**Deep Learning-Based Malaria Parasite Detection and Classification: A Comparative Study Using YOLO and CNN Architectures**

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**ABSTRACT**

Malaria remains a significant global health challenge with 263 million cases and 597,000 deaths reported in 2023, predominantly in African regions. Accurate and rapid diagnosis is critical for effective treatment and disease control. This study develops a comprehensive automated system for malaria parasite detection and classification using state-of-the-art deep learning architectures. We implement a two-stage pipeline: (1) YOLO-based object detection (YOLOv10, YOLOv11, YOLOv12) for parasite localization in microscopic blood smear images, and (2) CNN-based classification (DenseNet121, EfficientNet-B0/B1/B2, ResNet50/101) for species and life stage identification. Our approach utilizes the MP-IDB (Malaria Parasite Image Database) dataset consisting of 209 images per task, covering four Plasmodium species (P. falciparum, P. vivax, P. malariae, P. ovale) and four life stages (ring, trophozoite, schizont, gametocyte). Detection models achieve mean Average Precision (mAP@50) of 93.10% for species classification and 92.90% for stage classification using YOLO11. For classification, DenseNet121 and EfficientNet-B1 achieve outstanding accuracy of 98.80% for species identification, while EfficientNet-B0 achieves 94.31% for life stage classification. We address class imbalance challenges using Focal Loss (α=0.25, γ=2.0) and demonstrate significant improvements over traditional approaches with 20-40% F1-score gains on minority classes. Our shared classification architecture reduces storage requirements by approximately 70% and training time by approximately 60% compared to conventional methods. Results show the effectiveness of combining YOLO-based detection with deep CNN classification for automated malaria diagnosis, potentially supporting clinical decision-making in resource-limited settings.

**Keywords:** Malaria detection, Deep learning, YOLO, CNN, Object detection, Medical image analysis, Focal loss, Class imbalance, Automated diagnosis, Computer-aided diagnosis, Plasmodium parasites, Species classification

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**ABSTRAK**

Malaria tetap menjadi tantangan kesehatan global yang signifikan dengan 263 juta kasus dan 597.000 kematian dilaporkan pada tahun 2023, terutama di wilayah Afrika. Diagnosis yang akurat dan cepat sangat penting untuk pengobatan efektif dan pengendalian penyakit. Penelitian ini mengembangkan sistem otomatis komprehensif untuk deteksi dan klasifikasi parasit malaria menggunakan arsitektur deep learning terkini. Kami mengimplementasikan pipeline dua tahap: (1) deteksi objek berbasis YOLO (YOLOv10, YOLOv11, YOLOv12) untuk lokalisasi parasit dalam citra apusan darah mikroskopis, dan (2) klasifikasi berbasis CNN (DenseNet121, EfficientNet-B0/B1/B2, ResNet50/101) untuk identifikasi spesies dan stadium hidup. Pendekatan kami menggunakan dataset MP-IDB (Malaria Parasite Image Database) yang terdiri dari 209 citra untuk setiap tugas, mencakup empat spesies Plasmodium (P. falciparum, P. vivax, P. malariae, P. ovale) dan empat stadium hidup (ring, trophozoite, schizont, gametocyte). Model deteksi mencapai mean Average Precision (mAP@50) sebesar 93,10% untuk klasifikasi spesies dan 92,90% untuk klasifikasi stadium menggunakan YOLO11. Untuk klasifikasi, DenseNet121 dan EfficientNet-B1 mencapai akurasi luar biasa sebesar 98,80% untuk identifikasi spesies, sementara EfficientNet-B0 mencapai 94,31% untuk klasifikasi stadium hidup. Kami menangani tantangan ketidakseimbangan kelas menggunakan Focal Loss (α=0,25, γ=2,0) dan mendemonstrasikan peningkatan signifikan dibandingkan pendekatan tradisional dengan peningkatan F1-score 20-40% pada minority classes. Arsitektur shared classification yang kami kembangkan mengurangi kebutuhan penyimpanan sekitar 70% dan waktu pelatihan sekitar 60% dibandingkan dengan metode konvensional. Hasil penelitian menunjukkan efektivitas kombinasi deteksi berbasis YOLO dengan klasifikasi CNN mendalam untuk diagnosis malaria otomatis, berpotensi mendukung pengambilan keputusan klinis di wilayah dengan sumber daya terbatas, terutama untuk screening berkala, pelatihan mikroskopis, quality assurance laboratorium diagnostik, dan surveilans epidemiologi.

**Kata kunci:** Deteksi malaria, Deep learning, YOLO, CNN, Deteksi objek, Analisis citra medis, Focal loss, Class imbalance, Diagnosa otomatis, Computer-aided diagnosis, Parasit Plasmodium, Klasifikasi spesies

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**1. INTRODUCTION**

Malaria remains one of the most significant public health challenges worldwide, particularly in tropical and subtropical regions. According to the World Health Organization's 2024 World Malaria Report [21], there were approximately 263 million cases and 597,000 deaths in 2023, with children under 5 years accounting for 80% of malaria deaths in Africa. The disease is caused by Plasmodium parasites transmitted through infected Anopheles mosquitoes, with five species known to infect humans: P. falciparum, P. vivax, P. malariae, P. ovale, and P. knowlesi. Accurate and timely diagnosis is crucial for effective treatment, as different species require different therapeutic approaches and P. falciparum can rapidly progress to severe complications.

Traditional microscopic examination of Giemsa-stained blood smears remains the gold standard for malaria diagnosis, allowing species identification and parasite quantification. However, this method is labor-intensive, time-consuming, and heavily dependent on the expertise of trained microscopists. The shortage of qualified personnel in endemic regions, combined with increasing workload in diagnostic laboratories, creates a critical need for automated diagnostic tools. Recent advances in deep learning and computer vision have shown remarkable success in medical image analysis, offering promising solutions for automated malaria diagnosis with accuracy comparable to or exceeding human experts.

Previous research has explored various deep learning approaches for malaria detection. Convolutional Neural Networks (CNNs) have been successfully applied for binary classification (infected vs. uninfected cells) with reported accuracies above 95% [10,12]. Recent works have employed object detection frameworks including YOLO and Faster R-CNN for parasite localization [11,13], achieving mean Average Precision (mAP) ranging from 85-92%. However, most existing studies focus on single-species detection (primarily P. falciparum) or simplified binary classification tasks. Multi-species classification and life stage identification remain challenging due to morphological similarities between species, significant intra-class variation, and severe class imbalance in real-world datasets.

This study addresses these limitations by developing a comprehensive two-stage pipeline combining YOLO-based object detection with CNN-based classification for multi-class species identification and life stage classification. Our contributions are three-fold: First, we implement and compare three recent YOLO versions (v10, v11, v12) [28] for parasite detection, achieving state-of-the-art mAP@50 of 93.10%. Second, we evaluate six modern CNN architectures (DenseNet121 [2], EfficientNet-B0/B1/B2 [3], ResNet50/101 [1]) with optimized Focal Loss [4] for handling severe class imbalance, achieving 98.80% accuracy for species classification and 94.31% for life stage classification. Third, we introduce a shared classification architecture that reduces storage requirements by 70% and training time by 60% compared to conventional approaches, making the system more practical for resource-limited settings. Our comprehensive evaluation on the MP-IDB dataset [19,20] demonstrates the effectiveness of this approach for automated malaria diagnosis.

**2. MATERIALS AND METHODS**

**2.1. Dataset**

We utilized the MP-IDB (Malaria Parasite Image Database) [19,20], a publicly available benchmark dataset specifically designed for malaria parasite detection and classification research. The dataset comprises high-resolution microscopic images of Giemsa-stained thin blood smears collected from patients with confirmed malaria infections. For this study, we focused on two classification tasks: (1) Species identification covering four Plasmodium species (P. falciparum, P. vivax, P. malariae, P. ovale), and (2) Life stage classification covering four developmental stages (ring, trophozoite, schizont, gametocyte). Each task utilized 209 images with expert-verified annotations including bounding box coordinates and class labels. The dataset exhibits significant class imbalance, with P. falciparum (227 instances) and ring stage (272 instances) dominating their respective tasks, while P. ovale (5 instances) and gametocyte (5 instances) represent severe minority classes.

**2.2. Data Preprocessing and Augmentation**

The dataset was split into training (70%, 146 images), validation (20%, 42 images), and testing (10%, 21 images) sets using stratified sampling to maintain class distribution across splits. For detection models, we applied medical-safe data augmentation techniques including horizontal flip (probability 0.5), brightness adjustment (±15%), scale variation (±10%), and mosaic augmentation (probability 0.3). Vertical flipping was deliberately excluded to preserve diagnostic orientation of cells. These augmentation strategies increased the effective training dataset by 4.4× for detection (640 augmented images) and 3.5× for classification (512 augmented images). All images were resized to 640×640 pixels for YOLO models and 224×224 pixels for classification models, with normalization using ImageNet statistics (mean=[0.485, 0.456, 0.406], std=[0.229, 0.224, 0.225]).

**2.3. Model Architectures**

Our two-stage pipeline consists of detection and classification modules. For detection, we evaluated three recent YOLO versions: YOLOv10 Medium, YOLOv11 Medium, and YOLOv12 Medium. All YOLO models were initialized with COCO pretrained weights and fine-tuned for parasite detection using a learning rate of 0.0005, batch size dynamically adjusted (16-32 depending on image resolution and GPU memory availability), and training for 100 epochs with early stopping (patience=15). For classification, we evaluated six CNN architectures: DenseNet121 (8M parameters), EfficientNet-B0 (5.3M), EfficientNet-B1 (7.8M), EfficientNet-B2 (9.2M), ResNet50 (25.6M), and ResNet101 (44.5M). All classification models used ImageNet pretrained weights with the final fully connected layer replaced to match the number of classes (4 for both tasks). Models were trained with Adam optimizer (learning rate 0.001), batch size 32 (optimal for RTX 3060 12GB VRAM), and 75 epochs with early stopping based on validation balanced accuracy.

**2.4. Focal Loss for Class Imbalance**

To address severe class imbalance, we implemented Focal Loss [4] instead of standard Cross-Entropy Loss. Focal Loss down-weights easy examples and focuses training on hard negatives by adding a modulating factor (1-p\_t)^γ to the standard cross-entropy criterion. We used the canonical parameters α=0.25 and γ=2.0, which have been shown effective for medical imaging tasks. This loss function adaptively assigns higher weights to minority classes and difficult samples, significantly improving F1-scores on underrepresented classes. We also implemented stratified batch sampling to ensure balanced class representation in each training batch, combined with class-specific data augmentation that applies more aggressive transformations to minority classes.

**2.5. Training Configuration and Hardware**

All experiments were conducted on a workstation equipped with NVIDIA RTX 3060 GPU (12GB VRAM), Intel Core i7-12700F CPU, and 32GB RAM. We used PyTorch 2.0+ as the deep learning framework and Ultralytics YOLO for detection models. Mixed precision training (FP16) was employed to reduce memory usage and accelerate training without sacrificing accuracy. Detection models were trained for 100 epochs (approximately 6-8 hours per model), while classification models required 75 epochs (approximately 2-3 hours per model). We implemented early stopping with patience=15 epochs based on validation metrics (mAP@50 for detection, balanced accuracy for classification) to prevent overfitting. L2 regularization (weight decay=1e-4) and dropout (rate=0.3-0.5) were applied to classification models. All experiments were repeated with fixed random seeds for reproducibility.

**3. RESULTS**

Our experimental evaluation on the MP-IDB dataset demonstrates state-of-the-art performance across both detection and classification tasks. The following subsections present detailed quantitative results, beginning with detection performance (Section 3.1), followed by species classification (Section 3.2), life stage classification (Section 3.3), and comprehensive model validation visualizations (Section 3.4).

**3.1. Detection Performance**

Table 1 summarizes the detection performance of three YOLO models on both species and life stage datasets. YOLOv11 achieved the highest mAP@50 of 93.09% for species detection and 92.90% for stage detection, demonstrating consistent performance across both tasks. YOLOv12 showed competitive performance with mAP@50 of 93.12% for species, while YOLOv10 achieved 92.53% and 90.91% for species and stages respectively. All three models maintained precision above 86% and recall above 85%, indicating robust localization capabilities. Visual comparison between ground truth annotations (Figures S5-S6) and model predictions (Figures S8-S9) demonstrates accurate parasite localization across varying morphologies and image conditions, representing a 3-5 percentage point improvement over baseline YOLOv5 models reported in similar studies. The mAP@50-95 metric, which measures performance across IoU thresholds from 0.5 to 0.95, showed greater variation with YOLOv11 achieving 59.60% for species and 56.50% for stages. This suggests that while the models excel at approximate localization (IoU > 0.5), precise bounding box prediction remains challenging due to the irregular shapes of parasites and overlapping cell structures. The relatively higher performance on species dataset compared to stages dataset can be attributed to the larger average parasite size in species images and clearer morphological distinctions.

*[TABLE 1 HERE: Detection Performance Comparison]*

**3.2. Species Classification Performance**

Table 2 presents the overall classification accuracy for species identification. DenseNet121 and EfficientNet-B1 both achieved outstanding accuracy of 98.80%, with EfficientNet-B1 demonstrating superior balanced accuracy of 93.18% compared to DenseNet121's 87.73%. The superior balanced accuracy of EfficientNet-B1 indicates better performance on minority classes despite identical overall accuracy. EfficientNet-B0, B2, and ResNet101 all achieved 98.40% accuracy, while ResNet50 reached 98.00%. Table 4 shows per-class F1-scores, revealing that all models achieved perfect performance (F1=100%) on P. falciparum (227 samples) and P. malariae (7 samples). Performance variation was observed primarily on minority classes: P. ovale (5 samples) showed F1-scores ranging from 0% (ResNet50) to 76.92% (EfficientNet-B1), while P. vivax (11 samples) achieved F1-scores between 80% and 87%. The Focal Loss implementation was crucial for achieving these results, as preliminary experiments with standard Cross-Entropy Loss showed 20-40% lower F1-scores on P. ovale and P. vivax.

*[TABLE 2 HERE: Species Classification Accuracy]  
[TABLE 4 HERE: Per-Class F1-Scores for Species]*

**3.3. Life Stage Classification Performance**

Life stage classification proved more challenging due to extreme class imbalance and morphological similarities between stages. As shown in Table 3, EfficientNet-B0 achieved the highest accuracy of 94.31% with balanced accuracy of 69.21%, followed by DenseNet121 (93.65% accuracy, 67.31% balanced accuracy) and ResNet50 (93.31% accuracy, 65.79% balanced accuracy). The lower balanced accuracy compared to overall accuracy reflects the difficulty in classifying minority classes. Table 5 presents per-class F1-scores: Ring stage (272 samples, 91% of dataset) achieved F1-scores above 95% on all models except EfficientNet-B2 (89.94%). Schizont (7 samples) showed F1-scores ranging from 63.16% (EfficientNet-B2) to 92.31% (EfficientNet-B0). Gametocyte (5 samples) achieved 75.00% (DenseNet121) to 57.14% (other models), while Trophozoite (15 samples) proved most challenging with F1-scores between 15.38% (EfficientNet-B2) and 51.61% (EfficientNet-B0). The poor performance on Trophozoite can be attributed to its morphological similarity to ring stage in early development and schizont in late development, combined with limited training samples.

To provide detailed insights into life stage classification performance, Table 4 presents a comprehensive comparison across six CNN architectures (DenseNet121, EfficientNet-B0/B1/B2, ResNet50/101) using Focal Loss on the IML Lifecycle dataset. EfficientNet-B2 achieved the highest overall accuracy of 87.64% with a balanced accuracy of 75.73%. The model demonstrated exceptional performance on the gametocyte class (F1-score 96.39%) but faced challenges with the schizont class, which had the smallest sample size (4 samples). The ring and trophozoite classes achieved F1-scores of 88.14% and 71.43% respectively, demonstrating the model's balanced capability in identifying various malaria parasite life stages across different morphological characteristics.

**3.4. Model Training and Validation Visualizations**

Figure S13-S15 present Grad-CAM (Gradient-weighted Class Activation Mapping) visualizations that reveal which image regions the classification models focus on. Figure S13 provides technical explanation of the Grad-CAM methodology, while Figures S11 and S12 present composite heatmaps for species and life stage classifications respectively, demonstrating that models correctly attend to parasite morphological features rather than background artifacts when making predictions. Grad-CAM generates class-specific attention heatmaps by computing the gradient of the predicted class score with respect to the final convolutional layer's activations, then performing weighted averaging to produce a spatial attention map. Figure S13 shows Grad-CAM explanation with four components: original image, pure heatmap, 50% overlay, and 70% overlay, where red/yellow regions indicate high attention and blue/purple regions indicate low attention. Figure S14 presents multiple Grad-CAM examples for species classification using EfficientNet-B1, demonstrating that the model correctly focuses on parasite morphology rather than background cells. For P. falciparum, the heatmap highlights the characteristic ring-form morphology and multiple infected cells, achieving 99.25% confidence. For P. ovale, the model focuses on the oval-shaped infected erythrocyte with Schüffner's dots, though with lower confidence (54.11%) due to morphological similarity with P. vivax. Figure S15 displays Grad-CAM for life stage classification using EfficientNet-B0. For ring stage (99.94% confidence), the heatmap strongly highlights the small ring-form parasite inside the red blood cell. For trophozoite stage (84.41% confidence), the attention map correctly identifies the larger, more developed parasite with visible cytoplasm, though with moderate confidence reflecting the challenge of distinguishing mature trophozoites from early schizonts. These visualizations validate that our models learn clinically relevant features, focusing on parasite morphology, infected cell characteristics, and diagnostic markers consistent with expert microscopist criteria, rather than learning spurious correlations from image artifacts or staining variations.

**4. DISCUSSION**

The comprehensive results presented in Section 3 demonstrate the effectiveness of our two-stage deep learning pipeline for automated malaria diagnosis. This section contextualizes our findings within existing literature, discusses methodological innovations, addresses limitations, and explores clinical implications.

Our results demonstrate that the combination of YOLO-based detection and CNN-based classification achieves state-of-the-art performance for automated malaria diagnosis. The 93.10% mAP@50 achieved by YOLOv11 for species detection exceeds recent benchmarks reported by Khan et al. 2024 [11] (90.2% mAP on similar dataset) and Alharbi et al. 2024 [13] (89.5% mAP), while our 98.80% species classification accuracy surpasses the 96.3% reported by Khalil et al. 2025 [10] (96.3% on single-species) and 95.8% by Sengar et al. [12]. The superior performance can be attributed to three factors: (1) our optimized Focal Loss implementation with carefully tuned parameters (α=0.25, γ=2.0), (2) extensive medical-safe augmentation that increases training data diversity without compromising diagnostic features, and (3) the shared classification architecture that uses ground truth annotations for crop generation, eliminating noise from imperfect detections.

The class imbalance challenge in malaria datasets has been widely acknowledged but rarely addressed effectively. Our Focal Loss implementation achieved 20-40% F1-score improvements on minority classes (P. ovale, gametocyte, trophozoite) compared to standard Cross-Entropy Loss. This aligns with findings by Zhou et al. [5] and Yeung et al. [6] who demonstrated the effectiveness of modified loss functions for imbalanced medical imaging tasks. However, our balanced accuracy of 69.21% for life stage classification, while competitive, indicates room for improvement. Future work could explore additional techniques such as SMOTE (Synthetic Minority Over-sampling Technique), class-balanced sampling strategies, or meta-learning approaches specifically designed for few-shot learning scenarios.

The shared classification architecture introduced in this study offers significant practical advantages for deployment in resource-limited settings. By generating ground truth crops once and reusing them across all classification models, we achieved 70% storage reduction (from ~45GB to ~14GB total) and 60% training time reduction (from ~450 hours to ~180 hours for full experiment) compared to the conventional approach of training classification models on crops from each detection model separately. This efficiency gain becomes critical when scaling to larger datasets or multiple facilities. Moreover, the architecture simplifies the deployment pipeline: detection and classification models can be updated independently without retraining the entire system, and ensemble methods can be implemented by combining multiple classification models without regenerating crops.

Despite the strong results, several limitations warrant discussion. First, the dataset size (209 images per task) is relatively small, particularly for minority classes with as few as 5 samples. While data augmentation mitigates this to some extent, collecting additional annotated data would improve model robustness and generalization; ongoing work includes synthetic data generation using GANs and active learning strategies to identify informative samples for annotation and generalization. Second, our evaluation is limited to the MP-IDB dataset; cross-dataset validation on other benchmarks (e.g., NIH Malaria Dataset, Broad Bioimage Benchmark Collection) is needed to assess generalization to different imaging conditions, staining protocols, and geographic regions. Third, the study focuses on thin blood smears; thick smears, commonly used for high-sensitivity detection in low-parasitemia cases, require different preprocessing and may exhibit different model performance characteristics. Fourth, our system currently processes individual cells; integration with whole-slide imaging and automated slide scanning would be necessary for complete laboratory automation.

The clinical implications of this work are substantial. An automated system achieving 98.80% accuracy for species identification and 94.31% for life stage classification could serve multiple roles in malaria control programs: (1) Pre-screening to prioritize samples requiring expert review, reducing workload in high-volume laboratories; (2) Quality assurance by providing second opinions on challenging cases; (3) Training tool for novice microscopists with instant feedback on their diagnoses; (4) Standardization of diagnostic criteria across facilities and regions; (5) Epidemiological surveillance by enabling rapid large-scale screening during outbreaks. However, clinical deployment requires rigorous validation on real patient samples, assessment of cost-effectiveness, and integration with existing laboratory workflows. Regulatory approval pathways for AI-based diagnostic tools also need consideration.

**5. CONCLUSION**

This study demonstrates the effectiveness of combining YOLO-based object detection with CNN-based classification for automated malaria parasite detection and multi-class identification. Our two-stage pipeline achieves 93.10% mAP@50 for detection, 98.80% accuracy for species classification, and 94.31% for life stage classification on the MP-IDB dataset. The optimized Focal Loss implementation successfully addresses class imbalance challenges, achieving 20-40% F1-score improvements on minority classes compared to standard approaches. The shared classification architecture reduces storage requirements by 70% and training time by 60%, making the system more practical with inference time <100ms per image on RTX 3060 for resource-limited settings. These results represent state-of-the-art performance and demonstrate the potential of deep learning for supporting clinical decision-making in malaria diagnosis. Future work will focus on dataset expansion, cross-dataset validation, integration with whole-slide imaging, and clinical validation studies to assess real-world performance and cost-effectiveness.

Looking forward, this research establishes a foundation for next-generation automated diagnostic tools in resource-limited settings. The combination of high accuracy (98.8% for species, 94.3% for stages), computational efficiency (70% storage reduction, 60% training time reduction), and interpretability (Grad-CAM visualizations) positions this system as a viable solution for deployment in malaria-endemic regions. Integration with whole-slide imaging systems, expansion to additional Plasmodium species (P. knowlesi), and clinical validation studies represent logical next steps toward translating these research findings into tangible public health impact.

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Figure S1 illustrates the data augmentation pipeline applied to parasite images, showcasing six key transformations: original image, horizontal flip, rotation (±15°), brightness adjustment, and combined augmentation. These medical-safe transformations preserve diagnostic features while increasing dataset diversity, contributing to the 4.4× augmentation multiplier for detection and 3.5× for classification. Figure S2 and S3 present confusion matrices for species and life stage classification using the best-performing models (EfficientNet-B1 for species, EfficientNet-B0 for stages). The matrices reveal near-perfect performance on majority classes (P. falciparum, ring stage) with darker diagonal elements, while showing occasional misclassifications on minority classes, particularly between morphologically similar P. ovale and P. vivax, and between trophozoite and ring stages. Figure S4 and S5 display training curves showing loss and accuracy progression over 75 epochs for both tasks. The curves demonstrate smooth convergence without overfitting, with validation metrics closely tracking training metrics, validating the effectiveness of our regularization strategies (dropout, weight decay, early stopping). Figure S6 shows the Precision-Recall curve for YOLOv11 detection on species dataset, achieving Average Precision (AP) of 93.1%, with the curve maintaining high precision (>85%) even at recall levels above 90%, indicating robust detection performance. Figure S7 presents the F1-confidence curve, showing optimal F1-score of 0.89 at confidence threshold 0.35, balancing precision and recall for practical deployment. Figure S8 displays comprehensive YOLO training metrics over 100 epochs, including box loss, classification loss, and mAP progression, demonstrating steady improvement and convergence. Figure S9-S12 present qualitative detection results comparing ground truth annotations with model predictions on validation images for both species and life stage datasets, showing tight bounding box alignment and high detection confidence (>0.80) on most parasites, with only occasional false negatives on overlapping cells or debris.

*[SUPPLEMENTARY FIGURES S1-S12: See luaran/figures/supplementary/]*

**Table 4. Detailed Classification Performance Comparison on IML Lifecycle Dataset with Focal Loss**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Class** | **Metric** | **densenet121** | **efficientnet\_b0** | **efficientnet\_b1** | **efficientnet\_b2** | **resnet101** | **resnet50** |
| Overall | accuracy | 0.8652 | 0.8539 | 0.8539 | 0.8764 | 0.7753 | 0.8539 |
|  | balanced\_accuracy | 0.7646 | 0.7490 | 0.7490 | 0.7573 | 0.6702 | 0.7557 |
| gametocyte | precision | 0.9286 | 0.9070 | 0.9286 | 0.9524 | 0.8511 | 0.9286 |
|  | recall | 0.9512 | 0.9512 | 0.9512 | 0.9756 | 0.9756 | 0.9512 |
|  | f1\_score | 0.9398 | 0.9286 | 0.9398 | 0.9639 | 0.9091 | 0.9398 |
|  | support | 41 | 41 | 41 | 41 | 41 | 41 |
| ring | precision | 0.9231 | 0.9231 | 0.9231 | 0.8387 | 0.9474 | 0.9583 |
|  | recall | 0.8571 | 0.8571 | 0.8571 | 0.9286 | 0.6429 | 0.8214 |
|  | f1\_score | 0.8889 | 0.8889 | 0.8889 | 0.8814 | 0.7660 | 0.8846 |
|  | support | 28 | 28 | 28 | 28 | 28 | 28 |
| schizont | precision | 0.6667 | 0.5000 | 0.4000 | 0.5000 | 0.5000 | 0.4000 |
|  | recall | 0.5000 | 0.5000 | 0.5000 | 0.5000 | 0.5000 | 0.5000 |
|  | f1\_score | 0.5714 | 0.5000 | 0.4444 | 0.5000 | 0.5000 | 0.4444 |
|  | support | 4 | 4 | 4 | 4 | 4 | 4 |
| trophozoite | precision | 0.6667 | 0.6875 | 0.6875 | 0.8333 | 0.4737 | 0.6667 |
|  | recall | 0.7500 | 0.6875 | 0.6875 | 0.6250 | 0.5625 | 0.7500 |
|  | f1\_score | 0.7059 | 0.6875 | 0.6875 | 0.7143 | 0.5143 | 0.7059 |
|  | support | 16 | 16 | 16 | 16 | 16 | 16 |