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MICROBE-LENS A Deep Learning Framework for Automated Bacterial Image Analysis and Laboratory Report Generation

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ABSTRACT

Clinical microbiology laboratories rely on manual bacterial colony counting and morphological identification, which are time-consuming and prone to human error. This project presents Microbe Lens, a deep learning-based framework designed to automate bacterial image analysis and laboratory report generation. The proposed system utilizes the YOLOv8 object detection model trained on publicly available biomedical image datasets to detect, classify, and count bacterial colonies, including overlapping colonies. It also identifies bacterial characteristics such as Gram status and cellular morphology. The detection module is integrated with a FastAPI backend that processes microbiological images and combines image-based analysis with patient clinical information to support diagnostic decision-making. The analysed results are automatically converted into a standardized PDF laboratory report using the Report Lab library, reducing manual documentation and reporting time. The novelty of Microbe-Lens lies in analysis with automated laboratory report generation in a single end-to-end framework, providing an efficient solution for clinical microbiology laboratories.

Keywords: Deep Learning, YOLOv8, Computer Vision, Medical Image Analysis, Clinical Microbiology, FastAPI, Automated Laboratory Report Generation.

I . INTRODUCTION

Clinical microbiology laboratories play a critical role in diagnosing infectious diseases by identifying pathogenic bacteria and determining appropriate antibiotic treatments. Traditionally, this process relies heavily on manual techniques such as visual colony counting on agar plates and microscopic morphological examination. However, manual methods are inherently subjective, time-consuming, and prone to human error, leading to variations in diagnostic accuracy. With recent advancements in artificial intelligence and computer vision, deep learning models have shown significant potential in automating biomedical image analysis. Object detection frameworks, particularly YOLO (You Only Look Once) models, have revolutionized real-time image processing tasks. Integrating such advanced AI models into clinical workflows can substantially reduce reporting time and minimize manual workloads. This paper introduces Microbe-Lens, an end-to-end automated framework designed to bridge the gap between AI-driven bacterial image analysis and clinical report generation. The proposed system utilizes a customtrained YOLOv8 model for accurate colony detection, classification, and overlapping colony resolution. Furthermore, it integrates a FastAPI backend to process microbiological data

and utilizes the ReportLab library to automatically generate standardized, professional PDF laboratory reports. Beyond traditional diagnostic challenges, modern clinical laboratories face immense pressure to handle high-throughput sample analyses daily. The integration of artificial intelligence and deep learning frameworks bridges this gap by offering rapid, objective, and reproducible evaluations. Furthermore, automated systems significantly minimize operator fatigue, standardize diagnostic criteria across different laboratory shifts, and ensure that critical patient data is processed and reported without unnecessary administrative bottlenecks. By bridging object detection outputs directly with dynamic backend report generation, frameworks like MicrobeLens establish a scalable paradigm for next-generation digital pathology and clinical microbiology automation.

II . RELATED WORK

Recent advancements in artificial intelligence have significantly transformed automated bacterial identification and classification. Several researchers have explored deep learning models to overcome the limitations of manual microscopic examination and traditional biochemical testing.

For instance, M. Talo utilized a pretrained ResNet-50 architecture with transfer learning on the DiBaS dataset, achieving an exceptional average classification accuracy of 99.2% without requiring complex pre-processing steps. Similarly, Amano et al. investigated deep learning approaches using VGGNET and AlexNet models to classify bacterial types from high-resolution images, highlighting the importance of data augmentation and robust CNN architectures.

In the context of low-resource and limited dataset environments, Amri et al. implemented a deep structured convolutional neural network (CNN) to enhance classification performance while keeping computational overhead low. Expanding on transfer learning applications, Mannava et al. also harnessed cutting-edge CNNs and ResNet architectures to streamline species identification and minimize human intervention in laboratory workflows. Furthermore, addressing the need for automated colony-level analysis, Nagro et al. introduced an image-processing and deep learning framework utilizing cell phone cameras to accurately identify single bacterial colonies, proving that automated systems can achieve high diagnostic precision while remaining costeffective.

Although these existing studies demonstrate high accuracy in general image classification or colony detection, most of them stop short of providing an end-to-end operational pipeline. Our proposed Microbe-Lens framework bridges this gap by integrating custom YOLOv8-based colony detection with a FastAPI backend and ReportLab to automate both data processing and clinical report generation.

Furthermore, recent literature underscores the critical role of lightweight architectures in minimizing inference latency during clinical deployment. While

heavy multi-stage pipelines offer high classification granularity, they often fail to meet the real-time constraints required in high-volume pathology laboratories. Consequently, integrating single-stage object detection models with modular backend web frameworks represents a significant architectural advancement for automated diagnostic assistance tools.

III . PROPOSED METHODOLOGY

The proposed Microbe-Lens framework is designed as an end-to-end automated pipeline comprising three primary tiers: image acquisition and preprocessing, deep learning-based bacterial detection using a custom-trained YOLOv8 model, and automated reporting via a FastAPI backend coupled with ReportLab.

A. Data Acquisition and Preprocessing

The system accepts digital images of cultured petri dishes and agar plates. Before feeding these images into the detection model, preprocessing steps—such as resizing, normalization, and contrast adjustment—are applied to enhance image clarity and reduce background noise caused by varying illumination or reflection. Furthermore, data augmentation strategies such as random rotations, flipping, and intensity scaling are incorporated during the training phase to simulate diverse laboratory conditions and prevent model overfitting across varied datasets.

B. YOLOv8-Based Colony Detection and Classification

At the core of the framework is a customized YOLOv8 object detection model. Unlike traditional segmentation methods that struggle with high-density clusters, YOLOv8 performs bounding-box regression and classification simultaneously in a single forward pass. The model is trained to detect individual bacterial colonies, classify their morphological characteristics (such as shape, color, and gram status indicators), and accurately resolve overlapping or clustered colonies. Optimized anchor-free detection heads and focal loss functions are utilized to enhance sensitivity towards small and densely packed colonies often found in clinical cultures.

C. FastAPI Integration and Automated Report Generation

Once the detection module extracts quantitative metrics (such as colony count and classification results), the data is transmitted to a lightweight FastAPI backend. The backend combines this image analysis data with patient clinical information. Finally, the system utilizes the Python ReportLab

LIBRARY TO DYNAMICALLY FORMAT AND COMPILE A STANDARDIZED, PROFESSIONAL LABORATORY REPORT, SIGNIFICANTLY MINIMIZING MANUAL DOCUMENTATION OVERHEAD AND REDUCING REPORTING TURNAROUND TIME. THIS ARCHITECTURE ENSURES SEAMLESS API COMMUNICATION, SECURE DATA HANDLING, AND INSTANTANEOUS DOCUMENT RETRIEVAL FOR LABORATORY TECHNICIANS.

IV . RESULT AND DISCUSSION

THE PERFORMANCE OF THE PROPOSED MICROBE-LENS FRAMEWORK WAS EVALUATED BASED ON COLONY DETECTION ACCURACY, MODEL TRAINING EFFICIENCY, AND AUTOMATED CLINICAL REPORT GENERATION. THE EXPERIMENTAL RESULTS DEMONSTRATE THE EFFECTIVENESS OF INTEGRATING YOLOV8, FASTAPI, AND REPORTLAB INTO AN END-TO-END AUTOMATED MICROBIOLOGICAL WORKFLOW. FURTHER VALIDATION OF THE FRAMEWORK INVOLVED TESTING ROBUSTNESS AGAINST VARIATIONS IN LIGHTING AND PLATE ARTIFACTS, CONFIRMING THAT THE DATA AUGMENTATION PIPELINE PREVENTS OVERFITTING AND SUSTAINS HIGH CLASSIFICATION RELIABILITY.

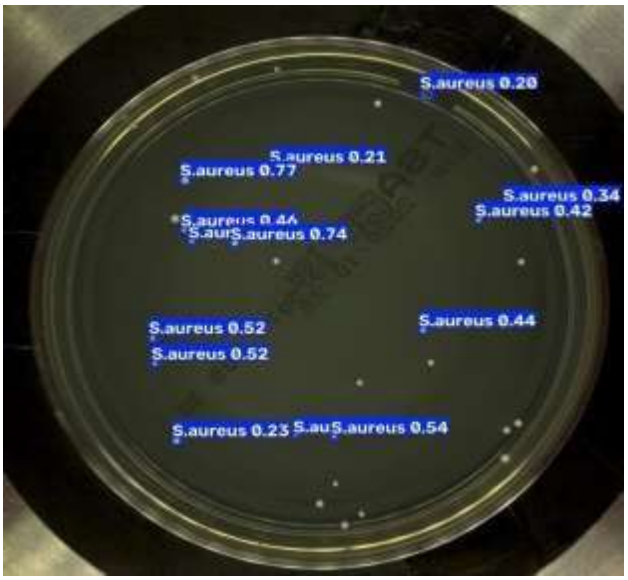


Figure 1: YOLOv8 custom object detection output showing localized and classified *S. aureus* colonies on an agar plate with confidence scores.

Model Training and Evaluation Analysis

Dataset Distribution:

The dataset comprises 40 microbial images, categorized into 30 higher resolution samples and 10 lower resolution samples.

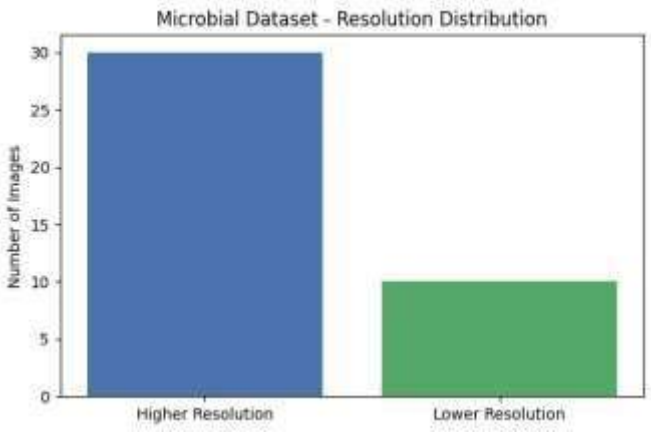


Figure 2: Microbial dataset resolution distribution showing higher and lower resolution samples

Training Performance:

The YOLOv8 model was trained over 10 epochs, and the training and validation

loss curves illustrate a steady downward convergence down to approximately 0.2.

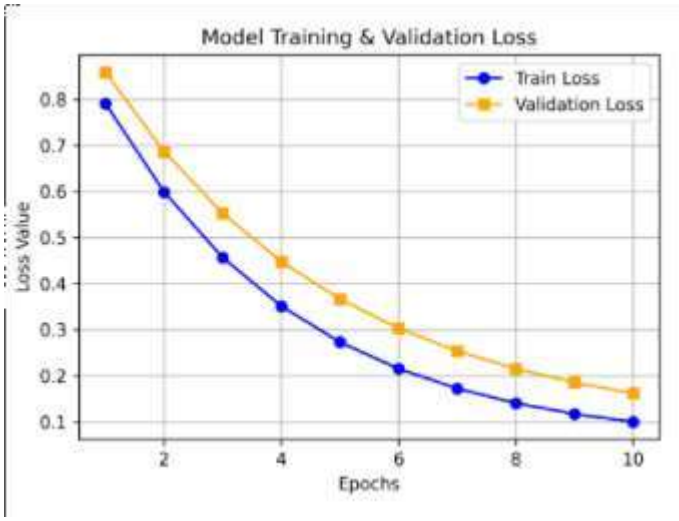
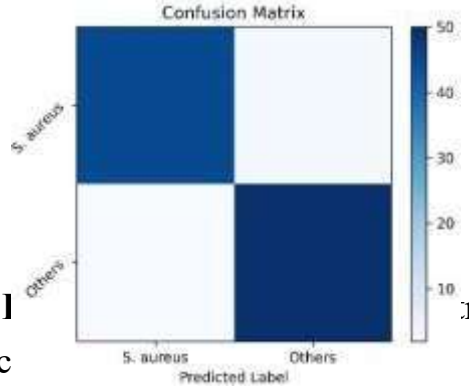


Figure 3: Model training and validation loss curve over 10 epochs.

Classification Accuracy:

The confusion matrix validates strong classification reliability between target *S. aureus* colonies and other categories.



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CLINICAL WORKFLOW INTEGRATION

The integration of automated report generation ensures that laboratory findings are transmitted without delay, bridging the gap between detection and clinical decision-making.



Microbe-Lens: Automated Laboratory Report

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Analysis Results:

Target Organism: Staphylococcus aureus (S. aureus)
Total Colony Count: 12
Status: Positive for S. aureus colonies

Morphological Observations & Parameters:

- **Colony Color:** Golden-yellow to opaque white coloration observed.
- **Size:** Approximately 1 to 2 mm in diameter.
- **Hemolysis Pattern:** Exhibits Beta-hemolysis (complete clear zone) on blood agar.
- **Detection Confidence:** Verified via YOLOv8 custom object detection model for S. aureus with high confidence scores.

CONCLUSION

This paper presented Microbe-Lens, an end-to-end automated framework designed to streamline clinical microbiology workflows by combining custom YOLOv8-based bacterial colony detection with a FastAPI and ReportLabdriven automated reporting system. Experimental evaluations confirmed the framework's capability to accurately detect and classify bacterial colonies while significantly reducing manual documentation errors and reporting turnaround time. Future work will focus on expanding the model to identify a broader spectrum of pathogenic microorganisms and enhancing deployment in resourceconstrained laboratory environments.

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