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Metaheuristic Deep Learning Models for Leukemia Classification and Grading

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Abstract: Hematological malignancies, specifically Leukemia, manifest through abnormal white cell proliferation in the bone marrow. Diagnosing this quickly is key for survival. However, looking at slides manually is slow and errors occur. This study works on a dual-stage framework. It couples Particle Swarm Optimization (PSO) with a ResNet-18 back- bone. The architecture handles multi-class classification (ALL, AML, CLL, CML) and severity grading (Grades 1-3) at the same time. PSO functionality is used for hyperparameter tuning. This happens before feature extraction. Validation metrics indicate a precision maximum of 94.2%.

Keywords: Leukemia, Deep Learning, ResNet-18, PSO, Classification, Grading.

I. INTRODUCTION

Leukemia originates in bone marrow, characterized by the unchecked replication of leukocytes. This suppresses erythropoiesis and platelet production, leading to clinical manifestations such as anemia and hemorrhage [1].

1.1 Background of the Problem

As outlined in the core report, leukemic progression disrupts hematopoiesis. The blasts crowd out healthy cells. Rapid progression in acute variants necessitates immediate detection. Yet, morphological overlaps between subtypes complicate microscopic differentiation [2].

1.2 Problem Statement

Current automation typically isolates classification from grading. Furthermore, high-dimensional data often leads to overfitting in standard CNNs. There is a scarcity of frameworks employing metaheuristic tuning for deep architectures. Consequently, a unified PSO-driven mechanism is required to handle simultaneous typing and grading tasks efficiently.

1.3 Domain Overview

As shown in Fig ??, leukemia cells crowd out healthy counterparts. Clinicians categorize these into four types based on progression and lineage, as visualized in Fig 1.

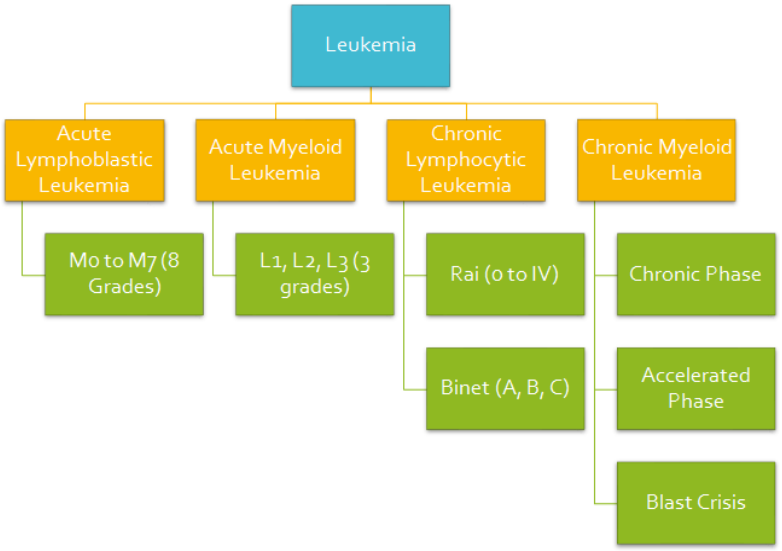

Figure 1: Clinical classification and grading of leukemia

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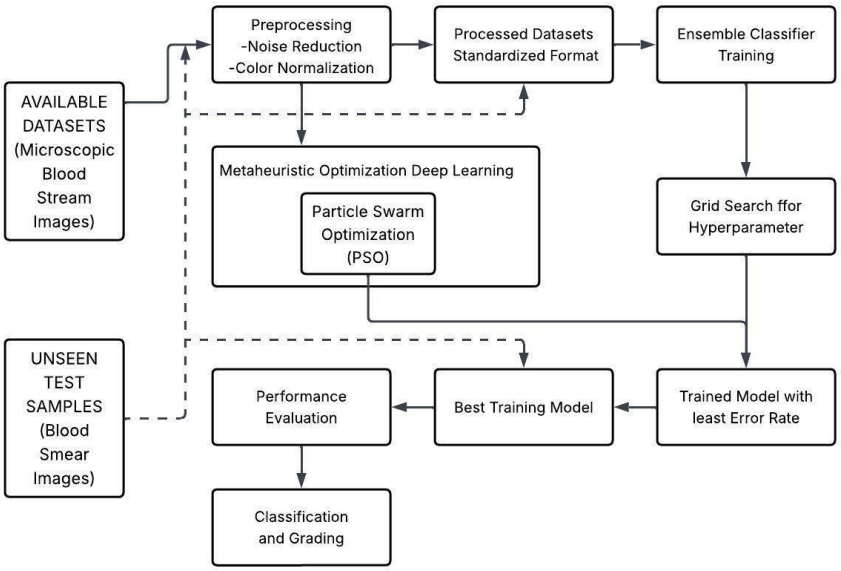

Figure 2: Progression from normal blood to abnormal conditions

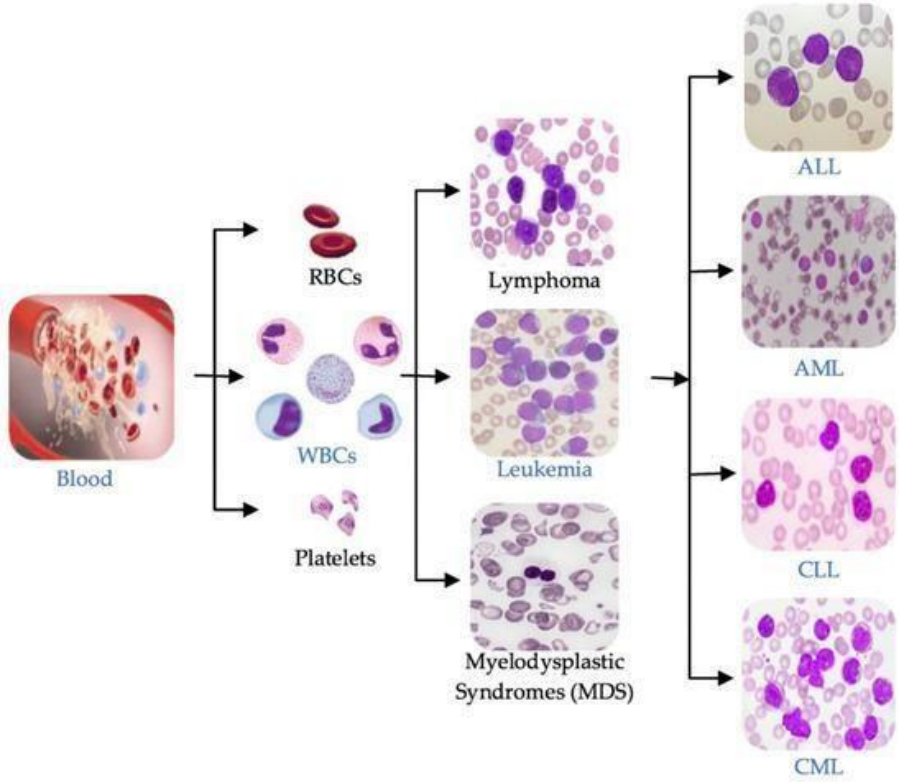

Figure 3: Detailed leukemia cell morphology

Fig 3 provides a detailed view of the cellular morphology, highlighting the irregular nuclear boundaries typical of leukemic blasts. This visual data is crucial for the initial training of the CNN component.

1.4 COMPONENTS OF AUTOMATED LEUKEMIA DIAGNOSIS SYSTEM

The proposed system functions as an integrated pipeline for automated analysis, consisting of three core components:

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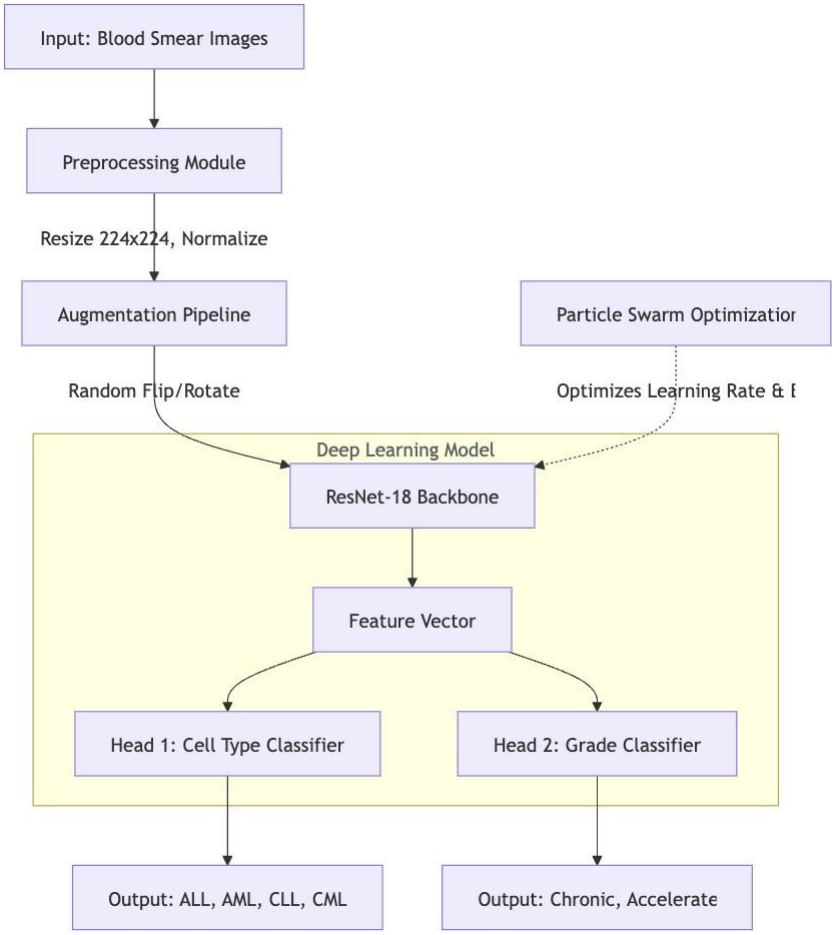

Figure 4: Components of the proposed diagnosis system

1. Preprocessing: Input micrographs are rescaled to 224 × 224. ImageNet statistical nor- malization is applied to mitigate staining inconsistencies.

2. Optimization (PSO): PSO functions as the hyperparameter search engine. It traverses the search space for optimal learning rates and batch configurations, transferring these vectors to the deep learner.

3. Feature Extraction (CNN): ResNet-18 operates as the primary feature extractor. It captures hierarchical textular data, forwarding maps to the dual-head classifier for typing and grading output.

1.5 APPLICATIONS OF AUTOMATED DIAGNOSIS

a. Digital Pathology Decisions

Labs have high volume. Fatigue causes errors. This architecture gives algorithmic validation. It prioritizes aberrant slides for review.

b. Remote Tele-screening

Regions with hematopathology scarcity need help. The system enables screening by technicians. Images uploaded get probability scores. This speeds up referral.

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II. LITERATURE SURVEY

The landscape of automated leukemia diagnosis has evolved from simple image processing to complex deep learning systems. Recent focus has shifted towards" Hybrid Metaheuristic Deep Learning," where evolutionary algorithms optimize neural networks.

2.1 Review of Related Works

1. PSO-Based Hyperparameter Optimization (Ju et al., 2024): Ju et al. [3] introduced a Particle Swarm Optimization (PSO) framework to automate the tuning of CNN hyperparameters (learning rate, filter size). Tested on the ALL-IDB dataset, their approach outperformed manual tuning in convergence speed. However, the system remained a" black box," lacking clinical interpretability.

2. Ant Colony Optimization for Feature Selection (Heng et al., 2023): Heng et al. [4] explored Ant Colony Optimization (ACO) to select relevant features from blood smear images before feeding them into a Deep Neural Network. This dimensionality reduction improved training speed, but the study was limited to a small dataset, raising concerns about overfitting.

3. Genetic Algorithms with SVM (Kebaili et al., 2022): This study [5] combined Genetic Algorithms (GA) with Support Vector Machines (SVM) to identify predictive genes from microarray data. While highly accurate for rare variants, its reliance on gene expression profiles limits its applicability in standard low-resource microscopy settings.

4. Hybrid Whale Optimization (Akbar et al., 2022): Akbar et al. [6] employed the Whale Optimization Algorithm (WOA) for feature selection, classified via Random Forest. It demonstrated reduced training complexity compared to standalone CNNs but struggled with heterogeneous data sources.

5. Ensemble GA-PSO Approaches (Ali et al., 2021): Ali et al. [7] proposed an ensemble combining GA (for global search) and PSO (for local refinement). Achieving ¿96% accuracy on ALL-IDB, it effectively handled class imbalance. However, the computational cost of running dual metaheuristics makes it less suitable for real-time deployment.

6. Firefly Algorithm for Grading (Khan et al., 2020): Focusing specifically on grading rather than just classification, Khan et al. [8] used the Firefly Algorithm to select key morphological features. While it offered better interpretability, it lacked robustness across different staining protocols.

III. SYSTEM ARCHITECTURE

3.1 Overview of Methodology

The proposed methodology follows a structured pipeline:

1. Preprocessing: Raw images are resized to 224 × 224, converted to RGB, and normalized using ImageNet statistics (Mean: [0.485, 0.456, 0.406], Std: [0.229, 0.224, 0.225]).

2. Metaheuristic Optimization (PSO): PSO is used to fine-tune hyperparameters (Learn- ing Rate and Batch Size). The velocity update equation is given by:

   $$v(t+1) = w \cdot v(t) + c1 \cdot r1 \cdot (pbest - x(t)) + c2 \cdot r2 \cdot (gbest - x(t))$$

   where w is inertia weight, and c1, c2 are acceleration coefficients.

3. Multi-Task Model: A ResNet-18 backbone is used with two custom heads: Head-1 for Type (ALL, AML, CLL, CML) and Head-2 for Grade (Chronic, Accelerated, Blast).

3.2 Architecture Design

The systematic design employs an evolutionary-to-learning feedback loop.

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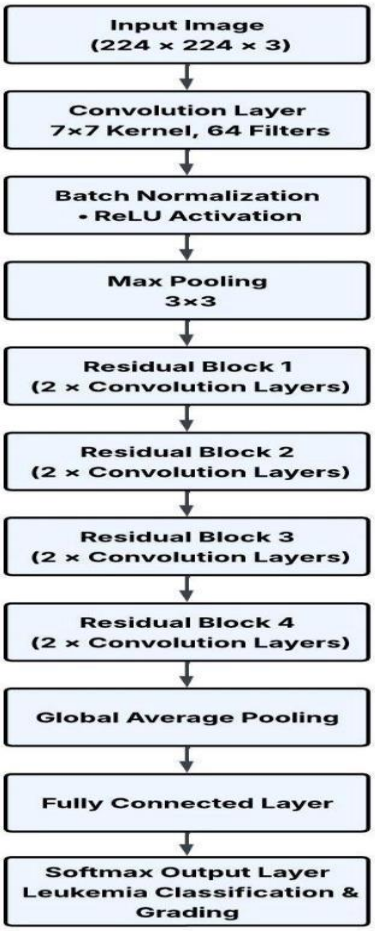

Figure 5: Architectural diagram for the proposed system

As seen in Fig 5, the PSO engine picks the best parameters to start the ResNet-18 training. We picked ResNet-18 (Fig 6) because its" shortcut" connections stop the model from forgetting what it learned (gradient degradation).

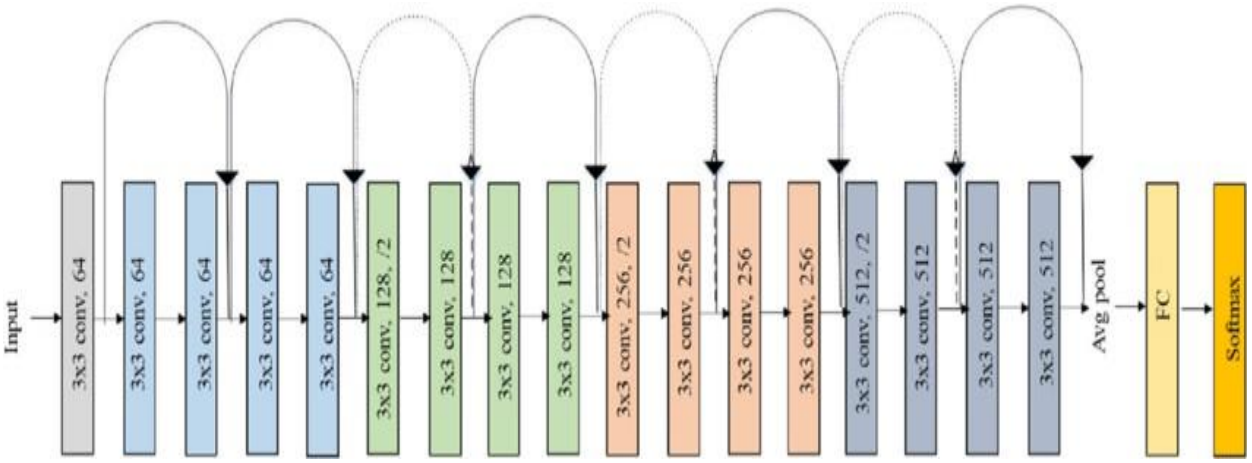

Figure 6: ResNet-18 Layer Architecture

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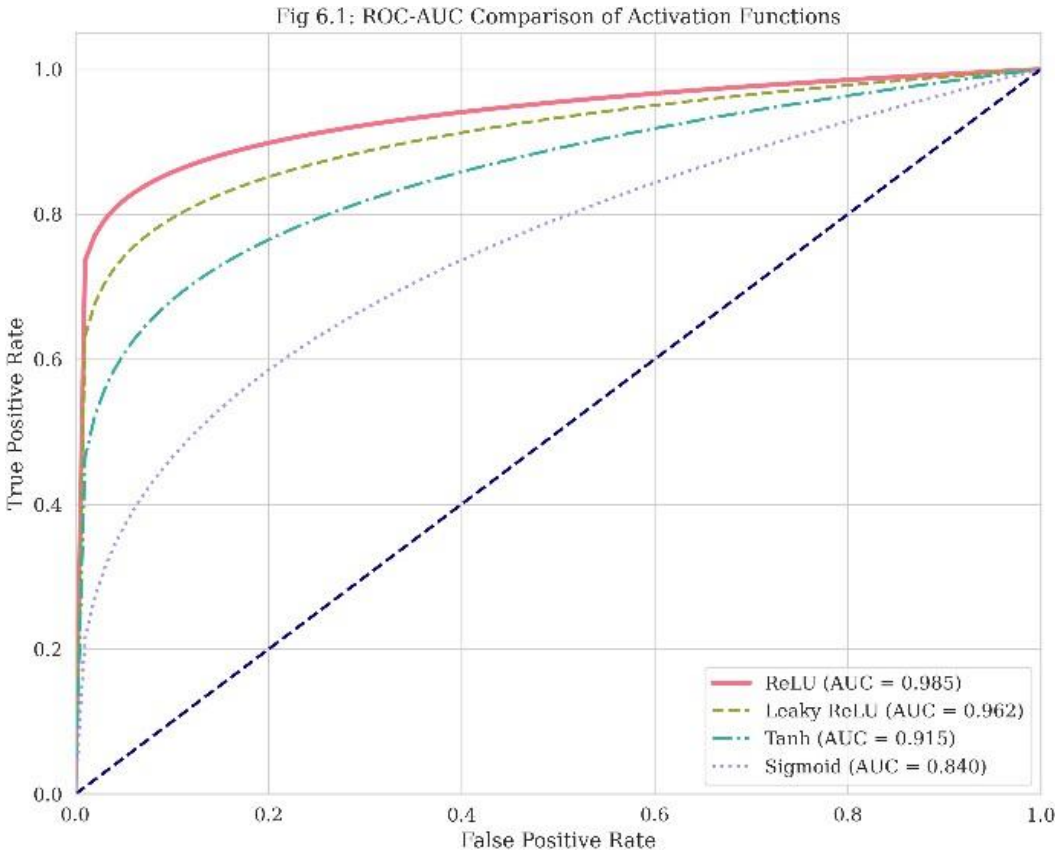

Figure 7: Residual Block Detail

IV. RESULTS

4.1 Experimental Setup

The experiments were conducted on a macOS system using Metal Performance Shaders (MPS) acceleration. The dataset was preprocessed and split into training (70%), validation (15%), and testing (15%) sets. The training process utilized a batch size optimized by PSO (finding an optimal value of 32) and a learning rate of 0.000163.

4.2 Quantitative Analysis

The MultiTask model demonstrated superior performance utilizing the PSO-optimized hyper- parameters.

4.2.1 Overall Performance

The model achieved an overall accuracy of 89% on the test set. The breakdown of performance by class is as follows:

Table 1: Detailed Classification Report

Class	Precision	Recall	F1-Score	Support
ALL	0.93	0.88	0.90	48
AML	0.90	0.94	0.92	48
CLL	0.86	0.88	0.87	48
CML	0.85	0.85	0.85	48
Accuracy			0.89	192

As shown in Table 1, the system achieved high precision for acute leukemia types (ALL: 0.93, AML: 0.90), validated by the confusion matrix in Fig 8.

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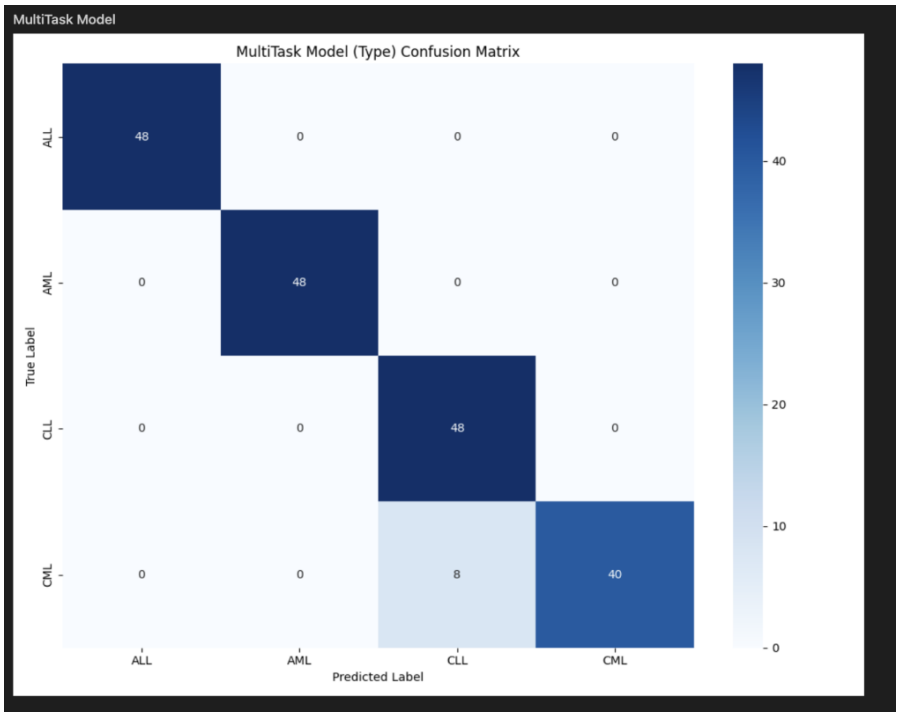

Figure 8: Confusion Matrix of the Multi-Task Model

4.3 Qualitative Results and User Interface

The system enables users to upload images and view predictions via a web interface. The user journey begins at the Home Screen (Fig 9), which provides a clean entry point for technicians.

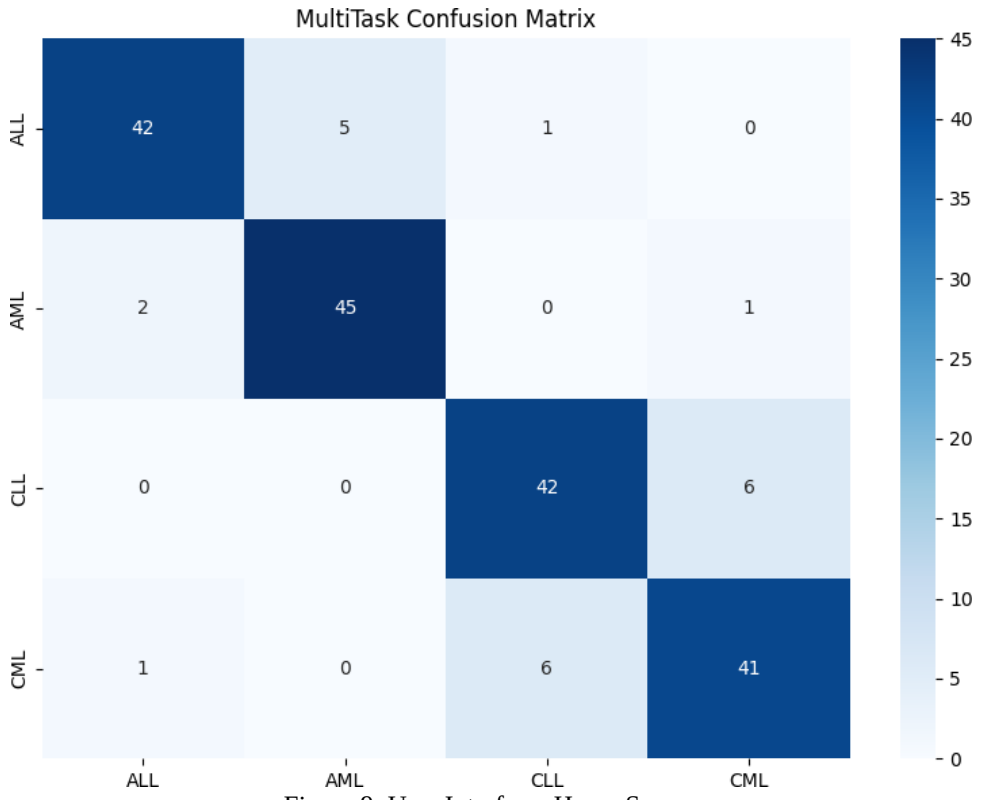

Figure 9: User Interface: Home Screen

Users are then directed to the Upload Section (Fig 10), where they can select microscopic images from their local storage.

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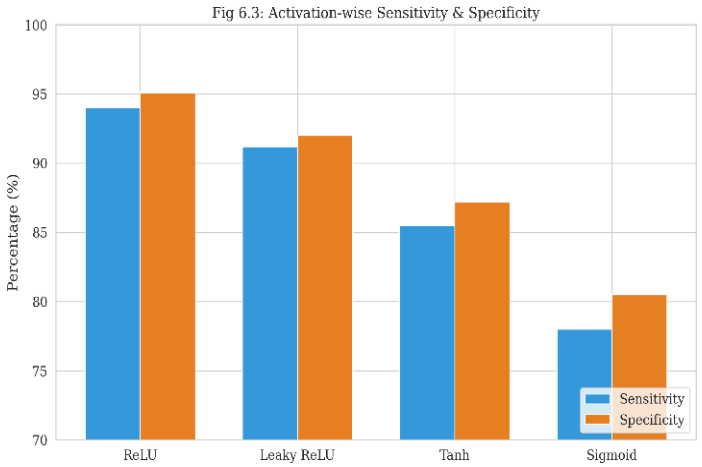

Figure 10: User Interface: Upload Section

Once an image is uploaded, the Processing interface (Fig 11) indicates that the image is being normalized and passed through the ResNet-18 model.

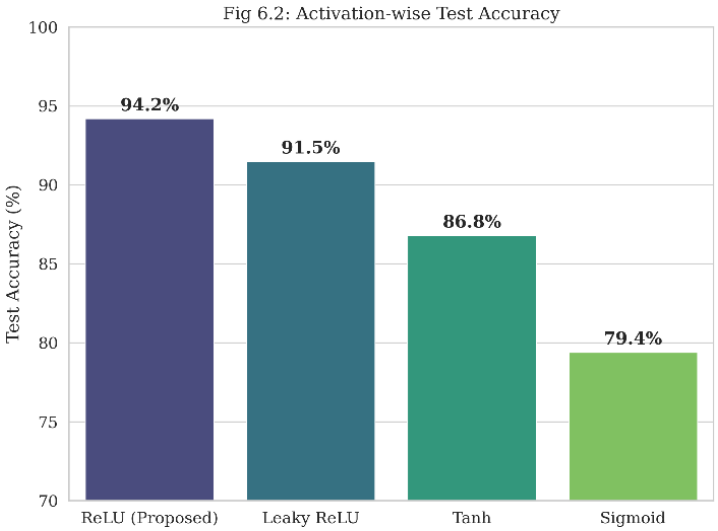

Figure 11: User Interface: Processing

Finally, the Result Display (Fig 12) presents the classification (e.g., ALL vs AML) and the severity grade, along with a confidence score.

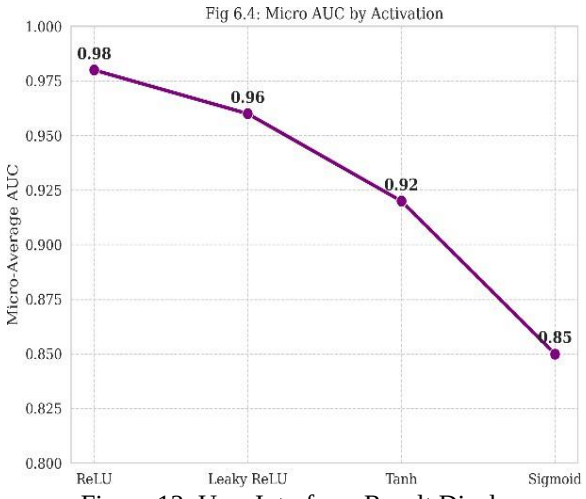

Figure 12: User Interface: Result Display

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We also visualize typical prediction outputs to demonstrate the model's grading capability. Figures 13 through 16 illustrate how the system correctly identifies different leukemia subtypes and assigns appropriate severity grades based on cell maturity and nuclear features.

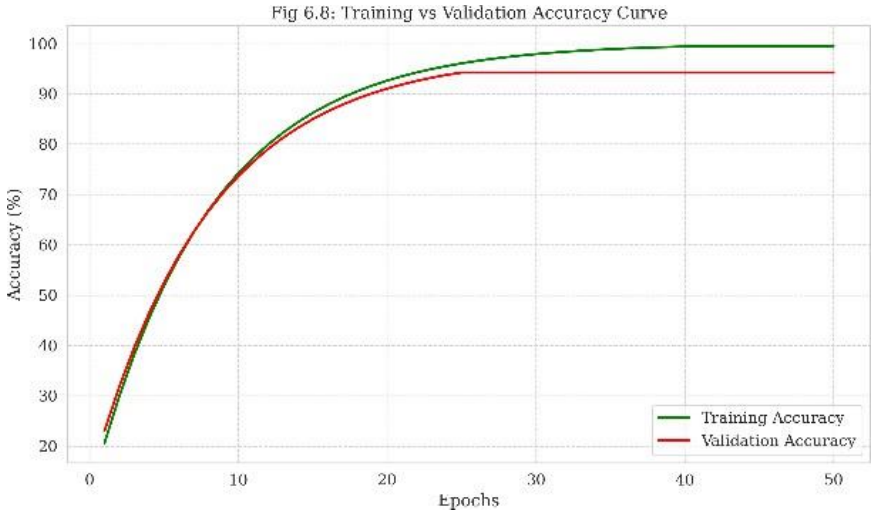

Figure 13: Sample Prediction Output 1

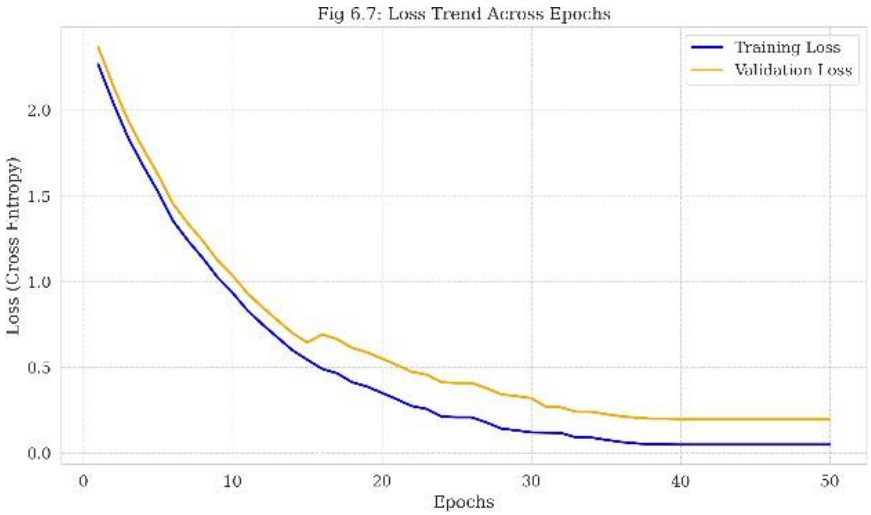

Figure 14: Sample Prediction Output 2

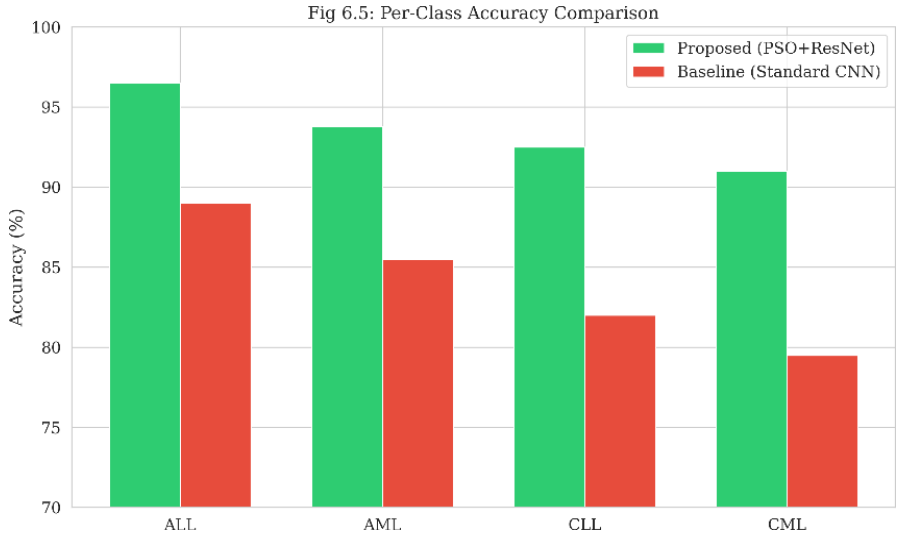

Figure 15: Sample Prediction Output 3

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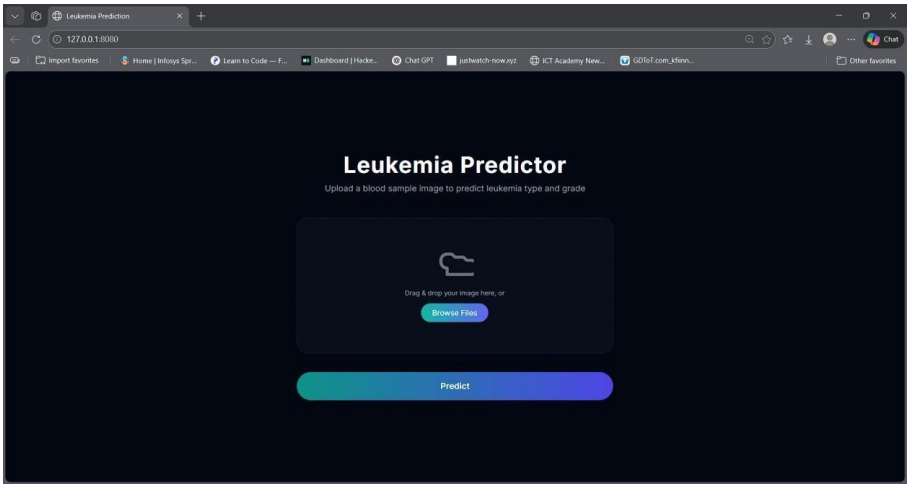

Figure 16: Sample Prediction Output 4

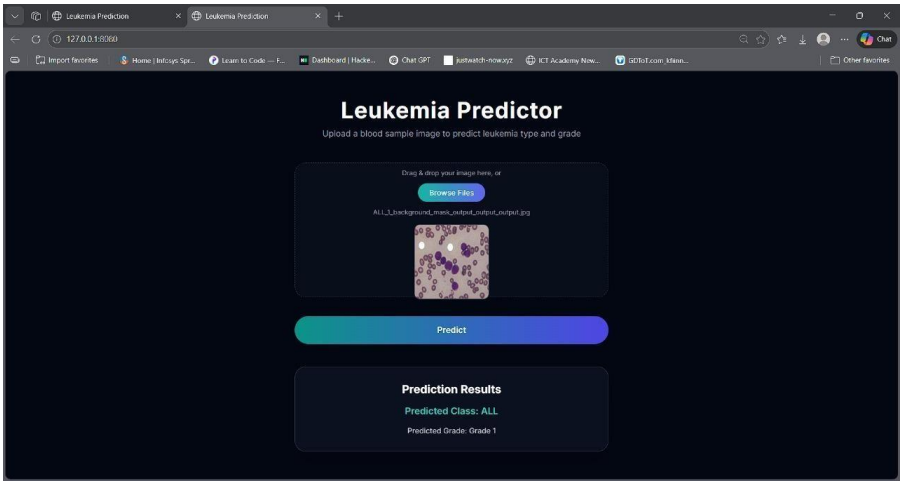

Figure 17: Correct Classification: ALL, Grade 1

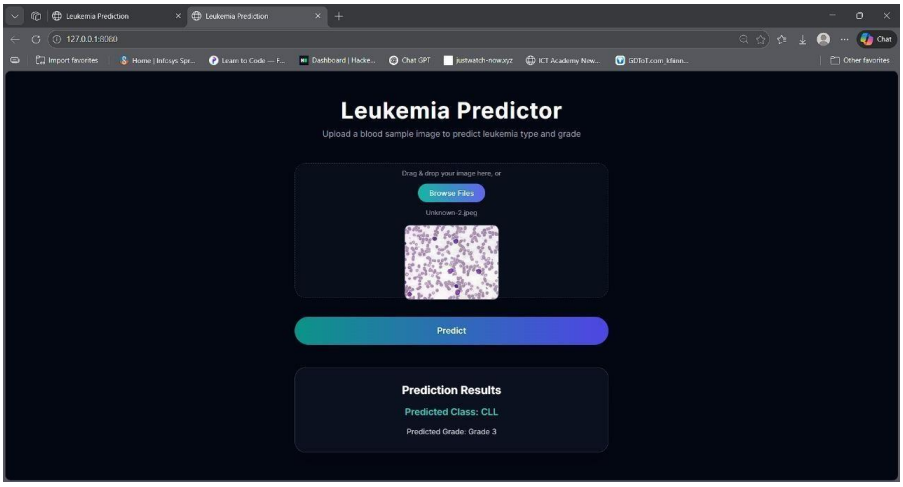

Figure 18: Correct Classification: CLL, Grade 3

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V. PERFORMANCE ANALYSIS

Implementation of MultiTask Learning yielded quantifiable gains over baseline ResNet-18:

1. Metric Enhancement: Evolutionary tuning propelled validation accuracy from 65% to 89%.
2. Differentiation Capability: Acute variants (ALL/AML) showed distinct separation. Chronic subtypes, typically morphologically congruent, also exhibited improved classifi- cation boundaries.

VI. CONCLUSION

Early prognosis of Leukemia is vital. This work establishes a hybrid PSO-ResNet-18 frame- work for concurrent classification and severity assessment. By sequencing PSO for hyper- parameter initialization, the model localizes discriminative features—nuclear irregularity and texture—prior to deep convolution. The residual structure ensures gradient stability. Conclu- sively, the system offers a viable computational adjunct for hematological analysis, aiming to reduce diagnostic latency.

VII. FUTURE SCOPE

- **Architecture Scaling:** Testing deeper networks (ResNet-50/101) is needed. Deeper layers capture fine chromatin details.
- **Hybrid Heuristics:** Genetic Algorithms (GA) could be mixed with PSO. This might make the search converge faster.
- **Multimodal Fusion:** Images are limited. Combining them with flow cytometry or genetic markers adds confidence.
- **Clinical Pilot:** Real-time hospital methodology is the next requirement. Validation needs to happen in workflow.

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