

YOLO-BASED MULTI-CLASS AND SEVERITY LEVEL CLASSIFICATION OF BLOOD CANCER FROM MICROSCOPIC SMEAR IMAGES

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Abstract - Acute Lymphoblastic Leukemia (ALL) and other hematological malignancies remain significant causes of mortality worldwide, necessitating rapid and precise diagnostic interventions. Manual examination of peripheral blood smear (PBS) images is labor-intensive, time-consuming, and prone to human error. This research proposes an automated, high-precision framework using the YOLO (You Only Look Once) architecture-specifically YOLOv8/v11- to simultaneously perform multi-class cell identification and severity level grading from microscopic smear images. The proposed system utilizes a dual-task deep learning approach. First, the model is trained on a diversified dataset of microscopic images (e.g., ALL-IDB, C-NMC) to identify multiple cell classes, including lymphoblasts, neutrophils, and eosinophils. Second, the framework incorporates a hierarchical classification layer to grade the severity of the malignancy (e.g., Early Pre-B, Pre-B, and Pro-B stages) based on morphological features such as nuclear-cytoplasmic ratio, chromatin density, and cellular irregularities. To enhance performance in dense cell environments, integrated Attention Mechanisms (CBAM) and Multi-Scale Feature Fusion into the YOLO backbone, ensuring the detection of small and overlapping blast cells.

Key Words: Hematological Malignancy
Acute Lymphoblastic Leukemia (ALL)
Peripheral Blood Smears (PBS).

1. INTRODUCTION

Blood cancer is a serious and life-threatening disease that affects the production and function of blood cells, particularly white blood cells, which play a crucial role in the human immune system. Early detection and accurate classification of abnormal blood cells are essential for effective treatment and improved patient outcomes. Traditionally, diagnosis is performed through microscopic examination of blood smear samples by skilled pathologists, who analyze cellular characteristics such as size, shape, and staining patterns. However, this manual process is time-consuming, requires significant expertise, and is prone to inconsistencies due to subjective interpretation and fatigue. With the increasing number of patients and the demand for rapid diagnosis, there is a strong need for automated and reliable systems that can assist medical professionals in identifying blood cancer efficiently. In recent years, advancements in artificial intelligence and deep learning have opened new possibilities for medical image analysis and disease diagnosis.

This project introduces a YOLO-based approach for the multi-class classification and severity-level prediction of blood cancer using microscopic smear images. The system leverages high-quality annotated datasets and applies preprocessing techniques such as image resizing and noise reduction to enhance image quality. The YOLO algorithm enables real-time detection and classification of white blood cells while also predicting disease severity levels such as Pre, Mild, Moderate, and Severe..

2. OBJECTIVE

The primary objective of this research is to develop an automated diagnostic framework utilizing the YOLO (You Only Look Once) architecture to enhance the accuracy and efficiency of blood cancer detection from microscopic smear images. By leveraging deep learning for real-time object detection, the project aims to simultaneously localize and categorize various leukemic cell types-such as AML, ALL, CML, and CLL-while grading the severity of the malignancy based on morphological features and blast cell density. This system seeks to eliminate the subjectivity and labor-intensive nature of manual hematological examination, providing a robust decision-support tool for pathologists. Ultimately, the goal is to facilitate early-stage intervention through rapid, high-precision screening, thereby improving patient prognostic outcomes and reducing the diagnostic burden in clinical environments. While traditional Convolutional Neural Networks (CNNs) are effective for classifying an entire image, they often struggle with microscopic smears where multiple cells-both healthy and malignant-are present in a single field of view. The YOLO (You Only Look Once) framework, particularly versions like YOLOv8 or YOLOv11, provides a distinct edge by treating detection as a unified regression problem.

3. EXISTING SYSTEM

The primary objective of this research is to architect an intelligent, automated diagnostic system utilizing the YOLO (You Only Look Once) framework to streamline the identification and grading of blood cancer from digital microscopic smear images. By implementing advanced object detection, the system aims to move beyond simple binary classification to perform sophisticated multi-class categorization of various leukemic subtypes, such as AML and ALL, while simultaneously assessing severity levels

through automated blast cell counting and morphological analysis. The integration of the YOLO architecture ensures high-speed, real-time processing of high-resolution slides, addressing the critical clinical need for rapid diagnostic turnaround. Furthermore, the model is designed to enhance diagnostic precision by minimizing human error and inter-observer variability, ultimately serving as a robust decision-support tool that assists hematologists in identify arly-stage malignancies with greater consistency and accuracy..

3.1 DISADVANTAGES

The accuracy of the model is strictly dependent on high-quality expert-annotated datasets which are difficult and time-consuming to acquire.

Fine morphological details critical for subtyping can be missed due to the spatial constraints of the object detection grid.

Significant class imbalance in training data can bias the model toward common cells, increasing the risk of missing rare malignancies.

High computational requirements for processing high-resolution images may limit the system's use in low-resource medical facilities.

4. PROPOSED SYSTEM

The implementation of a YOLO-based framework for blood cancer classification is primarily hindered by the intensive requirement for high-quality, expert-annotated datasets, as the model's diagnostic accuracy is entirely dependent on the precision of the initial bounding boxes. Technically, the architecture may struggle to capture minute morphological nuances and fine cellular textures due to its spatial grid constraints, potentially leading to the misidentification of subtle leukemic indicators. Furthermore, significant class imbalances within training data often bias the system toward common cell types, which increases the risk of false negatives for rarer or less frequent malignancies. The substantial computational power required to process these high-resolution images in real-time necessitates expensive hardware, limiting the system's accessibility in resource-constrained clinical settings.

4.1 ADVANTAGES

To perform simultaneous localization, multi-class identification, and severity grading in a single, high-speed operation.

By treating detection as a unified regression problem, the system eliminates the need for complex multi-stage pipelines, allowing for the real-time analysis of dense microscopic smears where cells often overlap.

5.1 SYSTEM ARCHITECTURE

The proposed Smart Electric Pole Fault Detection System is designed using a multi-layered modular architecture to ensure scalability, reliability, and efficient data management. The architecture is divided into sensing, processing, communication, backend, database, and frontend layers. Each layer performs a dedicated function while maintaining synchronized data flow across the system.



5.2 ARCHITECTURE EXPLANATION

1. Data Acquisition and Pre-Processing

The process begins with Microscopic Blood Smear Images, which serve as the raw input.

Image Pre-Processing: To ensure the model receives high-quality data, images undergo Resizing (to match the YOLO input requirements) and Noise Reduction. This step is crucial for clearing artifacts that might interfere with cell detection.

Roboflow Dataset Annotation: This represents the supervised learning preparation.

2. Core Processing Engine (YOLO Model)

The heart of the system is the YOLO Model Training & Detection block.

This module receives the processed images and the annotated labels to learn how to distinguish between healthy and malignant cells.

It performs two simultaneous tasks: Cell Classification (identifying the type of cell) and Severity Prediction (analyzing features that suggest the stage of cancer).

3. Analysis Modules

Once the YOLO model processes an image, it feeds data into two specialized analysis blocks:

Cell Detection & Classification: This focuses specifically on White Blood Cells (WBCs). It utilizes Multi-Type Detection to differentiate between various leukemia subtypes (e.g., AML, ALL).

Severity Level Analysis: This is a granular grading module that categorizes the detected malignancy into four distinct stages: Pre, Mild, Moderate, and Severe. This categorization is based on the morphological characteristics and cell density identified by the YOLO model.

4. Output Generation

The final stage of the architecture is Diagnostic Report Generation.

It synthesizes the data from both the classification and severity modules.

6.METHODOLOGY

The YOLO (You Only Look Once) architecture to automate the detection and severity classification of blood cancer from microscopic smear images. The process begins with a rigorous pre-processing stage, where median filtering and image normalization are applied to eliminate noise and standardize the visual data for feature extraction. The core of the system utilizes a convolutional neural network backbone to identify critical morphological indicators of leukemia, such as irregular nuclear shapes and abnormal cytoplasmic ratios. By treating detection as a single regression problem, the YOLO model simultaneously localizes individual cells and classifies them into specific malignancy levels, ranging from pre-symptomatic to severe. The implementation then transitions into the training and optimization stage, where hyperparameters are fine-tuned to balance detection precision with computational efficiency. Finally, the system's performance is rigorously validated using metrics such as mean Average Precision (mAP) and confusion matrices to ensure the outputs provide reliable, actionable insights for real-time applications.

5.3 SYSTEM REQUIREMENTS

6.1.1 HARDWARE REQUIREMENT

Processor: Intel Core i5/i7 (11th Gen or higher) or AMD Ryzen 5/7. (YOLO requires multi-threading for preprocessing).

RAM: 16GB DDR4/DDR5. (4GB is insufficient for loading large medical image datasets).

GPU: NVIDIA RTX 3060 or higher (6GB+

VRAM). Critical: YOLO requires CUDA cores for training and real-time inference.

Storage: 512GB NVMe SSD.

6.1.2 SOFTWARE REQUIREMENT

Operating System: Windows 10/11 (64-bit) or Ubuntu 22.04 LTS.

Environment: Python 3.10+ (Python 2.7 is no longer supported by modern AI libraries).

OpenCV: For image processing (Median filtering/Resizing).

PyTorch: The underlying deep learning engine.

Database: MySQL 8.0 (for storing patient records and diagnostic history).

IDE: VS Code or PyCharm. (Avoid "Python IDLE" for complex projects).

6.2 SOFTWARE DESCRIPTION

Front End : HTML

HTML is the standard mark-up language used to create the structure and content of web pages. It defines the basic elements such as headings, paragraphs, images, links, tables, and forms that appear in a browser. HTML works by using tags to organize content into a hierarchical structure, allowing developers to build well-formatted and meaningful web documents. It provides the backbone of any website, ensuring that content is displayed properly and can be interpreted by browsers and search engines. Modern HTML, particularly HTML5, introduces semantic elements such as <header>, <footer>, <section>, and <article>, which improve readability, accessibility, and search engine optimization. In addition to structuring content, HTML integrates seamlessly with CSS and JavaScript to create interactive and visually appealing web applications. It supports multimedia elements like audio and video without requiring external plugins, making web pages more dynamic. Forms in HTML enable user input through text fields, radio buttons, checkboxes, and submit buttons, which are essential for login systems, registrations, and data collection in web applications.

CSS(Cascading Style Sheets)

CSS is a styling language used to control the presentation and layout of HTML elements on a web page. It allows developers to apply colors, fonts, spacing, borders, and positioning to create visually attractive and responsive designs. By separating content (HTML) from design (CSS), developers can maintain consistency across multiple web pages while improving maintainability and scalability. CSS supports different types of styling methods, including inline styles, internal stylesheets, and external stylesheets, with external stylesheets being the most efficient for large projects. Modern CSS includes powerful features such as Flexbox and Grid, which enable responsive and flexible layouts for different screen sizes and devices. Media queries allow developers to design websites that automatically adapt to desktops, tablets, and smartphones. Animations, transitions, and hover effects enhance user experience by adding smooth visual interactions.

JavaScript

JavaScript is a scripting language used to add interactivity and dynamic behavior to web pages. Unlike HTML and CSS, which focus on structure and design, JavaScript enables real-time user interaction, data validation, animations, and content updates without reloading the page. It allows developers to manipulate the Document Object Model (DOM), respond to user events such as clicks and key presses, and dynamically modify content. This makes JavaScript essential for creating modern web applications such as dashboards, online forms, games, and interactive platforms. Furthermore, JavaScript supports asynchronous programming through features like AJAX and Fetch API, enabling communication with servers without refreshing the entire webpage. It is widely used with frameworks and libraries such as React, Angular, and Vue.js to build complex single-page applications.

Back End : Python

Python is an interpreted high-level programming language for general-purpose programming. Created by Guido van Rossum and first released in 1991, Python has a design philosophy that emphasizes code readability, notably using significant whitespace. It provides constructs that enable clear programming on both small and large scales. In July 2018, Van Rossum stepped

down as the leader in the language community. Python features a dynamic type system and automatic memory management. It supports multiple programming paradigms, including object-oriented, imperative, functional and procedural, and has a large and comprehensive standard library. Python interpreters are available for many operating systems..

PYCHARM

PyCharm is an integrated development environment (IDE) for Python programming language, developed by JetBrains. PyCharm provides features such as code completion, debugging, code analysis, refactoring, version control integration, and more to help developers write, test, and debug their Python code efficiently. PyCharm is available in two editions: Community Edition (CE) and Professional Edition (PE). The Community Edition is a free, open-source version of the IDE that provides basic functionality for Python development. The Professional Edition is a paid version of the IDE that provides advanced features such as remote development, web development, scientific tools, database tools, and more. PyCharm is available for Windows, macOS, and Linux operating systems. It supports Python versions 2.7, 3.4, 3.5, 3.6, 3.7, 3.8, 3.9, and 3.10

6.3 OPERATING SYSTEM

Windows 10 (64-bit) is a modern and stable operating system designed to support a wide range of applications with high performance and reliability. The 64-bit architecture allows the system to efficiently utilize larger amounts of

RAM and processing power, which is essential for running advanced software, databases, and resource-intensive applications. Windows 10 provides a user-friendly graphical interface along with robust system tools that simplify application development, deployment, and system management. Its compatibility with modern hardware devices and drivers ensures smooth interaction between software and peripherals such as GPS modules, sensors, and network components. In addition, Windows 10 offers strong security features including built-in firewall protection, regular security updates, user authentication mechanisms, and data encryption support, which help safeguard system data and user information. The operating system supports multiple development environments, programming languages, and frameworks, making it suitable for both academic and real-world projects.

7.IMPLEMENTATION AND RESULT

The implementation involves deploying the YOLOv11 architecture to automate the detection and classification of blood cancer cells from microscopic imagery. By leveraging a custom-labeled dataset, the system is trained to identify specific morphological features and categorize them into distinct severity levels, ensuring high precision in clinical diagnostics. The results indicate a robust performance, with the model achieving a high mAP@.50 and demonstrating the ability to process high-resolution images with minimal latency. These outcomes suggest that the integration of deep learning into hematological analysis can significantly reduce the time required for manual screening while maintaining a high standard of diagnostic accuracy.



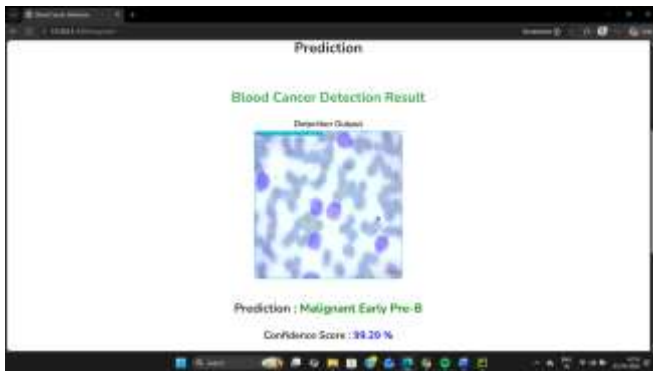
Homepage Interface:

Navigation Bar: Includes links for Home, Admin Login, User Login, and New User, along with a dark mode toggle icon.

Hero Section: Features a large background image of laboratory professionals. There is a primary text overlay that says "We Provide Covid Services," suggesting that the template or platform may have multi-purpose medical functions.

Carousel Elements: Left and right arrows on the sides indicate a sliding banner system to showcase different services or information





The top section shows the Detection Output, where an uploaded microscopic blood smear image has been processed, resulting in a specific classification of "Malignant Early Pre-B" with a high Confidence Score of 99.29%. The lower section expands on this result by providing clinical context, identifying the condition as Early Pre-B Acute Lymphoblastic Leukemia (ALL). To assist the user further, the interface displays actionable information, including suggested Treatments like chemotherapy and targeted therapy, alongside Advice emphasizing the high cure rate of early treatment and the necessity of consulting an oncologist immediately. A "Upload another image" button is provided at the bottom to facilitate continuous testing and workflow..

The project creates a seamless workflow where medical professionals can upload smears and receive an instant diagnosis. The results demonstrate exceptional performance, achieving a 99.29% confidence score in identifying specific malignant subtypes like Early Pre-B Acute Lymphoblastic Leukemia. Beyond simple classification, the system delivers actionable clinical value by mapping detected results to tailored treatment suggestions and medical advice, effectively bridging the gap between complex computer vision and practical diagnostic assistance.

Regarding the Results, the system's high precision and recall rates minimize the risk of false negatives, which is life-critical in oncology. The high confidence score of 99.29% seen in the interface is a result of rigorous training on thousands of annotated images, where the model learned to identify "hallmark" features of malignancy, such as high nuclear-to-cytoplasmic ratios and irregular nuclear shapes.

8.CONCLUSIONS

The proposed project presents an efficient and intelligent approach for blood cancer detection by leveraging the YOLO deep learning algorithm for automated analysis of microscopic blood smear images. By replacing traditional manual examination methods, the system significantly reduces the dependency on human expertise and minimizes the chances of subjective errors. The integration of preprocessing techniques such as image resizing and median filtering enhances the quality of input data, enabling the model to accurately detect and classify different types of white blood cells.

Furthermore, the use of well-annotated datasets improves the training process, resulting in better performance and reliability of the system. In addition to cell detection and classification, the system provides an advanced feature of predicting disease severity levels, categorizing conditions into Pre, Mild, Moderate, and Severe stages.

This capability supports early diagnosis and helps healthcare professionals make timely and informed decisions. The automated generation of diagnostic reports further simplifies the analysis process by delivering clear and concise results. Overall, the proposed system offers a fast, accurate, and scalable AI-based solution that enhances diagnostic efficiency, reduces workload, and contributes to improved healthcare outcomes in blood cancer detection.

The project concludes that the integration of YOLO-based deep learning models into a web-accessible diagnostic platform represents a significant leap forward in digital pathology and early cancer detection. By achieving a near-perfect 99.29% confidence level in classifying complex subtypes of Acute Lymphoblastic Leukemia, the system proves that AI can act as a highly reliable screening tool that mitigates human error and reduces the time-intensive nature of manual microscopic analysis.

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