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Automated Blood Cell Detection System for Infection Diagnosis from Body Fluids

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Abstract

Detecting and counting blood cells accurately is essential for diagnosing many medical conditions. Conventional methods such as manual counting can be time consuming, require expertise and prone to human errors. To overcome these challenges, our project uses a deep-learning based system that can recognize and count the blood cells from microscopic images. Our model helps in improving the speed and reliability and ease the testing process. The future versions of this model can enhance performance through advanced image processing.

Keywords: Blood Cell Detection; Blood Count; Deep Learning; Object Detection; Red Blood Cells; White Blood Cells; Neural Network.

1. Introduction

Infectious diseases remain one of the leading challenges that causes millions of deaths every year. To prevent such spreading of infections early detection and diagnosis plays a vital role in improving treatment outcomes. Analysis of body fluids such as blood, urine, cerebrospinal fluid and lymph plays an important role in diagnosis of infectious cells. Many medical examinations rely on analysis of red blood cells (RBCs) and white blood cells (WBCs) which serve as critical indicators of numerous diseases. Recent advancements in medical imaging and deep learning has enabled the automation of the diagnosis procedure. Automation of blood cell detection can reduce the workload on laboratory personnel and minimizes human error. This research focuses on developing an Automated Blood Cell Detection System that analyses the red blood cells (RBCs) and white blood cells (WBCs) from body fluid samples through machine learning models and predicts the class and count of cells. The ultimate goal is to create a reliable and cost effective tool that seamlessly integrates into modern healthcare workflows.

2. Literature Review

Campus-Medina et al. (2024) created a web based system using the IKOSA platform for automatic cell detection used for classification and counting of different types of cell in WBCs and platelets. They used gray level occurrence matrices that showed high accuracy and consistency with known cell size values. It performed well in monochrome images, public datasets and easily detected small shape variables. Overall the study showed that web based automated microscopy can analyze faster and accurately. [1]

Cruz, Gracia, and Feitosa (2024) developed a system to detect blood cells reducing the drawbacks of manual microscopy by using CNNs trained on the BCCD datasets. It detected RBCs, WBCs and platelet cells with high accuracy. This method improved accuracy and speed while lowering human error. It only lacked in limited availability of white blood cell data which reduced diagnostic detail. Still the work shows the reliability of cell detection is possible without costly lab tools. [2]

Martín et al. (2021) also reviewed the traditional method of cell counting and compared the results with automated blood cell counting only to find out that the traditional methods are slow and subjective. Automated analyzers are able to count red, white and total nucleated cells and even separate polymorphonuclear from mononuclear cells. These systems offered faster results, needed smaller samples and improved consistency. However the results with low cell samples like cerebrospinal fluids required manual checks. In the end they concluded that automation improves accuracy but still needs support of microscopy in complex cases. [3]

Wick et al. (2021) evaluated how well cerebrospinal fluid (CSF) can be automatically examined by commercial blood cell analyzers compared to manual microscopy. They found out that the accuracy is limited by detection thresholds but efficient in time saving. They work well for leukocyte counts but in real cases like meningitis manual checks are still needed. The analyzers can broadly identify lymphocytes. The analyzers can broadly identify WBCs or abnormal cells like blasts, tumor cells and plasma cells which are key in diagnosing cancers and other conditions. So in the end automation improved speed still manual review remains essential for accurate diagnosis. [4]

Chadha et al. (2020) designed an automated system which counts RBCs using image processing. This method was introduced to reduce human efforts and errors seen in traditional manual microscopy. The system applies thresholding and morphological steps like edge detection to separate each cell. This system can also detect abnormal cells by analyzing their texture, colour and shape showing accuracy of 91.6% and 100% sensitivity and strong consistency. However the system struggles with overlapping cells , samples from the fluids and change in lightning. [5]

Xia et al. (2019) explored a method to count and detect WBCs using Faster R-CNN with transfer learning. Their goal was more accurate for small diagnostic devices and faster processing at the point of care. They got 98% accuracy by training the model on 364 microscopic images with very few missed detections. The system proved more reliable than manual counting and suitable for lab on chip applications. However, the authors noted that it still needs more testing but imaging conditions confirm its reliability and consistency.[6]

Shu et al. (2020) introduced AIRFIHA, a reagent free imaging hematology analyzer that usually uses quantitative phase microscopy to study WBCs without chemicals and dyes. The system captures phase

images and applies a residual neural network to identify different cell types along with their subtypes for example. B-cells, T-cells and CD4/CD8 groups. It achieved around 90% accuracy while keeping the natural state of cells intact. This method requires quick, low-cost and requires minimal preparation useful for limited resources. However, It still needs validation as it is only tested on healthy samples. [7]

Chen et al. (2024) proposed MFDS-DETR, a new method to detect WBCs in microscopic images. This new method tackles problems like low quality images, missing details and varying cell sizes. The model captures both global and fine details effectively. It was tested on private datasets called WBCCD and on public datasets like LISC and BCCD. The results showed higher precision and accuracy better than models such as Faster R-CNN, SDD. Some limitations stayed, such as handling overlapping cells. Still this method proved to be more robust and generalizable than either approach. [8]

Choudhary et al. (2024) compared several modern models on cell detection including YOLOv10, ShuffleNetV2 and DarkNet and trained these models on labeled 640x640 pixel images. YOLOv10 gave the best performance and accuracy on training, DarkNet was strong at feature extractions and ShuffleNetV2 ran faster and with less computation. Most models achieve above 0.9 precision and recall. However since the testing was done on a single dataset and generalization may be limited in the case. In the end YOLOv10 offers the best balance of speed and accuracy when trained properly. [9]

Chen, Tsai, and Ho (2022) built a Blood cell detection system using a Single Shot Detector (SSD) with ResNet-50. It identifies WBCs, RBCs and platelets in microscopic smear images. Learning rate and batch size is optimized by applying Taguchi method. By testing this model on BCCD dataset it showed better results with larger input image size especially for detecting platelets of small cells. In the end results showed strong accuracy for WBCs and moderate for RBCs and platelets. The choice of optimization played the biggest role in performance. [10]

Sawant and Singh (2024) built a deep learning system using a CNN based on ResNet50. The model was trained on Kaggle Malaria Cell Images Dataset which includes 27,000 labeled images that achieved high accuracy, recall and precision making it effective for reducing human error and malaria diagnosis. A Streamlit-based web app for quick image upload and real time predictions which can be useful in low resourceful areas. The system offered more consistent results than traditional methods using man work, still they faced challenges with poor image quality and overlapping cells. [11]

Manescu et al. (2022) proposed a method called MILLIE (Multiple Instance Learning for Leukocyte Identification) to detect bone marrow samples and Acute Promyelocytic Leukemia. They achieved a strong performance score with AUC of 0.94 for blood firms and 0.99 for bone marrow aspirated. This reduces the need for manual labeling and minimization of human prone errors. The study shows that this model can make leukemia diagnosis faster, scalable and reliable in limited- resource settings.[12]

3. Proposed System

Module 1: In this module, we explore the existing methods used in automated blood cell detection and infection diagnosis systems. Recent studies highlight various approaches from traditional computer vision algorithms that contribute valuable insights into the field. We aim to identify their strengths and limitations that require further improvements.

Module 2: In this module, we focus on collecting a diverse dataset of microscopic images obtained from various body fluids. This dataset is used for training and validating the machine learning model used in automated detection systems.

Module 3: In this module, the focus is on building the core functionality of automated detection systems which includes development of blood cell detection algorithm and design of intuitive user interface.

Designing the Image Upload Interface:

A web interface will be developed which allows users to upload microscopic images of fluid samples.

Implementing Automated Blood Cell Detection and Infection Diagnosis:

Machine learning algorithms will be built and integrated to the web interface that detects and classifies different types of blood cells. The model will process the uploaded images, apply segmentation masks and analyze cell patterns.

Module 4: In this module, the developed deep learning algorithm is applied to the uploaded microscopic images of body fluid samples.

Blood Cell Detection Algorithm:

The system will process each image to detect and classify blood cells including red blood cells (RBCs) and white blood cells (WBCs) and platelets and determine their count.

Report Generation:

A clear and comprehensive diagnostic report is generated for the user which contains the classification of cell and predicted infection and count.

Module 5: In this module, the blood cell detection undergoes thorough testing to evaluate its accuracy and performance. This phase ensures that the system performs correctly across different samples.

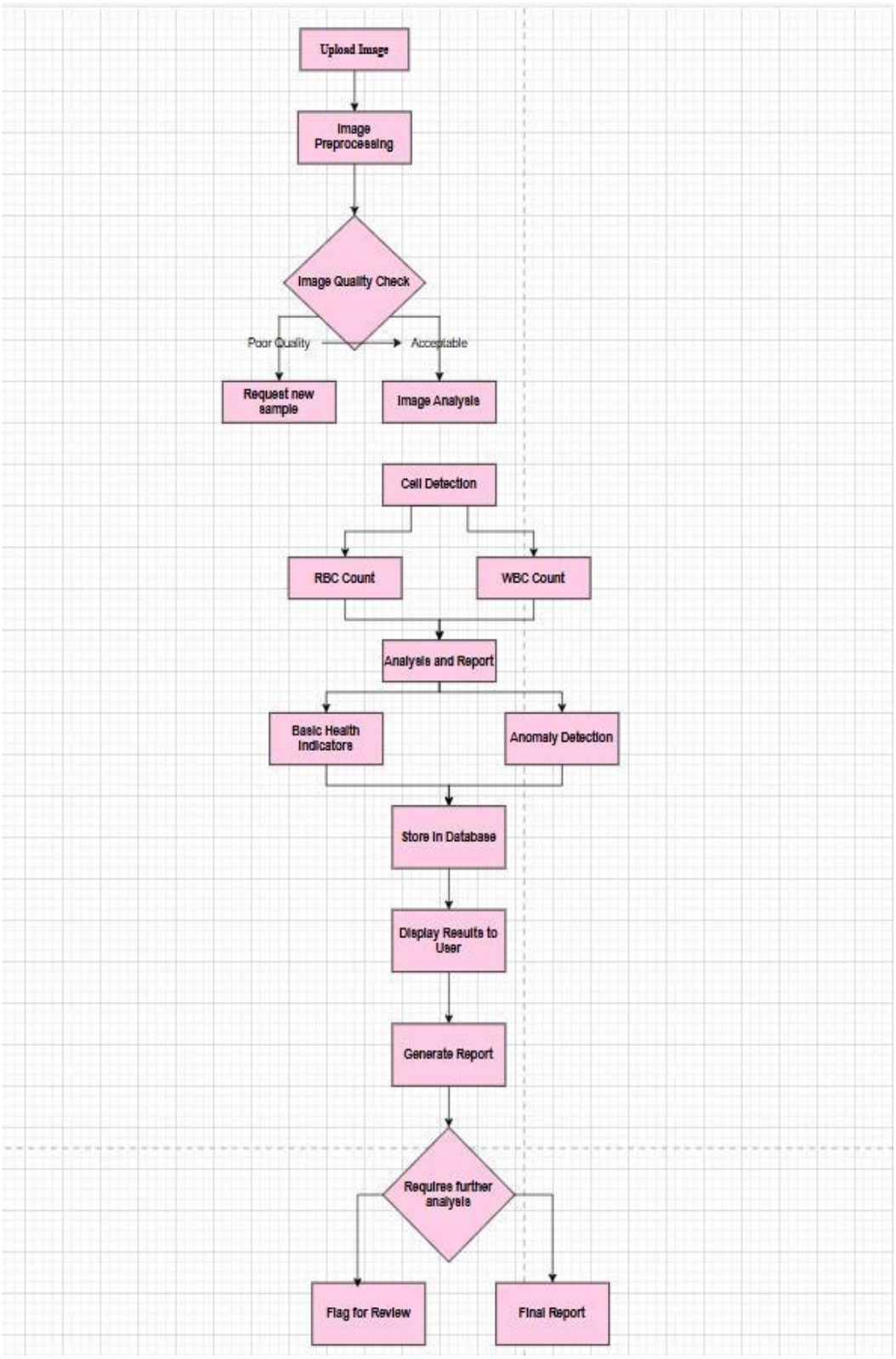

Fig 1. Block Diagram of Follow Up System.

4. Methodology

The Automated Blood Cell Detection and Infection Diagnosis System follows a structured approach dividing key modules to ensure the system is reliable, accurate and user friendly. The process starts with a literature review where existing techniques related to cell detection and diagnosis are studied in depth. This includes modern machine learning and deep learning approaches and traditional image processing methods which are used for microscopic image classification. This review focuses on understanding the advantages and drawbacks of classical techniques such as thresholding, edge detection and morphological operations and some models like Convolutional Neural Networks (CNN) , YOLO that are usually applied for identifying leukocytes and erythrocytes. The insights gathered in the whole process and analysis help in designing a detection system that is accurate and adaptable to various sample types and imaging conditions. After the literature review the next major step is dataset collection, where a wide range of well labeled data of microscopic images from body fluids such as blood, saliva, urine and cerebrospinal fluid (CSF) are collected for training and evaluation. [1]

The **core mathematical operation** in CNNs is the convolution between the image and the kernel (filter).

If the input image is I and the kernel is K, then the convolution output (feature map) F is given by:

$$F(i,j) = \sum_m \sum_n I(i+m, j+n) \cdot K(m,n)$$

- i, j are the coordinates of the **output feature map** F.
  - i represents the **row index** in the output.
  - j represents the **column index** in the output.
- m, n are indices that iterate over the **kernel/filter** K.
- $I(i+m, j+n)$ is the value of the input image at the location covered by the kernel.

Fig 2. Convolutional Operation formulas and Key to variables in the 2D Convolution Formula

The methodology involves collecting and sourcing microscopic labeled images from publicly available medical datasets and collaborating with medical institutions and laboratories to ensure the encompassing both normal and pathological samples of diverse dataset. Direct and accurate image annotation server as the ground truth for supervised learning and impacts both the performance and reliability of the classifiers. The following steps focuses then on the development of the blood cell detection algorithm and a user centric web interface that improves interactivity and seamless image upload resulting in better user experience. [2]

- **Confusion Matrix**:

$$C_{ij} = \text{number of samples with true class } i \text{ and predicted class } j$$

- **Precision, Recall, F1-score** from `classification_report()`:

$$\text{Precision} = \frac{TP}{TP + FP}, \quad \text{Recall} = \frac{TP}{TP + FN}$$

$$\text{F1} = 2 \times \frac{\text{Precision} \times \text{Recall}}{\text{Precision} + \text{Recall}}$$

Fig 3. Core Classification Evaluation Metrics

These metrics are derived from the Confusion Matrix and are critical for evaluating a machine learning classifier. Precision measures the accuracy of positive predictions, Recall measures the fraction of actual positives correctly identified and F1-score is the harmonic mean that provides measure of model performance. [3]

This user interface is equipped with automated preprocessing images, including resizing, normalization, and enhancement, to optimize image quality for analysis. In parallel, machine learning and Deep learning algorithms are developed and integrated into the system to detect, segment, and classify different blood cell primarily red blood cells (RBCs), white blood cells (WBCs), and platelets—while identifying morphological abnormalities that may indicative of infections or other abnormalities.The detection pipelines involves advance image processing and cell detection using deep neural network architecture to generate accurate cell count and classifications.These outputs are then compiled into comprehensive diagnostic report summarizing detected cell types helpful for further diagnosis of any medical issues. To ensure data privacy and regulatory compliance the system incorporates user authentication which allows control over the information. Because of this, users can manage report sharing and viewing permissions. Following the development phase the system undergoes rigorous testing and validation to ensure and evaluate the accuracy, efficiency and robustness under different imaging conditions and sample variations. Performance is usually measured using metrics such as precision, recall, F1-score and noise tolerance. Based on the evaluation outcomes, iterative refinements are to be applied to both the detection algorithm to improve the diagnostic accuracy The methodology concludes with the preparation of a comprehensive thesis documenting design, experimentation, implementation and evaluation process establishing strong foundation for future research and real world deployment of automated blood cell detection and diagnosis systems. [4]

5. Results and Discussion

The proposed Blood Cell Detection System provides clear advantages over manual microscopy with efficiency and ease of use. By using machine learning algorithms the system is capable of learning recursively, making the system adaptable to varying sample conditions. This learning method results in improvement in detection accuracy. The model can analyze multiple slides and different types of cells using parallel processing, reducing the time required for conventional microscopy. Potential medical conditions can be flagged using cell morphology and count which can offer diagnostic suggestions.

The intuitive web interface blends advanced analysis tools with easy to use controls making it more accessible to everyone.

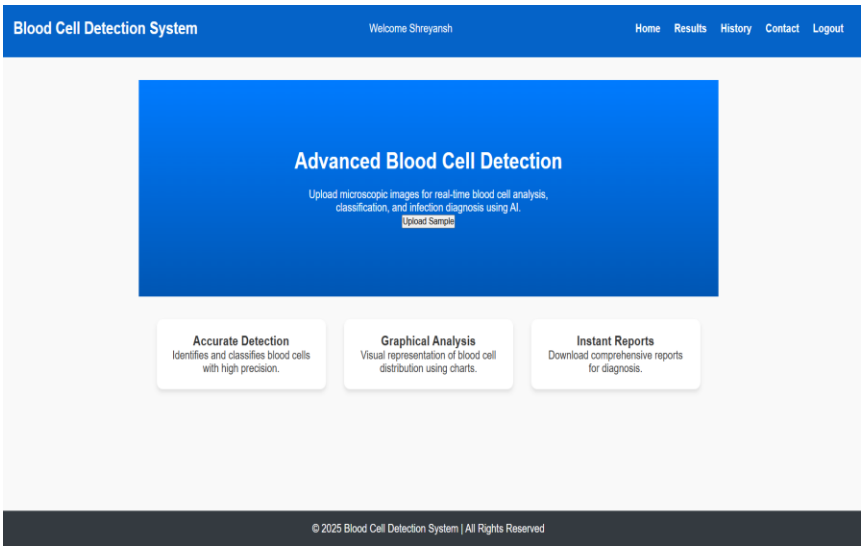

Fig 4. Web Interface of the Automated Blood Cell Detection System.

The system is capable of analysing a variety of bodily fluids such as blood, urine, cerebrospinal fluid, saliva and lymph. Cross-referencing results across these samples improves diagnostic accuracy by revealing systemic patterns that might otherwise go unnoticed. The proposed system takes an image through the web interface.

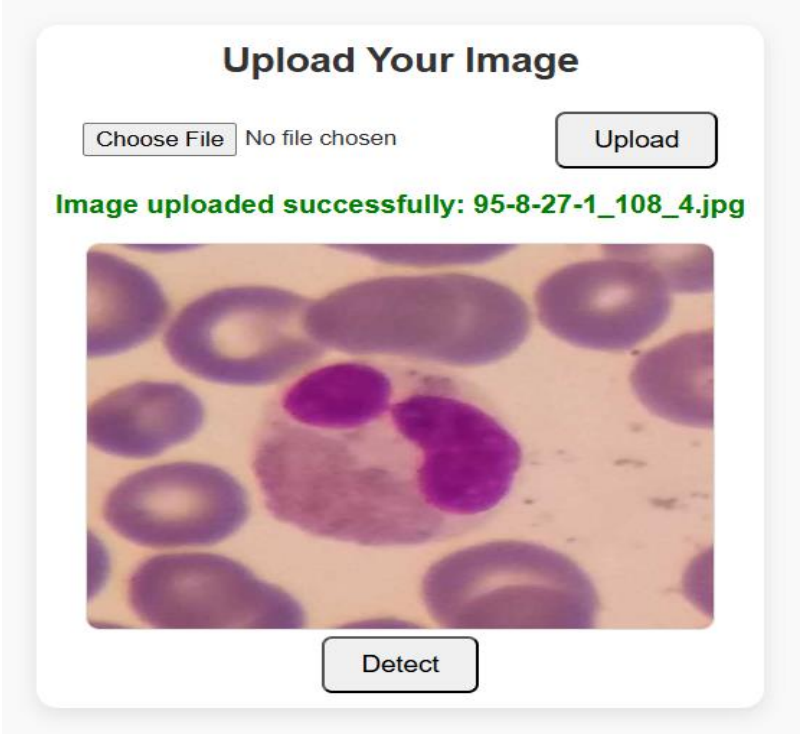

Fig 5. Image Upload Interface for Blood Cell Detection.

This image is then processed through the model which applies a variety of segmentation masks to identify the cell.

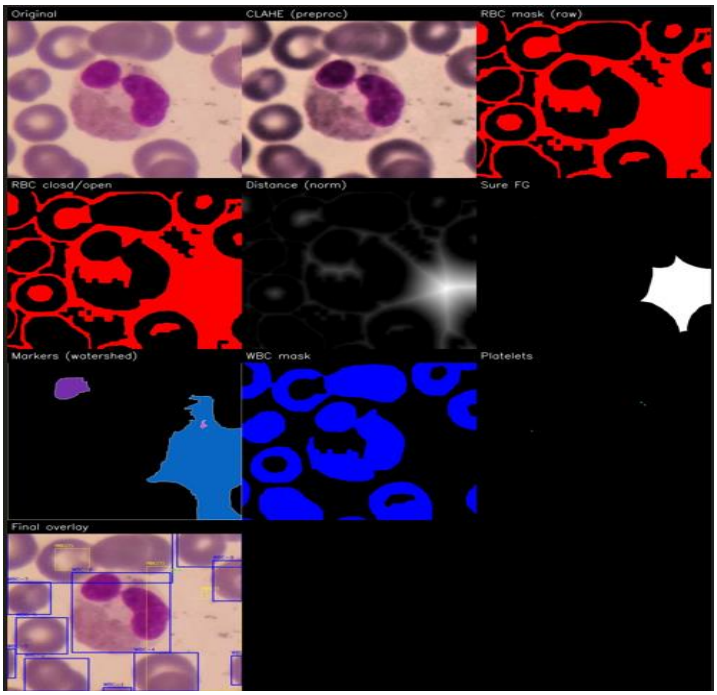

Fig 6. Visualization of Segmentation Stages.

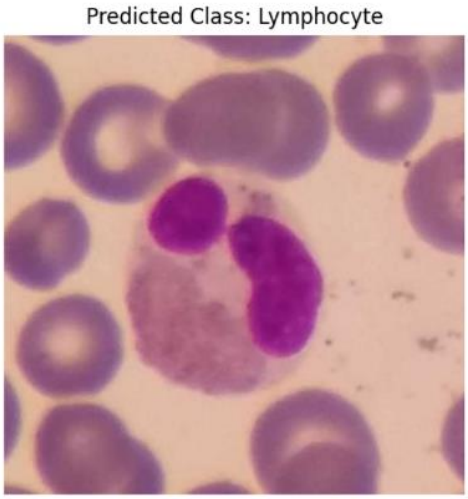

Fig 7. Predicted Cell

6. Conclusion

This research proposes an Automated Blood Cell Detection System that is designed to make microscopic analysis faster and easy to access. By integrating deep learning techniques with an intuitive interface, the system can detect and classify different types of blood cells, such as RBCs, WBCs and platelets. This approach reduces human efforts and speeds up the diagnosis process with consistent results.

The system is flexible enough to analyse cells from various bodily fluids and generate a report on it. Such adaptability makes the system useful for well-equipped laboratories and remote healthcare centers with limited resources. Overall, this work demonstrates the remarkable application of machine learning and automation that takes a step forward towards smarter and technology-driven healthcare solutions. Future developments may focus on expanding the model's dataset and capabilities that can support a broader range of medical applications.

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