Deep Learning for Automated Malaria Parasite Detection: A Cross-Dataset Validation Study

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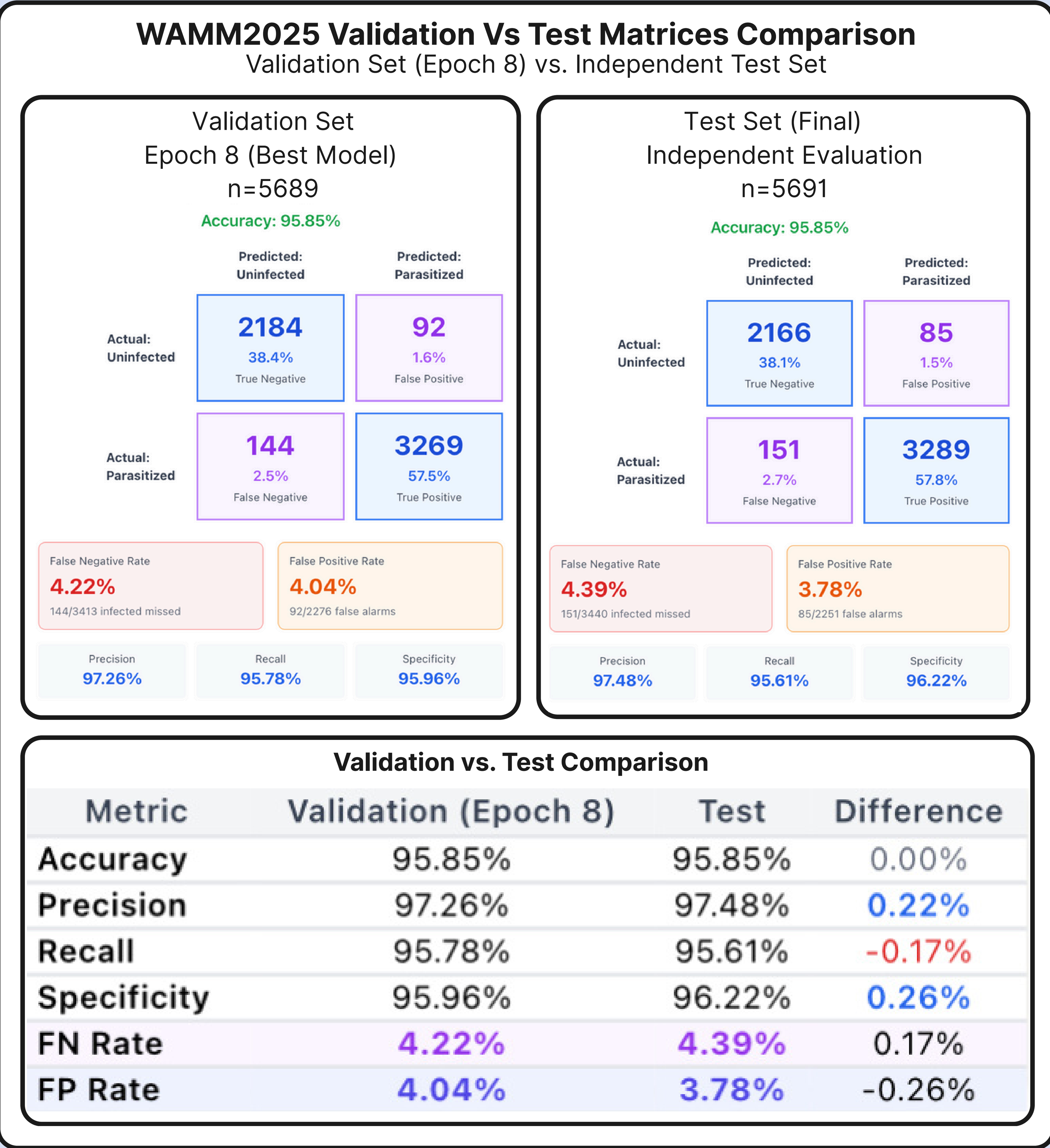
Background: Malaria accounts for 249 million cases and 608,000 deaths annually, with 95% in sub-Saharan Africa. Conventional microscopy requires 20-30 minutes per sample with 60-85% inter-observer variability, limiting diagnostic capacity in resource-constrained settings.

Objective: To develop a geographically diverse and univesal deep learning system for automated malaria detection using MaxViT-Small architecture with a validation protocol.

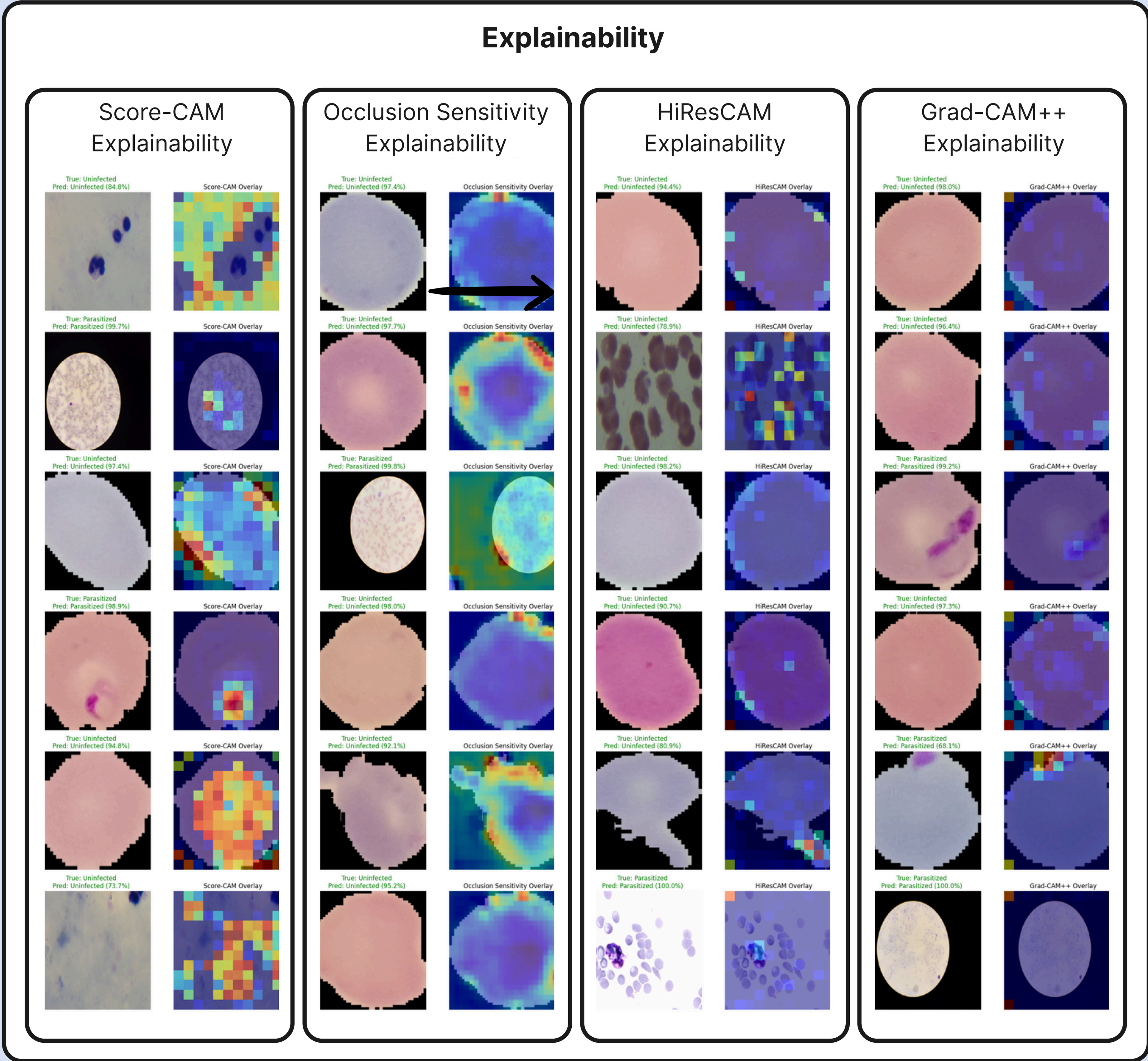
Methods: A 6-stage pipeline processed 6 datasets from 4 continents (NIH, MP-IDB, Broad Institute, Tek, Lacuna, Tanzania) including thin and thick blood films of infected and uninfected samples. Datasets contained four Plasmodium species (P. falciparum, P. vivax, P. malariae, P. ovale), predominantly P. falciparum. From 38,622 images, 689 corrupted files (1.8%) were excluded, yielding 37,933 images split 70/15/15: 26,553 training, 5,689 validation, 5,691 test. Preprocessing included CLAHE, gray-world color constancy, Macenko stain normalization, and resizing to 384×384. MaxViT-Small (68.3M parameters) was trained on Google Colab A100 with Kornia augmentation, mixed-precision training, and early stopping. Explainability assessed using Grad-CAM++, HiResCAM, Occlusion Sensitivity, and Score-CAM. Claude Sonnet 4.5 assisted with coding.

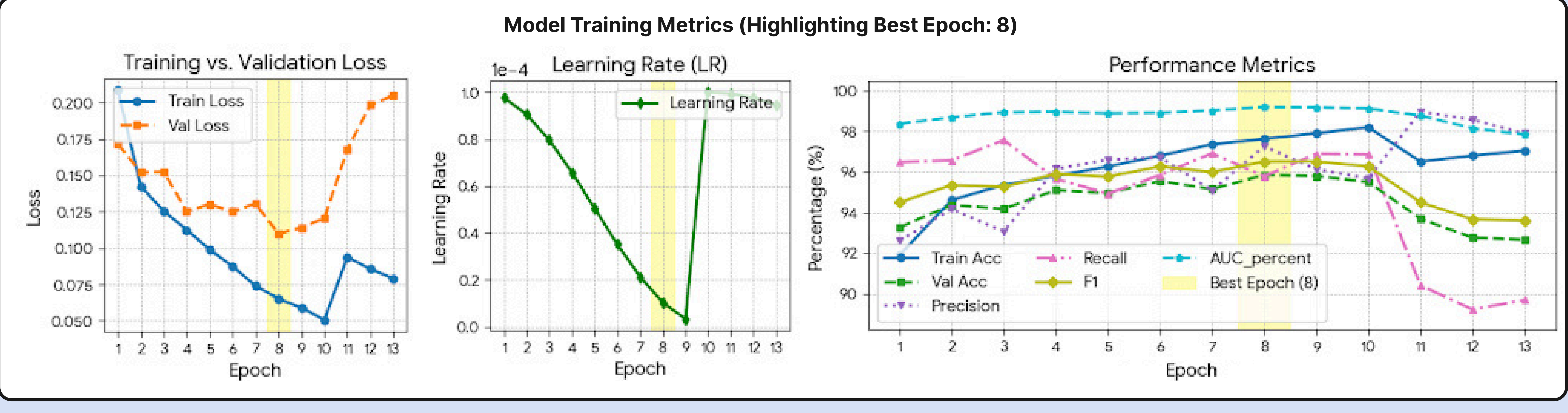
Results: Training for 13 epochs selected epoch 8 as optimal (validation AUC 0.9921). Independent test evaluation (n=5,691) achieved: accuracy 95.85%, precision 97.48%, recall 95.61%, specificity 96.22%, F1 96.54%, AUC-ROC 0.9897. Confusion matrix: 2,166 true negatives, 85 false positives (3.77%), 151 false negatives (4.39%), 3,289 true positives. Perfect validation-test concordance (95.85%) with 1.78% train-validation gap demonstrated robust generalization. Explainability confirmed correct parasite focus. Training: 2.07 hours.



Validation vs. Test Comparison

Metric	Validation (Epoch 8)	Test	Difference
Accuracy	95.85%	95.85%	0.00%
Precision	97.26%	97.48%	0.22%
Recall	95.78%	95.61%	-0.17%
Specificity	95.96%	96.22%	0.26%
FN Rate	4.22%	4.39%	0.17%
FP Rate	4.04%	3.78%	-0.26%





Conclusion: This is one of the firs multi-continental model integrating 6 datasets achieved strong performance (95.85% accuracy, 0.9897 AUC-ROC). However, 4.39% false negative rate exceeds clinical standards (<2%). We used H&E-based stain normalization; Giemsa-specific normalization would improve performance. Augmented training required to achieve projected 97-98% accuracy with <2% false negatives for clinical deployment.