocytes, and identifying lymphoblasts. Their system had 92.15% accuracy, 96.92% sensitivity, and 91.35% precision, proving the merit of conventional image processing.

4. Methodology

This study employs a systematic review methodology following the PRISMA (Preferred Reporting Items for Systematic Reviews and Meta-Analyses) guidelines to evaluate the application of artificial intelligence (AI) techniques in leukemia detection and classification. The methodology is structured to address research questions, identify relevant studies, and synthesize findings to highlight advancements, limitations, and future directions.

We started off by searching relevant research using academic databases, filtering out studies (from 86 to 40) that encompassed PubMed, Scopus, IEEE Xplore, and Google Scholar. Search terms including "leukemia detection," "blood smear examination," "ML in hematology," and "DL for health imaging" defined the search. Studies were eligible if they centered on computational or image-based diagnosis of leukemia, were peer-reviewed, published in the past ten years, and English language.To understand the various methods used in the literature, we categorized the shortlisted studies into four broad themes that encapsulate the typical workflow in computational hematology:

1-Traditional method (image processing) :

There are numerous studies that rely on image processing and statistical methods to identify and clustering of leukemia .

2-ML Methods:

Multiple papers describe the procedure of extracting custom features from segmented images. Custom features are generally cell shape, size, color, and surface texture. After that, the classification is carried out using conventional machine learning models like support vector machines (SVMs), random forests, and gradient boosting models. The models provide understanding and act as good performance metrics.

3-DL Methods

More research studies use convolutional neural networks (CNNs) and other DL algorithms to automatically extract features from image data. The models are typically trained on very large labeled datasets and have high ability in recognizing fine morphological differences.

4-Hybrid and Integrative Methods

Some studies integrate classical and deep learning techniques to leverage the strengths of both interpretability and predictive ability. For example, human-crafted features can be combined with the output of CNNs to enhance the model's performance or provide more clarity in prediction.

Through the analysis and comparison of these methods, this review illustrates the intersection of machine learning and hematological wisdom to develop more precise, effective, and scalable systems for the diagnosis of leukemia. This methodology gives a formalized basis to review existing trends and explore potential avenues for additional research in computational pathology.

4.1. Research Questions (RQs)

To guide the systematic review, the following research questions were formulated to assess the role of AI in leukemia detection:

RQ1: Which (ML), (DL), and traditional (image processing) or hyperid models are currently used for leukemia detection and classification?

RQ2: What datasets (e.g., blood smear images, genetic markers) are most frequently employed in AI-driven leukemia studies?

RQ3: What performance metrics (e.g., accuracy, sensitivity, specificity) and limitations (e.g., dataset size, spectral noise) are reported for these AI models?

RQ4: What are advantages and disadvantages of AI models and traditional ?

RQ5: How do hybrid approaches (e.g., DL combined with ML and image processing) enhance diagnostic accuracy and clinical applicability?

4.2. Search Strategy and Study Selection

The reviewed approaches demonstrate how integrating traditional image processing techniques and hematological expertise with artificial intelligence (AI) including both (ML) and (DL) can lead to more scalable and accurate diagnostic tools for leukemia. This review focuses on how these methods are being used to support blood smear image analysis, from early-stage image preparation to advanced classification models.

A common pattern across the literature is the use of hybrid analytical strategies. In many cases, researchers extract handcrafted features such as cell shape, size, and texture, which are then used to train classical machine learning models like support vector machines (SVMs) or random forests. At the same time, more recent studies increasingly adopt deep learning approaches, especially convolutional neural networks (CNNs), to automate feature extraction and uncover complex patterns in blood smear images. These models are often trained on large annotated datasets, enabling them to learn representations directly from the data without manual input. Table 1 summarizes the inclusion and exclusion of papers criteria.

Table 1: Inclusion and Exclusion Criteria

Inclusion Criteria	Exclusion Criteria
Studies published in the last 7 years(2018-2025).	**Studies published more than 7 years ago.**
Research that have used image processing techniques , ML or DL in blood smears analysis.	**Studies that do not use AI techniques or image processing.**
Studies using real-world or public datasets to train or test AI models for leukemia diagnosis .	**Studies that do not use blood images or are not focused on leukemia.**
Research involving blood smear imaging, genetic data.	**Duplicate studies or datasets with fewer than 100 samples.**
Articles written in English and available in full text.	**Studies not written in English or not available in full text .**

RQ1: Which ML, DL, traditional, or hyperid models are currently used for leukemia detection and classification?

There are few models for leukemia diagnosis Using image processing as a traditional method in the last three years as presented in Table 2.

Table 2: Traditional methods.

Ref	Year	Methodology	Result	Dataset	Advantage	Limitation	Future direction
46	2023	(Gaussian Blurring & HSV Segmentation) GBHSV-Leuk method has two main stages: 1.Preprocessing:The Gaussian Blurring technique to reduce noise and blur. 2.Segmentation and classification	achieved an accuracy of 96.30% on the private dataset and 95.41% on the publicly available ALL-IDB1 datase	https://www.mdpi.com/search?q=ALL-IDB1	It achieved high accuracy in detecting ALL cancer cells which can help in early detection	limited detecti on of ALL cancer cells	the method may need to be extended to detect other types of leukemia and improved by adding more advanced image processing techniques or DL models

There are many applications of AI (ML,DL and Hyperid) models used in leukemia diagnosis in recent years.

ML models are summarized in the following table3.

Table 3:ML models.

Ref	Year	Methodology	Result	Dataset	Advantage	Limitation	Future direction
37	2022	collect, analyze, and summarize existing research on leukemia detection	Some model reach 98%	(NICHD) Datasets	Increased Accuracy, Reduced Human Error,Faster Diagnosis,Improved Early Detection	Variation in CBC Values Noisy and Missing Data ,Lack of Clinical Information Difficulty in Differentiating Between Leukemia Types	Digitization of pathology slides
38	2022	Explainable AI model, The dataset was split into training and testing sets.	97.45% accuracy	NICRH , Leukemia Dataset	Explain ability of AI result	Resource Constraints,Sample Size ,Geographical Limitation	Integration of AI into hospital
39	2022	drug response model Explainable Artificial Intelligence (XAI), a subfield of (ML) ,MOM	identified four AML patient subgroups based on biomarkers, and recommended targeted treatments	http://vizome.org/additional_figures_BeatAML.html	MOM's treatment recommendations are easy to understand, helps doctors optimize treatments.	computational complexity increases with the number of biomarkers and drugs,need more real-world validation	validation in clinical trials is still needed for MOM's treatment recommendations.

40	2022	Using regression and clustering then a decision tree model to detect leukaemia	Acute leukaemia is diagnosed with 97% Compared to manual ,and reduced analysis time	Data available upon request .	It reduced time ,improve classification accuracy	Need more diversity ,it was only based on one hospital data ,need more external validation	Intruduce deep learning (cnn) to improve sensitivity and reduce false positives ,integrates this tool into clinical decision-making system
41	2021	They used two machine learning models (XGBoost and LASSO) to predict the CML test result based on the blood cell count	The models were better able to predict CML when trained with data closer	Primary Data: Extracted from Electronic Health Records (EHR)	- Early Detection Capability -Non-Invasive & Cost-Effective -Integration with Routine Care	the retrospective, observational design and potential variability in the laboratory data	include prospective validation and investigation of whether earlier diagnosis leads to improved clinical outcomes
42	2020	Non-invasive blood test detecting ctDNA methylation across 595 genomic regions using semi-targeted PCR and machine learning (Logistic Regression)	88% sensitivity in post-diagnosis and 95% in pre-diagnosis	TZL	High accuracy,non surgical and early detection of cancer	Retrospective analysis.the type of tumor has not been determined. They didn't have cancer stage data for all patients.	Conduct a larger prospective study to confirm the results. Include identification of the tumor's tissue type of origin.
43	2020	Key marker selection and classification algorithm.a random forest algorithm to classify blood cancer stages.techniques like quantgene for enhanced detection	Improved accuracy ,effective classification.	HG-U133A microarray (Dataset 1) HG-U133 2.0 microarray (Dataset 2) Illumina RNA-seq (Dataset 3)	Combining feature selection with deep classification yields higher accuracy. Using Random Forest achieves a balance between performance and simplicity.	Performance variability when using the model in new environments or with new data. The data is heterogeneous (multiple sources and different objectives).	Improve the accuracy of models using deep learning, such as CNN or RNN. Expand the database to include more blood cancer types.

44	2023	analyze gene expression data from 72 patients diagnosed with acute myeloid leukemia (AML) and acute lymphoblastic leukemia (ALL),To identify the most relevant genes for distinguishing between AML and ALL,experimentin g with different values of the parameter p	Both RF and SVM classifiers achieved 100% accuracy in correctly classifying all AML and ALL samples.	ijpho.ssu.ac.ir	High Accuracy ,Efficiency ,Robustness	Sample Size, need a validation on larger datasets	Testing on more diverse datasets to validate and refine the gene selection and classification methods. ,Clinical Application for early and accurate diagnosis of leukemia.

DL models are summarized in the following table 4.

Table 4 :DL models.

REF	Year	methodology	result	dataset	advantages	limitations	Future directions
9	2020	-enhanced it with data augmentation. -performed feature selection	CNN with accuracy 97.2%	-used the SN-AM dataset	-Accuracy, -Efficiency, and -Compactness	-Not evaluated on larger -More diverse datasets	-Evaluate performance on more data
4	2021	The researchers developed ALNet, a two-step deep learning system	ALNet was able to correctly classify 100%.it had a sensitivity of 89% and specificity and precision of 100%	collected a large dataset of over 16,000 blood cell images	High Accuracy & Sensitivity Improved Patient Outcomes	-Single-Institution Data Bias -Compute Requirements	-Multi-Center Diverse Datasets -Hybrid Model Integration -Clinical Deployment
17	2019	CNN	achieving an impressive accuracy of 99.9%	GsE28497 dataset	Achieved a significant accuracy in blood cancer prediction	the study was limited to a single dataset	Merge multiple datasets. Develop a custom DL model.
27	2019	CNN	The analysis show that CNN and ViTs have a achieved a great classification of leuukemia	The study didn't use a single dataset ,review a popular datasets that used in previous studies such as ALL-IDB,c-NMC,ASH image bank.	it serves as a vital resource for reasearchers, helping to adoption of ai -driven solutions in leukemia diagnostics	Limited dataset and imbalance in categories	Create various datasets. . Developing explainable DL models.
45	2021	CNN to detect the type of white blood cancer (ALL or MM)	CNN achieved an accuracy of 97.2%	SN-AM.	Help in making a viable solution for practical deployment in clinical settings.	the study is limited to relatively small dataset.	should focus on exploring the model's scalability and performance on larger datasets.

Hyperid models are summarized in the following table5.

Table 5 :Hyperid models.

ref	year	methodology	result	dataset	advantages	limitations	environment	Future directions
8	2019	SMOTE-Tomek technique,Logistic Regression (LR), Random Forest (RF), Support Vector Classifier (SVC), Extra Trees Classifier (ETC), and Weighted VGG Convolutional Neural Network (WVCNN)	LR, RF, SVC, ETC, and WVCNNachieved an accuracy score of 97%	Leukemia_GSE28497	It used more than one model in ML and also used DL models , it used the SMOTE-Tomek oversampling technique to improve the performance of models	The study was limited with only one dataset	DL and ML	Development of a customised deep learning model specifically for small datasets
11	2022	GAN classifier (ML) ,CNNs models	98.67% In binary 95.5% multi-class	ALL-IDB , ASH Image Bank	Using GAN classifier (AC-GAN) which allow using small datasets for training (445 images)	limited dataset size, Lack of real-world clinical validation and needing of more focusing on images on the datasets	ML , DL Image processing	Expanding of dataset to collect more diverse and high quality data ,more clinical trials and real-world testing
23	2018	Image segmentation and classification of ALL using CNN	CNN-based method achieved an accuracy of 97.78%	this is a private dataset created by reasearchers from images taken from Amreek Clinical Laboratory – Saidu Sharif, Swat, Pakistan.	It help in speeding diagnosis of All and its subtypes.	The segmentation technique that used may not be clearly.	Image processing and DL.	Improve segmentation technique. Exloring different DL

24	2023	Conversion of blood microscopic images to the RGB,Utilization of (CNNs) to extract relevant features from the preprocessed images,enhancing the accuracy of leukemia cell classification.	Achieved an accuracy of 99.98%	Leukemia Classification Dataset	Enhances early leukemia detection	Dataset Specificity ,Data Augmentation ,Clinical Applicability	ML and image processing	Scalability ,Generalizability, Clinical Integration
25	2023	Features are extracted from individual blood cell images using CNN ,	Achieved an accuracy of 99.84	ResearchGate	Helps classify benign & malignant subtypes	Model has some drawbacks ,Computational Complexity,Algorithm Sensitivity	ML & DL	Algorithm Optimization ,Ensemble Learning ,Real-World Application
3	2020	reviews ML&DL approaches for leukemia classification, analyzing algorithm principles	SVM:92% k-NN:80% Neural networks:93.7% Naïve Bayes :80.88% CNNs: 97.78%	used different datasets Microscopic blood images of ALL & AML Blood smear images of ALL and AML Leukocyte images	lead to more accurate and efficient detection	The study's inability to directly compare algorithm performance due to using accuracy metrics from different datasets	DL & ML MATLAB	should conduct standardized benchmarking of ML/DL algorithms using a common leukemia dataset
5	2021	compared DL&ML for classifying leukemic	-ResNet-50: 81.63% -VGG-16:84.62% -convolutional network: 82.10%	The dataset used from a CodaLab	High accuracy for the VGG-16 network	used a limited dataset	DL & ML image processing	-improve the performance
26	2021	Hybrid Model (AlexNet + ML)	-the AlexNet CNN :100% -with the linear SVM classifier:98%	used the ALL-IDB2 dataset..	-Perfect Diagnostic Accuracy -Superior to Traditional Methods	-Small Dataset -Narrow Validation Scope -Architecture Constraints	DL & ML	-Expand Dataset -External Validation

15	2025	systematic mapping study (SMS) and a systematic literature review (SLR), to analyze 30 articles published between 2019 and 2023 Include Preprocessing with image processing then using CNNs	(CNNs), (ViTs),hybrid models, conclude high classification accuracy exceeding 90% in many cases.	ALL-IDB, C-NMC 2019, ASH image bank	Deep learning models were able to learn features from the blood smear images, leading to accurate differyentiation of leukemia subtypes and stages which is better than manual microscopic analysis, which can be subjective and time-consuming.	Limited datasets for training ,overfitting risks due to using complex models with small datasets,lack of understanding deep learning models (black box)	DL & image processing	Build large and high quality datasets ,use XAI so clinical can trust them ,use advanced segmentation for better accuracy
28	2023	preprocessed the data, including normalization, feature selection, and feature extraction, to prepare it for the ALLDM deep learning model then develop and train on the preprocessed data.	ALLDM model varies by treatment (up to 94.31%)	Diagnosis Dataset (DDS),Symptoms Dataset (SDS)	High accuracy in detecting ALL,reduces time for diagnosis compared to manual.	Model has not tested in real hospitals yet ,no specific public dataset name	DL & image processing	Expand dataset with larger patients data ,try the model on real hospital dataset
9	2021	analyzing methodologies across image acquisition, preprocessing (normalization, segmentation), feature extraction, and classification	- Segmentation Techniques - Feature Extraction - Classification Performance	-ALL-IDB1 -ALL-IDB2 -ASH some private dataset	- Comprehensive Resource for Researchers -Clinical Relevance - Accelerates Innovation	-Rapidly Evolving Field -Narrow Focus on Acute Leukemia - Preprocessing/Segmentation Bottlenecks	Image Processing, ML& DL	-Algorithm Improvements -Expand Subtype Coverage -Next-Gen AI Models -Clinical Deployment
29	2021	- Preprocessing -Feature Extraction - Classification (SVM)	system achieved an overall accuracy of 97.69%	520 blood smear images from Jimma Medical Center	The developed system outperformed previous studies	The study used a limited dataset from a single medical center	image processing & ML	-Dataset Expansion & Diversity -leukemia Progression & Staging -Advanced AI Techniques

10	2021	trained a deep learning model on blood cell images	-High Diagnostic Accuracy -Discovery of Distinct APL Features	—-	-Superior Diagnostic Performance - Novel Biological Insights - Clinical Impact -Research Potential	limited by the relatively small number of patients, since APL is a rare disease.	DL& image processing	-Enhanced Validation & Generalizability -Clinical Integration & Impact Studies -Model Advancements
30	2021	-Databases Searched -PBS image analysis	-average accuracy of ML methods 97%	The study does not explicitly name a specific dataset	-High Accuracy -Early Diagnosis -Improved Treatment -Potential Impact	-Limited Datasets -Risk of Overfitting	-Image Processing -python -ML	-Develop Larger Datasets -Standardization -Enhanced Augmentation
31	2020	Use the PRISMA article model.	The study concluded that both TML and DL have an important role in medical image analysis, but DL is superior in terms of performance and ease of use.	Researchers point out that the lack of high-quality public databases represents a major challenge in this field. Data augmentation and transfer learning have been recommended to address this gap.	Deep learning (DL) provides automatic feature learning from raw data without human intervention. DL offers higher accuracy.	Lack of well-labeled, public databases. Difficulty generalizing trained models to new data	ML and DL	Developing end-to-end approaches based on deep networks (DNNs, CNNs). Promoting the use of resource-light models for application on mobile or low-power devices.

32	2024	Applied image transformation techniques to reduce dimensionality and enhance data quality ,Used machine learning classifiers including:SVM ,ANN ,random trees ,Evaluated classification performance after applying the transformations.	Predictive insights on disease progression, studies achieve over **90%** accuracy	satellite imagery , geological maps	Enhanced classification accuracy of lithological units. Combining image processing with ML algorithms leads to more robust and reliable results. The method improves visual interpretation and geological understanding.	Requires high-quality, high-resolution data for accurate classification. Training machine learning models can be computationally expensive. Generalizability might be limited unless tested on various geographic regions.	Image processing -ML	Integration of Deep Learning (DL) techniques for possibly better performance. Applying the framework to different regions to test scalability and generalization. Exploration of hybrid models combining multiple ML or DL techniques.
33	2024	reviews the literature on the use of AI in CML, including studies that have used various AI techniques such as machine learning, neural networks, and decision trees.	improve the diagnosis and treatment of CML, which lead to better patient outcomes and more efficient healthcare delivery.	ALL-IDB, (ASH) Image Bank	highlighting the progress made and the areas that need more research and development	More researches needed to address the challenges	ML & DL	Developing more explainable systems ,improving data quality ,integrating AI into clinical workflows.

34	2023	introduces Mayfly optimization with Generative Adversarial Network (MayGAN) to enhance feature extraction and classification of leukemia. Generative Adversarial System (GAS) with Principal Component Analysis (PCA) is used to classify different types of blood cancer.	Achieved an 99.8% accuracy	TSPLIB	faster convergence to near-optimal solutions ,ability to handle larger TSP instances effectively. flexibility.	the solutions are approximate and may not always be optimal. Performance may heavily depend on the tuning of algorithm-specific parameters. Effectiveness may vary across different types of TSP instances.	DL & Image Processing	Combining multiple algorithms to leverage their respective strengths. Extending methods to handle real-time changes in the problem setup. Incorporating learning-based techniques to predict promising solution paths.
35	2023	combining the Grasshopper Optimization Algorithm (GOA) and the Simulated Annealing (SA) technique.The algorithm's performance is evaluated using benchmark TSP instances to assess its effectiveness and efficiency.	it achieves better results compared to several existing metaheuristic algorithms on standard TSP benchmarks indicating for solving complex problem,Achieved an 98.8% accuracy	TSPLIB	The hybrid approach leverages the strengths of both GOA and SA, leading to improved solution quality.The algorithm demonstrates efficient convergence, reducing computational time compared to some existing methods. flexibility.	The performance of the algorithm may be sensitive to the tuning of certain parameters, which could affect its robustness.its effectiveness on larger, real-world instances of TSP remains to be fully explored.	DL & Image Processing	Algorithm Enhancement, Real-World Applications, combining the proposed algorithm with other optimization techniques, such as machine learning methods, to further enhance performance.

36	2023	optimized for classifying ALL and normal cells ,the model reduces the number of trainable parameters, enhancing computational efficiency without compromising performance .	it achieved an accuracy of 99.31%,For multi-class classification (differentiating between various leukemia cell types), the model attained an accuracy of 96.81%	C_NMC_19 Dataset,ALL Dataset	High accuracy ,Computational Efficiency,Scalability	Dataset Dependency ,Potential Overfitting	DL & Image Processing	Dataset Expansion ,Model Optimization , clinical validation .

RQ2: What datasets (e.g., blood smear images, genetic markers) are most frequently employed in AI-driven leukemia studies?

The most commonly used datasets for leukemia are summarized as shown in Table 6.

Table 6 : Overview of Leukemia Datasets :

Ref	Dataset	classes	Images/samples per class	Total images/Samples	Class Balance	Number Of studies	Best Accuracy	Lowest Accuracy
71	SN-AM	1)B-ALL 2)MM	this dataset consists of 90 images of B-ALL, 100 images of MM.	190 images	The number of images is not equal between classes,the number of B-All is higher than MM.	60 studies	need to train a model to calculate it .	need to train a model to calculate it.
72	C-NMC 2019	1)ALL 2)Normal cell	Training Set: ALL (cancer) images: 7,272 Normal cell images: 3,389 Preliminary Test Set: ALL (cancer) images: 1,219 Normal images: 648	15,135 images	The number of ALL (cancer) cell images is significantly higher than that of normal cells.	118 studies	around 98.3%.	ranged between 85% and 90%.
73	All-IDB	1)Lymphoblasts (blast cells), 2)Normal lymphocytes	1)ALL-IDB2: 130 2)ALL-IDB1: 510	1)ALL-IDB1: 109; 2)ALL-IDB2: 260 (cropped)	1)Unbalanced (IDB1) 2)Balanced (IDB2)	The number of studies was not clearly mentioned.but the multiclass suggests 6 classes that might correspond	~92% (morphological + neural networks).	Significantly lower with basic threshold-based segmentation

						to 6 different studies.		
74	GsE28497	in Gene expression: 1)lymphoblastic leukemia (ALL) 2)Normal B-cell progenitors. In flow cytometry analysis: 1)B-lineage ALL 2)nonleukemic BM	this dataset consists of 270 samples of lymphoblastic leukemia (ALL) , 4 samples of Normal B-cell progenitors and 200 samples of B-lineage ALL,61 samples of nonleukemic BM	288 samples	The two classes are highly imbalanced	1 studies.	Not mentioned a specific accuracy percentages.but ,it showed high sensitivity,as the newly identified markers allowed for detection of one leukemic cell among 100,000 BM cells.	Not mentioned a specific accuracy percentages
75	Beat AML	1)Mutational categories(e.g., FLT3, TP53, NPM1 mutations) 2)Drug response categories (Sensitive vs. Resistant)	No image data available Genomic and drug response samples only.	Primary tumor samples: 672	Unbalanced 1)Some mutations are frequent 2)Others are rare (e.g., BCOR + SRSF2 co-mutations) 3)Drug response categories vary greatly in sample size per drug	562 patients	The dataset does not use classification accuracy like image-based tasks. High sensitivity (low AUC) observed for: FLT3-ITD mutation with FLT3 inhibitors (e.g., Ibrutinib, Midostaurin)	Poor drug sensitivity (high AUC) in:TP53, ASXL1, NRAS, KRAS mutated samples

RQ3: What performance metrics (e.g., accuracy, sensitivity, specificity) and limitations (e.g., dataset size, spectral noise) are reported for these AI models?

Type of Method	Accuracy	Sensitivity (Catching real cases)	Specificity (Avoiding false alarms)	Main Challenges

Deep Learning (DL)	Up to 99% (like Inception-v3, custom CNNs)	Up to 100%	Up to 97.8%	-need large and varied datasets -need data balance (too many examples of one type and not enough for others) -create new and smarter models -try to use these models in real hospitals to see how it works in practice -Sensitive to differences in image quality
Machine Learning (ML)	90–100% (like SVM, ANN)	Around 85–100%	Around 92–100%	– Results vary depending on the algorithm – Doesn't handle messy or complex data as well – Performance drops with poor-quality datasets -need more large and diverse datasets -need to make more models that are easy to understand -add DL methods like CNNs to catch more cases and reduce mistakes. -use it in real hospitals to help doctors make faster and more accurate decisions.
Traditional Methods	Less accurate and more variable	Depends on the person analyzing the data	Lower than AI-based methods	– Time-consuming – Relies on expert experience – Results can vary from person to person – Doesn't handle image noise or inconsistency well

Hybrid (ML + DL)	Often above 95%	High (close to 100%)	High	– Complex to set up – Needs to be set up properly to work well – Need data balance so it doesn't make overfit
Hybrid(ML+Image Processing)	Around 92–98%	Moderate to High	Moderate to High	– Image quality varies between sources – May miss patterns without DL support
Hybrid(DL+Image Processing)	Often above 98%	Very High	High	– Requires large, clean datasets – Needs a lot of computing power
Hybrid (DL+ML + Image Processing)	Up to 99.6%	Very High	High (83–100%)	– Most complex hybrid – Needs strong hardware – Can be hard to generalize to new data

Traditional methods still work, but they're slower, less consistent, and depend heavily on the skill of the person doing the analysis. They struggle with large datasets and image variation.

Machine Learning (ML) is also great but needs you to tell it what to look for. It works well with clean, well-prepared data, but it's not as good at handling messy situations.

Deep Learning (DL) is super accurate and powerful, but it needs lots of good data and can struggle if that's missing.

Hybrid Models combine the strengths of DL and ML. They're often the best performers, but they're more complex and require more time and computing power.

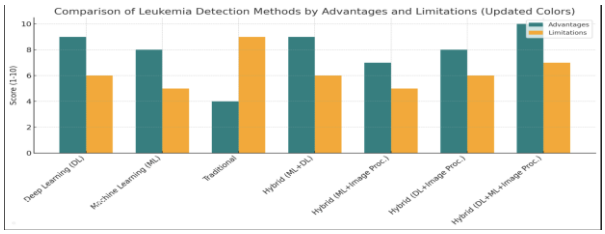
RQ4: What are the advantages and disadvantages of Ai models and traditional?

AI Models:

Advantages	Disadvantages
AI models can achieve very high accuracy in detecting leukemia types. It can make the process of diagnosis by analyzing data much quicker than humans. AI models (like blood tests or image processing) can help in detecting leukemia without surgery. It can reduce the chances of errors made by human doctors during diagnosis. AI can detect leukemia at earlier stages, which improves the chances of successful treatment AI can handle large amounts of data.	AI models are often trained using datasets that are small. Noisy, missing, or inconsistent data can impact its performance. This means the data's quality affects performance. Models can perform well on training data but fail on certain new datasets due to overfitting. Certain AI models are viewed as "black boxes," making it tough for doctors in understanding decisions' routes. Certain models are computationally expensive, require powerful hardware and lengthy processing times. They still need to be supervised as well as verified by medical experts.

Traditional Methods :

Advantages	Disadvantages
Traditional methods have been used for many years, as they are trusted by doctors. There is no need for overly advanced equipment or algorithms, making it far more accessible within resource-limited settings. AI models need large datasets for training, unlike others. There is more Flexibility in Rare Cases in which AI might battle. There Exist No Computational Requirements, which can make them easier for implementation in such an environment.	Traditional methods do need a lot of time in the diagnostic process. Human interpretation might yield inconsistencies or errors, particularly with involved diagnoses. Manual analysis may miss subtle patterns, leading to lower accuracy in diagnosis limited for it. Doctors can make mistakes, which leads to a higher risk of human error. This is especially true under pressure or with complex cases. Certain customary diagnostic methods call for intrusive procedures like biopsies, and these can be uncomfortable for the patients.



This bar chart compares different methods for detecting leukemia based on their advantages (teal) and limitations(orange):

A higher advantage score means the method works better — it's more accurate, flexible, and reliable.

A higher limitation score means it has more difficulties — like needing lots of data, being harder to use, or not handling messy images well.

What the chart shows:

Traditional methods have the lowest performance and the most challenges.

Hybrid methods, especially the ones that combine DL, ML, and Image Processing, give the best results — but they can be more complicated to set up and use.

RQ5: How do hybrid approaches (e.g., DL combined with ML, image processing) enhance diagnostic accuracy and clinical applicability?

It is obvious that hybrid techniques combining deep learning techniques, machine learning techniques, and image processing techniques contribute positively to the systems for the diagnosis of leukemia in terms of accuracy and practical.

These techniques complement one another nicely, with each component contributing some important aspect. But deep learning models including CNNs have also demonstrated promising performance, since they can learn representative patterns automatically from images of the blood cells. But once those features are extracted, machine learning algorithms like SVM or random forests tend to be better at coming to quick and explainable decisions. When these them two together, the outcome tends to be much more accurate and reliable than if only one of these approaches is utilized individually.

Image processing is also a critical component of the systems. Segmentation, color adjustment and noise reduction are among the techniques that help clean and prepare the images before they're analyzed.So, this really boosts the quality of the data, And that, in turn, helps the models to pinpoint leukemic cells and their various subtypes more accurately. It's honestly pretty remarkable how some of these models can achieve nearly 100% accuracy. But, you know, there's a catch—what truly counts is how they perform in actual clinical situations. They can cut down the time it takes to make a diagnosis and help spot issues early on, which is super important for patient care.

That said, there are definitely some bumps in the road. A lot of these models? They're trained on pretty small or specialized datasets, which can be a big limit when they're thrown into new environments. Plus, deep learning models tend to be a bit of a black box. This complexity can make doctors attentive, and who can blame them? Trust is key in healthcare.

So, to finish, hybrid methods really do enhance diagnosis in a few key ways:

- They improve accuracy by mixing the strengths of various model.

- They speed up the diagnosis process and might even make it easier to explain.

- They're better at dealing with smaller or trickier datasets, thanks to techniques like data enhancement or GANs.

Looking ahead, researchers really need to focus on assembly bigger and more varied datasets, testing these models in actual hospital settings, and simplifying the systems so that clinical staff can easily understand them. Taking these steps could help transform these advanced models into reliable tools that doctors can actually use every day.Many of the hybrid systems have worked with excellent accuracy—often greater than 95% and even up to 100%.

6. Conclusion

This review identifies the advances, and obstacles in implementing artificial intelligence (AI)— including deep learning (DL), machine learning (ML) and hybrid models— for medical image analysis. In general, from their accuracy and processing times perspective, DL methods have provided the best performances making

them a highly promising candidate for clinical decision support systems. Still, their greatest weakness lies in the requirement of massive, varied, and high-quality datasets. DL models will struggle to generalize reliably in the real world without such data.

The performance from ML methods is also quite competitive, especially when you have clean and labeled data. Their main limitation involves their sensitivity to data quality and complexity; they are not effective compared to noisy and unstructured input. Furthermore, ML models typically require explicit feature engineering, which can restrict flexibility and generalizability to diverse clinical contexts.

Traditional methods of analysis, though still used, remain the most constraining. Their performance depends on human skills, making them to be slow, less consistent and less scalable. They are especially challenged by variability in image quality and subjectivity in diagnosis.

The hybrid approaches—particularly those that incorporate DL, ML, and image-processing components—usually have the highest accuracy result.Yet, their major limitation is complexity. But their greatest shortcoming is complexity. These systems demand considerable computational power and careful configuration, making them infeasible to deploy in environments lacking robust technical support. Their success is also highly reliant on balanced datasets to prevent overfitting.

These tasks would help enhance the utility of AI in healthcare by overcoming key limitations of the method and paving the way for broader deployment: targeted follow-up work should ensure diversity and balance in training data; improvements in image preprocessing pipelines; and finally, simplify train-deploy widgets for on-ground clinical applications. Only then, can these technologies help doctors more consistently and equitably across different healthcare settings.

7-References

[1]Tsilingiris, D., Vallianou, N. G., Spyrou, N., Kounatidis, D., Christodoulatos, G. S., Karampela, I., & Dalamaga, M. (2024). Obesity and leukemia: biological mechanisms, perspectives, and challenges. Current obesity reports, 13(1), 1-34.

[2] Zand, A. M., Imani, S., Sa'adati, M., Borna, H., Ziaei, R., & Honari, H. (2010). Effect of age, gender and blood group on different types of leukemia. Kowsar Med J, 15, 111-4.

[3]Maria, I. J., Devi, T., & Ravi, D. (2020). Machine learning algorithms for diagnosis of leukemia. Int J Sci Technol Res, 9(1), 267-70.

[4], L., Merino, A., Acevedo, A., Molina, A., & Rodellar, J. (2021). A deep learning model (ALNet) for the diag Boldúnosis of acute leukaemia lineage using peripheral blood cell images. Computer Methods and Programs in Biomedicine, 202, 105999.

[5]Rezayi, S., Mohammadzadeh, N., Bouraghi, H., Saeedi, S., & Mohammadpour, A. (2021). Timely diagnosis of acute lymphoblastic leukemia using artificial intelligence-oriented deep learning methods. Computational Intelligence and Neuroscience, 2021(1), 5478157.

[6]Kampen, K. R. (2012). The discovery and early understanding of leukemia. Leukemia research, 36(1), 6-13

[7]Achir, A., Debbarh, I., Zoubir, N., Battas, I., Medromi, H., & Moutaouakkil, F. (2024). Advances in Leukemia detection and classification: A Systematic review of AI and image processing techniques. F1000Research, 13, 1536.

[8] Surya Sashank, G. V., Jain, C., & Venkateswaran, N. (2021). Detection of acute lymphoblastic leukemia by utilizing deep learning methods. In Machine vision and augmented intelligence—theory and applications: select proceedings of MAI 2021 (pp. 453-467). Springer Singapore.

[9]Shah, A., Naqvi, S. S., Naveed, K., Salem, N., Khan, M. A., & Alimgeer, K. S. (2021). Automated diagnosis of leukemia: a comprehensive review. IEEE Access, 9, 132097-132124.

[10]Sidhom, J. W., Siddarthan, I. J., Lai, B. S., Luo, A., Hambley, B. C., Bynum, J., ... & Shenderov, E. (2021). Deep learning for diagnosis of acute promyelocytic leukemia via recognition of genomically imprinted morphologic features. NPJ precision oncology, 5(1), 38.

[11]Karar, M. E., Alotaibi, B., & Alotaibi, M. (2022). Intelligent medical IoT-enabled automated microscopic image diagnosis of acute blood cancers. Sensors, 22(6), 2348

[12]Bechar, A., Medjoudj, R., Elmir, Y., Himeur, Y., & Amira, A. (2025). Federated and transfer learning for cancer detection based on image analysis. Neural Computing and Applications, 1-46.

[13]Quentmeier, H., Pommerenke, C., Dirks, W. G., Eberth, S., Koeppel, M., MacLeod, R. A., ... & Drexler, H. G. (2019). The LL-100 panel: 100 cell lines for blood cancer studies. Scientific reports, 9(1), 8218.

[14]Shallis, R. M., Wang, R., Davidoff, A., Ma, X., & Zeidan, A. M. (2019). Epidemiology of acute myeloid leukemia: Recent progress and enduring challenges. Blood reviews, 36, 70-87.

[15]Oybek Kizi, R. F., Theodore Armand, T. P., & Kim, H. C. (2025). A Review of Deep Learning Techniques for Leukemia Cancer Classification Based on Blood Smear Images. Applied Biosciences, 4(1), 9.

[16]Assi, S. A., Bonifer, C., & Cockerill, P. N. (2019). Rewiring of the transcription factor network in acute myeloid leukemia. Cancer Informatics, 18, 1176935119859863.

[17]Alabdulqader, E. A., Alarfaj, A. A., Umer, M., Eshmawi, A. A., Alsubai, S., Kim, T. H., & Ashraf, I. (2024). Improving prediction of blood cancer using leukemia

microarray gene data and Chi2 features with weighted convolutional neural network. Scientific Reports, 14(1), 15625.

[18]Kantarjian, H. M., DiNardo, C. D., Kadia, T. M., Daver, N. G., Altman, J. K., Stein, E. M., ... & Ravandi, F. (2025). Acute myeloid leukemia management and research in 2025. CA: A Cancer Journal for Clinicians, 75(1), 46-67.

[19]Kaiser, M. F., Sonneveld, P., Cairns, D. A., Raab, M. S., San-Miguel Izquierdo, J., Zhang, R., ... & Weinhold, N. (2025). Co-Occurrence of Cytogenetic Abnormalities and High-Risk Disease in Newly Diagnosed and Relapsed/Refractory Multiple Myeloma. Journal of Clinical Oncology, JCO-24.

[20]Braun, T., Rade, M., Merz, M., Klepzig, H., Große, F., Fandrei, D., ... & Richardson, T. (2025). Multiomic profiling of T cell lymphoma after therapy with anti-BCMA CAR T cells and GPRC5D-directed bispecific antibody. Nature Medicine, 1-9.

[21]Siegel, R. L., Kratzer, T. B., Giaquinto, A. N., Sung, H., & Jemal, A. (2025). Cancer statistics, 2025. Ca, 75(1), 10.

[22]Sturgeon, C. M., Wagenblast, E., Izzo, F., & Papapetrou, E. P. (2025). The Crossroads of Clonal Evolution, Differentiation Hierarchy, and Ontogeny in Leukemia Development. Blood Cancer Discovery, OF1-OF16.

[23]Rehman, A., Abbas, N., Saba, T., Rahman, S. I. U., Mehmood, Z., & Kolivand, H. (2018). Classification of acute lymphoblastic leukemia using deep learning. Microscopy Research and Technique, 81(11), 1310-1317.

[24]Talaat, F. M., & Gamel, S. A. (2023). A2M-LEUK: attention-augmented algorithm for blood cancer detection in children. Neural Computing and Applications, 35(24), 18059-18071.

[25]Rahman, W., Faruque, M. G. G., Roksana, K., Sadi, A. S., Rahman, M. M., & Azad, M. M. (2023). Multiclass blood cancer classification using deep CNN with optimized features. Array, 18, 100292.

[26]Surya Sashank, G. V., Jain, C., & Venkateswaran, N. (2021). Detection of acute lymphoblastic leukemia by utilizing deep learning methods. In Machine vision and augmented intelligence—theory and applications: select proceedings of MAI 2021 (pp. 453-467). Springer Singapore.

[27]Ahmed, N., Yigit, A., Isik, Z., & Alpkocak, A. Identification of leukemia subtypes from microscopic images using convolutional neural network. Diagnostics 9 (3), 104 (2019). A Survey on Deep Learning Techniques, 45.

[28]Jiwani, N., Gupta, K., Pau, G., & Alibakhshikenari, M. (2023). Pattern recognition of acute lymphoblastic Leukemia (ALL) using computational deep learning. IEEE Access, 11, 29541-29553.

[29]Dese, K., Raj, H., Ayana, G., Yemane, T., Adissu, W., Krishnamoorthy, J., & Kwa, T. (2021). Accurate machine-learning-based classification of leukemia from blood smear images. Clinical Lymphoma Myeloma and Leukemia, 21(11), e903-e914.

[30]Ghaderzadeh, M., Asadi, F., Hosseini, A., Bashash, D., Abolghasemi, H., & Roshanpour, A. (2021). Machine learning in detection and classification of leukemia using smear blood images: a systematic review. Scientific Programming, 2021(1), 9933481.

[31]Khan, S., Sajjad, M., Hussain, T., Ullah, A., & Imran, A. S. (2020). A review on traditional machine learning and deep learning models for WBCs classification in blood smear images. Ieee Access, 9, 10657-10673.

[32]Aby, A. E., Salaji, S., Anilkumar, K. K., & Rajan, T. (2024). A review on leukemia detection and classification using Artificial Intelligence-based techniques. Computers and Electrical Engineering, 118, 109446.

[33]Bernardi, S., Vallati, M., & Gatta, R. (2024). Artificial Intelligence-based management of adult chronic myeloid leukemia: where are we and where are we going?. Cancers, 16(5), 848.

[34]Veeraiah, N., Alotaibi, Y., & Subahi, A. F. (2023). MayGAN: Mayfly Optimization with Generative Adversarial Network-Based Deep Learning Method to Classify Leukemia Form Blood Smear Images. Comput. Syst. Sci. Eng., 46(2), 2039-2058.

[35]Jain, S., Vishnawat, P., Shukla, P. K., & Khatri, N. (2023, November). Detection of Acute Lymphoblastic Leukemia Using CollateNet. In 2023 3rd International Conference on Technological Advancements in Computational Sciences (ICTACS) (pp. 1095-1100). IEEE.

[36]Batool, A., & Byun, Y. C. (2023). Lightweight EfficientNetB3 model based on depthwise separable convolutions for enhancing classification of leukemia white blood cell images. IEEE access, 11, 37203-37215.

[37]Malik, S., Iftikhar, A., Tauqeer, F. H., Adil, M., & Ahmed, S. (2022). A Systematic Literature Review on Leukemia Prediction Using Machine Learning. Journal of Computing & Biomedical Informatics, 3(02), 104-123.

[38]Hossain, M. A., Islam, A. M., Islam, S., Shatabda, S., & Ahmed, A. (2022). Symptom based explainable artificial intelligence model for leukemia detection. IEEE Access, 10, 57283-57298.

[39]Gimeno, M., San José-Enériz, E., Villar, S., Agirre, X., Prosper, F., Rubio, A., & Carazo, F. (2022). Explainable artificial intelligence for precision medicine in acute myeloid leukemia. Frontiers in Immunology, 13, 977358.

[40]Zhong, P., Hong, M., He, H., Zhang, J., Chen, Y., Wang, Z., ... & Ouyang, J. (2022). Diagnosis of acute leukemia by multiparameter flow cytometry with the assistance of artificial intelligence. Diagnostics, 12(4), 827.

[41]Hauser, R. G., Esserman, D., Beste, L. A., Ong, S. Y., Colomb Jr, D. G., Bhargava, A., ... & Rose, M. G. (2021). A machine learning model to successfully predict future diagnosis of chronic myelogenous leukemia with

retrospective electronic health records data. American journal of clinical pathology, 156(6), 1142-1148.

[42]Chen, X., Gole, J., Gore, A., He, Q., Lu, M., Min, J., ... & Jin, L. (2020). Non-invasive early detection of cancer four years before conventional diagnosis using a blood test. Nature communications, 11(1), 3475.

[43]Madanan, M., Venugopal, A., & Velayudhan, N. C. (2020, July). Designing an artificial intelligence model using machine learning algorithms and applying it to hematology for the detection and classification of various stages of blood cancer. In International Conference on Innovative Technical Advances in Disaster Management (ICITADM).

[44]Mehrabani, S., Zangeneh Soroush, M., Kheiri, N., Sheikhpour, R., & Bahrami, M. (2023). Prediction of blood cancer using leukemia gene expression data and sparsity-based gene selection methods. Iranian Journal of Pediatric Hematology and Oncology, 13(1), 13-21.

[45]Kumar, D., Jain, N., Khurana, A., Mittal, S., Satapathy, S. C., Senkerik, R., & Hemanth, J. D. (2020). Automatic detection of white blood cancer from bone marrow microscopic images using convolutional neural networks. IEEE Access, 8, 142521-142531.

[46]Devi, T. G., Patil, N., Rai, S., & Philipose, C. S. (2023). Gaussian blurring technique for detecting and classifying acute lymphoblastic leukemia cancer cells from microscopic biopsy images. Life, 13(2), 348.

[47]Agrawal, R.; Satapathy, S.; Bagla, G.; Rajakumar, K. Detection of White Blood Cell Cancer using Image Processing. In Proceedings of the 2019 International Conference on Vision Towards Emerging Trends in Communication and Networking (ViTECoN), Vellore, India, 30–31 March 2019; pp. 1–6.

[48]Kassani, S.H.; Kassani, P.H.; Wesolowski, M.J.; Schneider, K.A.; Deters, R. A Hybrid Deep Learning Architecture for Leukemic B-lymphoblast Classification. In Proceedings of the 2019 International Conference on Information and Communication Technology Convergence (ICTC), Jeju, Republic of Korea, 16–18 October 2019; pp. 271–276.

[49]Loey, M.; Naman, M.; Zayed, H. Deep Transfer Learning in Diagnosing Leukemia in Blood Cells. Computers 2020, 9, 29.

[50]Mathur, P.; Piplani, M.; Sawhney, R.; Jindal, A.; Shah, R.R. Mixup Multi-Attention Multi-Tasking Model for Early-Stage Leukemia Identification. In Proceedings of the ICASSP 2020—2020 IEEE International Conference on Acoustics, Speech and Signal Processing (ICASSP), Barcelona, Spain, 4–8 May 2020; pp. 1045–1049.

[51]Safuan, S.N.M.; Tomari, M.R.M.; Zakaria, W.N.W.; Othman, N.; Suriani, N.S. Computer Aided System (CAS) of Lymphoblast Classification for Acute Lymphoblastic Leukemia (ALL) Detection Using Various Pre-Trained Models. In Proceedings of the 2020 IEEE Student Conference on Research and Development (SCOReD), Batu Pahat, Malaysia, 27–29 September 2020; pp. 411–415.

[52]Anwar, S.; Alam, A. A convolutional neural network–Based learning approach to acute lymphoblastic leukaemia detection with automated feature extraction. Med. Biol. Eng. Comput. 2020, 58, 3113–3121.

[53]Ridoy, M.A.R.; Islam, M.R. An Automated Approach to White Blood Cell Classification Using a Lightweight Convolutional Neural Network. In Proceedings of the 2020 2nd International Conference on Advanced Information and Communication Technology (ICAICT), Dhaka, Bangladesh, 28–29 November 2020; pp. 480–483.

[54]Bibi, N.; Sikandar, M.; Ud Din, I.; Almogren, A.; Ali, S. IoMT-Based Automated Detection and Classification of Leukemia Using Deep Learning. J. Healthc. Eng. 2020, 2020, 6648574.

[55]Schouten, J.P.; Matek, C.; Jacobs, L.F.; Buck, M.C.; Bošnački, D.; Marr, C. Tens of images can suffice to train neural networks for malignant leukocyte detection. Sci. Rep. 2021, 11, 7995.

[56]Das, P.K.; Meher, S. Transfer Learning-Based Automatic Detection of Acute Lymphocytic Leukemia. In Proceedings of the 2021 National Conference on Communications (NCC), Kanpur, India, 27–30 July 2021; pp. 1–6.

[57]Jiang, Z.; Dong, Z.; Wang, L.; Jiang, W. Method for Diagnosis of Acute Lymphoblastic Leukemia Based on ViT-CNN Ensemble Model. Comput. Intell. Neurosci. 2021, 2021, 7529893.

[58]De Sant, Y.F.D.; De Oliveira, J.E.M.; Dantas, D.O. Lightweight Classification of Normal Versus Leukemic Cells Using Feature Extraction. In Proceedings of the 2021 IEEE Symposium on Computers and Communications (ISCC), Athens, Greece, 5–8 September 2021; pp. 1–7.

[59]Hosseini, A.; Eshraghi, M.A.; Taami, T.; Sadeghsalehi, H.; Hoseinzadeh, Z.; Ghaderzadeh, M.; Rafiee, M. A mobile application based on efficient lightweight CNN model for classification of B-ALL cancer from non-cancerous cells: A design and implementation study. Inform. Med. Unlocked 2023, 39, 101244.

[60]Abunadi, I.; Senan, E.M. Multi-Method Diagnosis of Blood Microscopic Sample for Early Detection of Acute Lymphoblastic Leukemia Based on Deep Learning and Hybrid Techniques. Sensors 2022, 22, 1629.

[61]Bukhari, M.; Yasmin, S.; Sammad, S.; Abd El-Latif, A.A. A Deep Learning Framework for Leukemia Cancer Detection in Microscopic Blood Samples Using Squeeze and Excitation Learning. Math. Probl. Eng. 2022, 2022, 2801227.

[62]Boreiri, Z.; Azad, A.N.; Ghodousian, A. A Convolutional Neuro-Fuzzy Network Using Fuzzy Image Segmentation for Acute Leukemia Classification. In Proceedings of the 2022 27th International Computer Conference, Computer Society of Iran (CSICC), Tehran, Iran, 23–24 February 2022; pp. 1–7.

[63]Mustaqim, T.; Fatichah, C.; Suciati, N. Modification of YOLO with GhostNet to Reduce Parameters and Computing Resources for Detecting Acute Lymphoblastic Leukemia. In Proceedings of the 2022 International Conference on Advanced Computer Science and Information Systems (ICACSIS), Depok, Indonesia, 1–3 October 2022; pp. 167–172.

[64]Eckardt, J. N., Bornhäuser, M., Wendt, K., & Middeke, J. M. (2020). Application of machine learning in the management of acute myeloid leukemia: current practice and future prospects. Blood Advances, 4(23), 6077-6085.

[65]Ahammed, P., Faruk, M. F., Raihan, N., & Mondal, M. (2022, December). Inception V3 Based Transfer Learning Model for the Prognosis of Acute Lymphoblastic Leukemia from Microscopic Images. In 2022 4th International Conference on Electrical, Computer & Telecommunication Engineering (ICECTE) (pp. 1-4). IEEE.

[66]Anilkumar, K. K., Manoj, V. J., & Sagi, T. M. (2020). A survey on image segmentation of blood and bone marrow smear images with emphasis to automated detection of Leukemia. Biocybernetics and Biomedical Engineering, 40(4), 1406-1420

[67]Asar, T. O., & Ragab, M. (2024). Leukemia detection and classification using computer-aided diagnosis system with falcon optimization algorithm and deep learning. Scientific Reports, 14(1), 21755.

[68]Saleem, S., Amin, J., Sharif, M., Mallah, G. A., Kadry, S., & Gandomi, A. H. (2022). Leukemia segmentation and classification: A comprehensive survey. Computers in Biology and Medicine, 150, 106028.

[69]Aby, A. E., Salaji, S., Anilkumar, K. K., & Rajan, T. (2025). Classification of acute myeloid leukemia by pre-trained deep neural networks: A comparison with different activation functions. Medical Engineering & Physics, 135, 104277

[70]Ramagiri, A., Jahnavi, V., Gottipati, S., Monica, C., Afrin, S., Jyothi, B., & Chinnaiyan, R. (2023, March). Image classification for optimized prediction of leukemia cancer cells using machine learning and deep learning techniques. In 2023 International Conference on Innovative Data Communication Technologies and Application (ICIDCA) (pp. 193-197). IEEE.

[71]Gupta, A., & Gupta, R. (2019). SN-CanData: White Blood Cancer Dataset of B-ALL and MM for Stain Normalization (Version 1) [Data set]. The Cancer Imaging Archive

[72]Mourya, S., Kant, S., Kumar, P., Gupta, A., & Gupta, R. (2019). ALL Challenge dataset of ISBI 2019 (C-NMC 2019) (Version 1) [dataset]. The Cancer Imaging Archive.

[73]Labati, R. D., Piuri, V., & Scotti, F. (2011, September). All-IDB: The acute lymphoblastic leukemia image database for image processing. In 2011 18th IEEE international conference on image processing (pp. 2045-2048). IEEE.

[74]Coustan-Smith E, Song G, Clark C, Key L et al. New markers for minimal residual disease detection in acute lymphoblastic leukemia. Blood 2011 Jun 9;117(23):6267-76. PMID: 21487112

[75]Tyner, J. W., Tognon, C. E., Bottomly, D., Wilmot, B., Kurtz, S. E., Savage, S. L., ... & Druker, B. J. (2018). Functional genomic landscape of acute myeloid leukaemia. Nature, 562(7728), 526-531