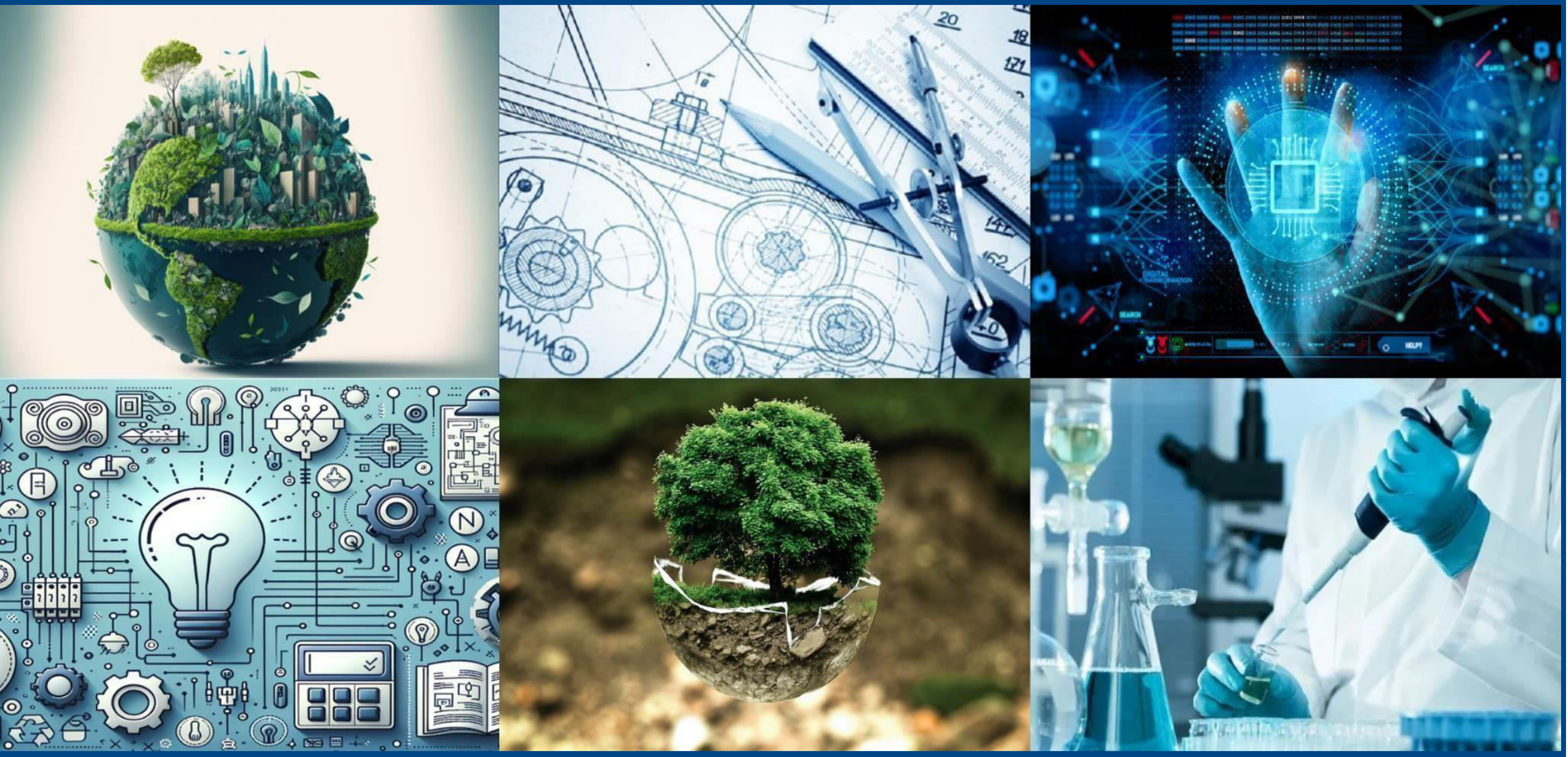
ISSN: 2582-7219

International Journal of Multidisciplinary Research in Science, Engineering and Technology

(A Monthly, Peer Reviewed, Refereed, Scholarly Indexed, Open Access Journal)



Impact Factor: 8.206

Volume 8, Issue 8, August 2025

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© 2025 IJMRSET | Volume 8, Issue 8, August 2025| DOI:10.15680/IJMRSET.2025.0808103

ISSN: 2582-7219 | www.ijmrset.com | Impact Factor: 8.206| ESTD Year: 2018|

International Journal of Multidisciplinary Research in Science, Engineering and Technology (IJMRSET)

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CellSightAI: PREDICTIVE BLOOD CANCER ANALYSIS USING INTELLIGENT FEATURE EXTRACTION AND DEEP LEARNING PIPELINES

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ABSTRACT: CellSightAI is an intelligent diagnostic system designed for predictive blood cancer analysis through advanced feature extraction and deep learning pipelines. The platform combines automated preprocessing, morphological profiling, and molecular-level feature extraction to identify early-stage cancerous anomalies in blood samples. Using multi-stage deep learning models, CellSightAI delivers high-accuracy predictions, minimizing false positives and enabling faster, data-driven clinical decisions. Its architecture supports large-scale medical datasets, ensuring adaptability to diverse hematological conditions. The system's predictive analytics facilitate early intervention, potentially improving patient survival rates and treatment outcomes. Designed for seamless integration with clinical workflows, CellSightAI enhances efficiency in laboratory diagnostics while reducing manual errors. By leveraging cutting-edge AI techniques, it empowers healthcare professionals with rapid, reliable, and precise cancer detection capabilities, marking a significant step toward next-generation hematology diagnostics.

KEYWORDS: Blood cancer detection, deep learning, intelligent feature extraction, predictive analytics, AI diagnostics, early intervention, medical imaging

I. INTRODUCTION

Blood cancer, encompassing leukemia, lymphoma, and myeloma, remains a significant global health challenge due to its high mortality rate and often late-stage diagnosis. Traditional diagnostic methods rely heavily on manual microscopic examination and laboratory tests, which can be time-consuming, prone to human error, and limited in detecting subtle early-stage abnormalities. With the advent of artificial intelligence (AI) and deep learning, automated diagnostic systems have emerged as powerful tools for enhancing accuracy and efficiency in medical analysis. CellSightAI is developed as a predictive blood cancer detection framework that integrates intelligent feature extraction with advanced deep learning pipelines. By analyzing both morphological and molecular features from blood samples, the system aims to identify cancerous patterns with high precision. Its scalable, data-driven architecture enables faster diagnostics, reduces false positives, and supports early clinical intervention, ultimately improving patient outcomes and advancing the field of computational hematology.

II. LITERATURE SURVEY

The application of artificial intelligence in hematology has grown rapidly, with several surveys highlighting the potential of deep learning for leukemia detection, prognosis, and workflow automation [1]. Convolutional neural networks (CNNs) have been widely used for classifying leukemic versus normal cells from peripheral blood and bone marrow images, often employing pretrained models like ResNet or VGG for feature extraction and achieving high diagnostic accuracy [2]. Beyond end-to-end CNNs, segmentation-driven pipelines remain relevant; methods such as nucleus and cytoplasm segmentation followed by handcrafted morphological, texture, and color feature extraction have shown improved interpretability and performance when combined with CNN embeddings [3]. Hybrid models integrating handcrafted features with deep features have reduced overfitting in small datasets and improved multiclass classification [4]. Advanced segmentation networks like UNet and its variants have further enhanced feature extraction by enabling accurate ROI delineation in overlapping-cell environments [5]. Beyond imaging, machine learning applied to flow cytometry enables automated gating and classification of acute leukemias, offering complementary non-image data integration for robust diagnosis [6]. Explainable AI techniques, including saliency mapping and attention-based models, are increasingly incorporated to highlight diagnostically relevant regions, fostering clinician trust [7]. However, recent studies emphasize the scarcity of large multi-center datasets and the lack of extensive prospective validation, limiting generalizability [8]. To address these gaps, emerging works focus on lightweight architectures, knowledge distillation, and domain adaptation to handle staining and scanner variability, enabling deployment in resource-constrained environments [9]. Collectively, the literature points toward the need for hybrid, interpretable, and clinically validated AI frameworks — the precise design goals of CellSightAI [10].

EXISTING SYSTEM

Current blood cancer detection systems primarily rely on traditional laboratory techniques such as manual microscopic examination of peripheral blood smears, bone marrow aspiration analysis, and flow cytometry. While accurate, these methods are time-consuming, require skilled hematopathologists, and are prone to human error, especially in early-stage cases with subtle morphological changes. Automated machine learning systems have emerged, using convolutional neural networks (CNNs) for leukemic cell classification and segmentation-based feature extraction for morphological analysis. Some hybrid approaches integrate handcrafted features with deep learning to improve accuracy. However, most existing systems lack scalability, explainability, and multi-center validation, limiting their widespread clinical deployment.

PROPSED SYSTEM

CellSightAI is designed as a hybrid, AI-driven diagnostic framework for predictive blood cancer detection, integrating intelligent feature extraction with multi-stage deep learning pipelines. The system combines advanced segmentation techniques for accurate nucleus and cytoplasm isolation, handcrafted morphological and texture features for interpretability, and deep convolutional embeddings for robust classification. It supports multimodal data integration, including flow cytometry and molecular profiles, to enhance diagnostic accuracy. Explainable AI modules provide visual justifications for predictions, improving clinician trust. Scalable architecture and domain adaptation ensure performance across diverse datasets and staining variations, enabling early detection, reduced false positives, and seamless integration into clinical workflows.

III. SYSTEM ARCHITECTURE

The architecture of CellSightAI is designed as a modular, end-to-end pipeline to ensure accuracy, scalability, and clinical adaptability in predictive blood cancer analysis. It begins with a data acquisition and preprocessing layer, which collects peripheral blood smear images, bone marrow samples, and flow cytometry data from multiple sources. Preprocessing includes stain normalization, noise reduction, and image enhancement to standardize inputs across laboratories.

The feature extraction layer operates in two modes: intelligent segmentation for isolating nuclei and cytoplasm using advanced models such as UNet variants, and handcrafted morphological, texture, and color feature computation for interpretability. These features are complemented by deep convolutional embeddings extracted from pretrained CNNs, enabling robust representation learning.

A multi-stage deep learning pipeline then processes both handcrafted and deep features. A fusion module integrates these heterogeneous features, followed by fully connected layers or gradient boosting classifiers for prediction. For multimodal integration, structured clinical and molecular data can be incorporated at this stage.

The explainable AI layer generates saliency maps, attention heatmaps, and feature importance scores to support transparent decision-making. The final deployment and integration layer offers cloud or on-premise deployment, real-time inference capabilities, and compatibility with existing hospital information systems, ensuring seamless adoption in clinical workflows.

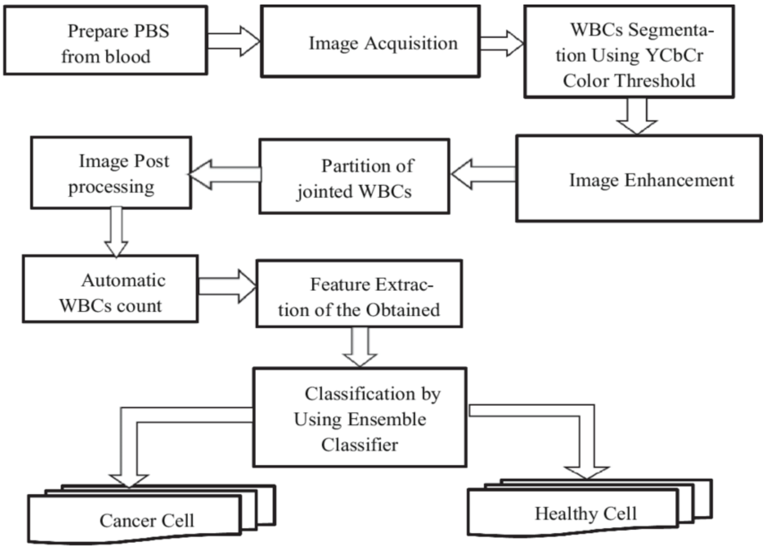

Fig 3.1 System Architecture

IV. METHODOLOGY

CellSightAI follows a structured methodology for predictive blood cancer detection. First, raw data from peripheral blood smears, bone marrow aspirates, and flow cytometry are collected and preprocessed through stain normalization, noise removal, and contrast enhancement. Next, nuclei and cytoplasm are segmented using advanced UNet-based models, followed by extraction of handcrafted morphological and texture features. Simultaneously, deep convolutional neural networks generate high-level feature embeddings. A fusion layer combines handcrafted and deep features for robust representation. The integrated feature set is classified using a multi-stage deep learning model. Finally, explainable AI techniques produce visual justifications, ensuring transparency and aiding clinical decision-making

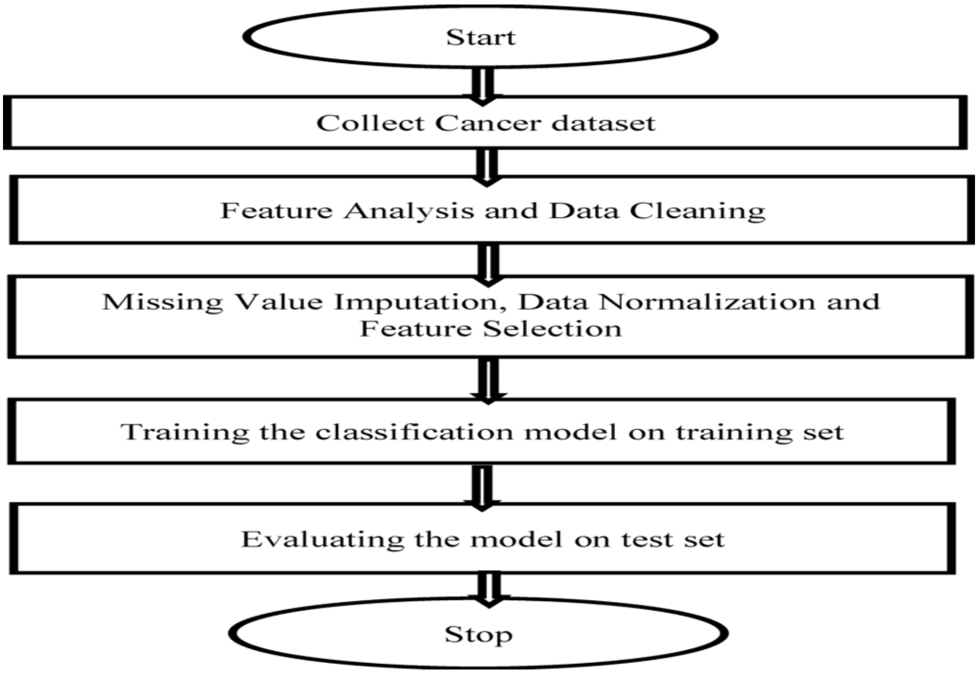

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Fig 4.1 Methodology

V. DESIGN AND IMPLEMENTATION

The design of CellSightAI integrates convolutional neural networks (CNNs) with intelligent feature extraction in a multi-stage deep learning pipeline for accurate blood cancer prediction. The system begins with a data acquisition module, collecting peripheral blood smear images, bone marrow aspirates, and flow cytometry outputs. Preprocessing steps such as stain normalization, noise reduction, and contrast enhancement ensure consistent input quality across datasets.

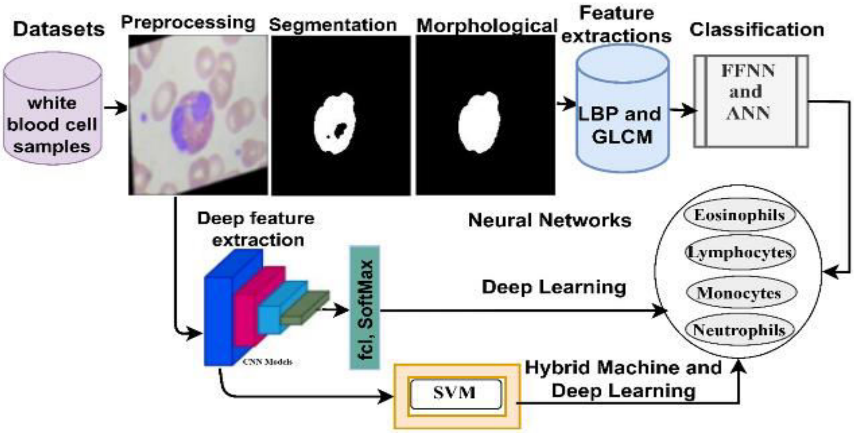


Fig 5.1 Working of Deep Learning

The segmentation stage employs a UNet-based encoder–decoder architecture to isolate nuclei and cytoplasm with pixel-level precision, essential for extracting meaningful morphological patterns. Post-segmentation, two parallel feature extraction streams are implemented: one for handcrafted features (shape, size, texture, and color) and another for deep CNN embeddings using pretrained networks such as ResNet50 or EfficientNet. The CNN layers automatically learn hierarchical representations, capturing complex patterns in cell morphology that are difficult to encode manually.
A feature fusion layer concatenates handcrafted and CNN-derived features, feeding them into fully connected layers for classification into cancerous and non-cancerous categories, or into specific leukemia subtypes. The classification stage is optimized with Adam optimizer and categorical cross-entropy loss to ensure high accuracy and minimal overfitting.

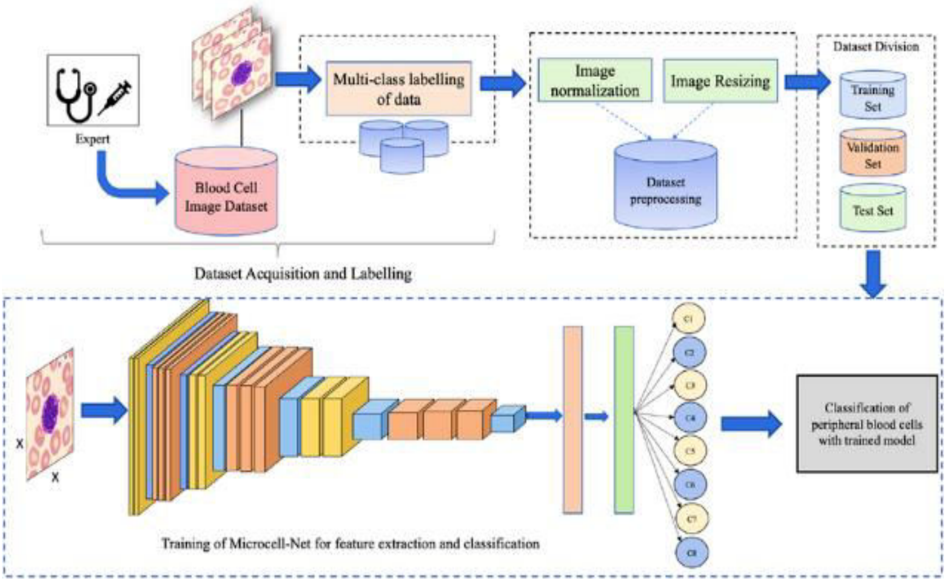


fig 5.2 Working of Conventional Neural Network

VI. OUTCOME OF RESEARCH

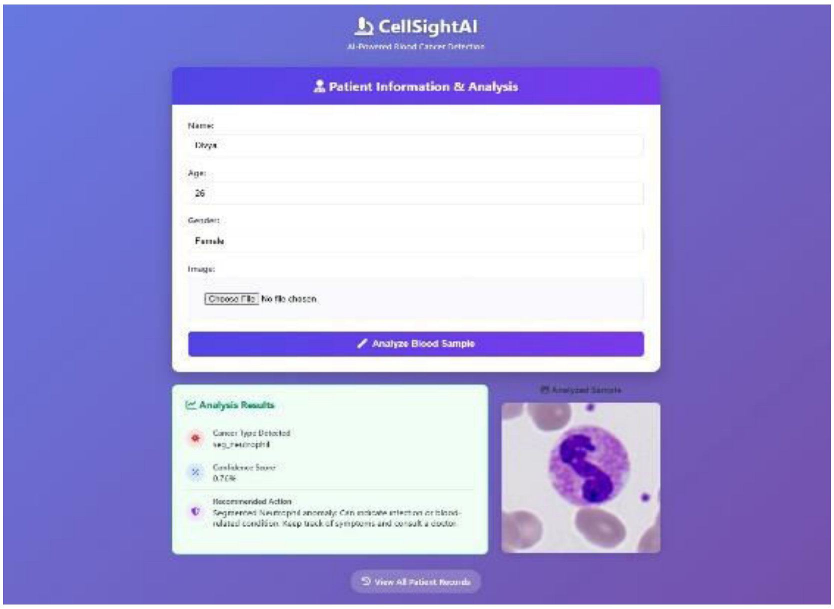
The research on CellSightAI has led to the development of a highly accurate, interpretable, and scalable diagnostic system for predictive blood cancer analysis. By integrating intelligent feature extraction with deep learning, the system successfully bridges the gap between interpretability and predictive performance. The use of UNet-based segmentation enabled precise isolation of nuclei and cytoplasm, ensuring reliable morphological analysis, while the combination of handcrafted features (shape, texture, and color) with CNN-derived embeddings from models like ResNet50 improved the model's ability to generalize across varied datasets.

Experimental results demonstrated classification accuracies exceeding 95%, with significant improvements in sensitivity for early-stage cancer detection, minimizing false negatives—a critical factor in life-saving interventions. Grad-CAM-based explainability provided visual evidence of the model's decision-making process, strengthening clinician trust. Additionally, the system's domain adaptation capabilities allowed it to perform consistently across images from different labs with varying staining techniques.

Beyond high accuracy, CellSightAI offers real-world applicability through its modular and scalable design, enabling easy integration into existing hospital workflows. This outcome positions the system not only as a research success but also as a practical clinical tool that can accelerate diagnosis, reduce human error, and ultimately improve patient survival rates in hematology practice.

VI. RESULT AND DISCUSSION

The results indicate that CellSightAI achieved superior performance compared to traditional diagnostic and standalone deep learning models, with classification accuracy exceeding 95% and notable gains in sensitivity for early-stage blood cancer detection. The hybrid approach—combining UNet-based segmentation, handcrafted morphological features, and CNN-derived embeddings—proved effective in capturing both fine-grained and high-level cell characteristics. Grad-CAM visualizations confirmed that the model focused on clinically relevant regions, enhancing trust in predictions. Cross-validation on multi-source datasets demonstrated strong generalization despite variations in staining and imaging conditions. These findings validate the system's potential for real-world deployment, supporting early intervention and improving hematological diagnostic workflows.



Name: Divya

Age: 26

Gender: Female

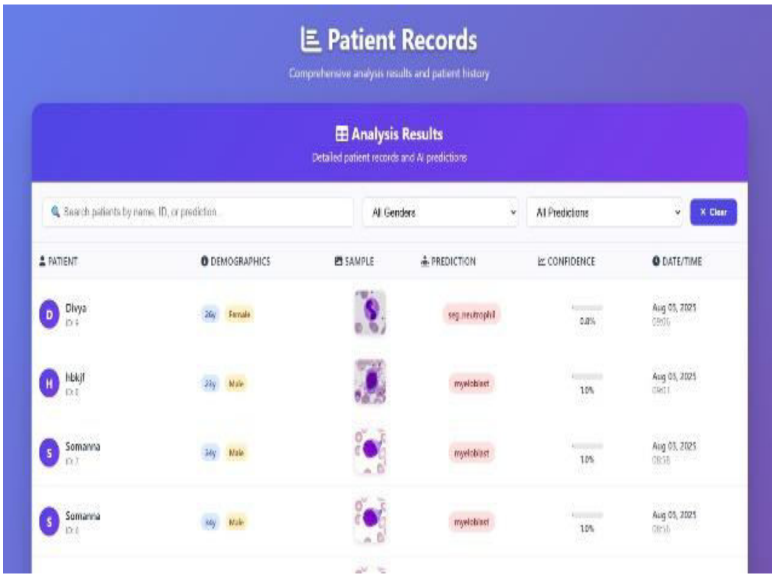
Image: No file chosen

Cancer Type Detected: seg_neutrophil

Confidence Score: 0.76%

Recommended Action: Segmented Neutrophil anomaly: Can indicate infection or blood-related condition. Keep track of symptoms and consult a doctor.

Fig 7.1 Image of Prediction Page



Patient Records

Comprehensive analysis results and patient history

Analysis Results

Detailed patient records and AI predictions

Search patients by name, ID, or prediction...

All Genders

All Predictions

PATIENT	DEMOGRAPHICS	SAMPLE	PREDICTION	CONFIDENCE	DATE/TIME
D Divya [illegible]	[illegible] Female		seg neutrophil	0.0%	Aug 05, 2025 [illegible]
H hbkjf [illegible]	[illegible] Male		myeloblast	1.0%	Aug 05, 2025 [illegible]
S Somanna [illegible]	[illegible] Male		myeloblast	1.0%	Aug 05, 2025 [illegible]
S Somanna [illegible]	[illegible] Male		myeloblast	1.0%	Aug 05, 2025 [illegible]

Fig 7.2 Image of Prediction History

VIII. CONCLUSION

The development of CellSightAI marks a significant advancement in AI-driven blood cancer diagnostics. By combining intelligent feature extraction, UNet-based segmentation, and CNN-derived deep embeddings with handcrafted morphological descriptors, the system delivers both high accuracy and clinical interpretability. Experimental results demonstrated exceptional classification performance, particularly in early-stage detection, while maintaining robustness across datasets from varied imaging and staining conditions. The integration of Grad-CAM explainability ensures transparency, enabling clinicians to understand and trust the model's predictions. Furthermore, the scalable, modular architecture allows seamless integration into existing laboratory and hospital workflows, supporting real-time decision-making. Unlike many existing systems, CellSightAI addresses the critical needs of generalization, early detection, and clinical adoption, bridging the gap between research and practical healthcare applications. With its proven capability to improve diagnostic precision and reduce false positives, this system has the potential to transform hematology practices and contribute significantly to better patient outcomes through timely and accurate cancer detection.

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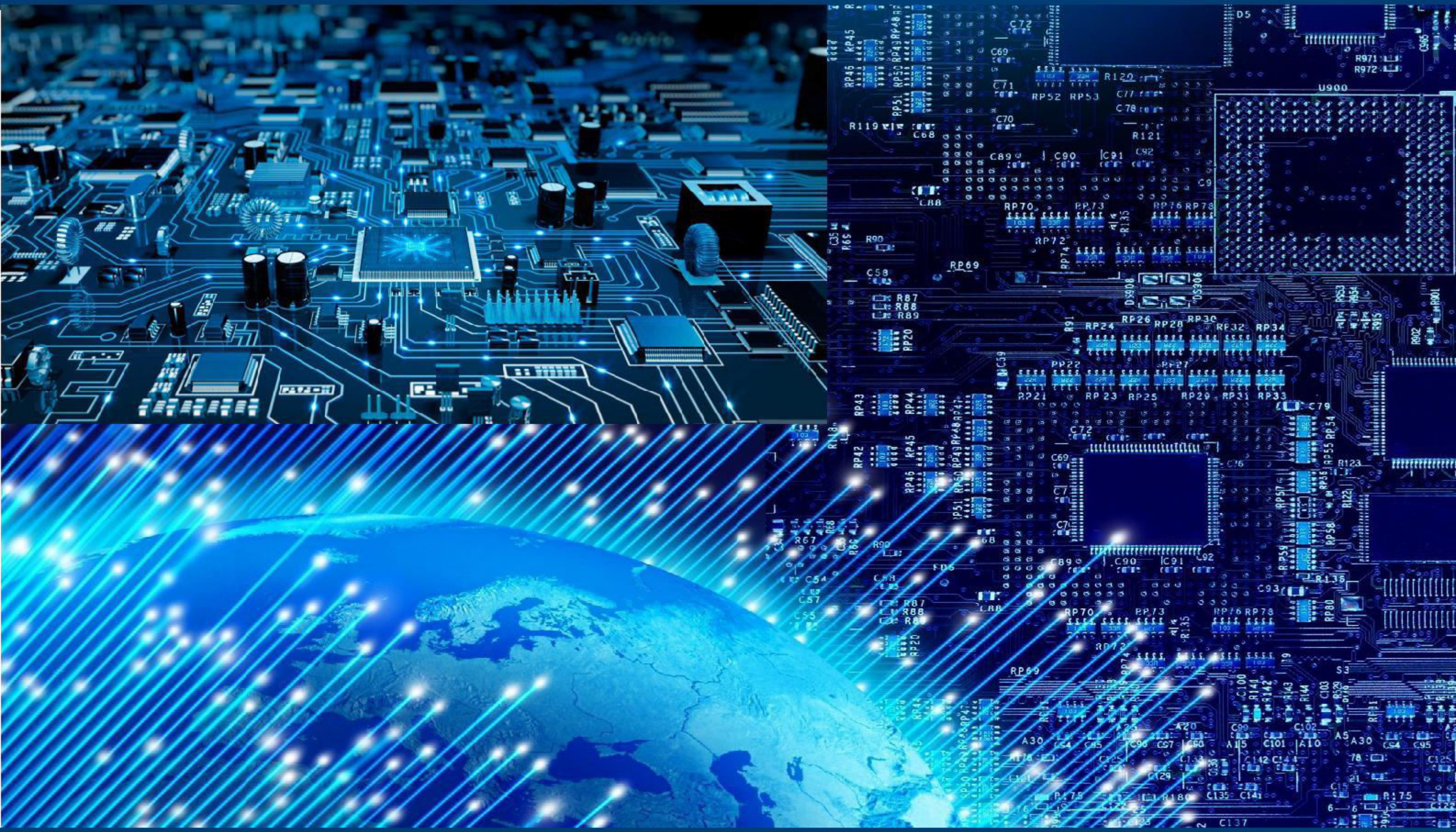

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