BRIDGING ACCURACY AND TRUST: EXPLAINABLE DEEP LEARNING VS. CLASSICAL COMPUTER VISION FOR MALARIA DIAGNOSIS

A COMPARATIVE ANALYSIS OF MOBILENETV2 AND HOG-RANDOM FOREST

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THE DUAL **CRISIS**

The Global Health Challenge

- **282 million cases of Malaria, 610,000 deaths (2024) [1]**
- Gold Standard (Microscopy) is slow, error-prone, and dependent on human expertise. [1]

The AI Dilemma:

- **High accuracy** is not enough
- The "Black Box" Paradox
  - Doctors cannot trust a model they cannot understand. [2]
- Safety Risk:
  - A False Negative can be fatal.

[1] World Health Organization, World malaria report 2025: Addressing the threat of antimalarial drug resistance, Geneva: WHO, 2025.
[2] F. Pesapane, M. Codari, and F. Sardanelli, "Artificial intelligence in medical imaging: threat or opportunity? Radiologists again at the forefront of innovation in medicine," European Radiology Experimental, vol. 2, no. 1, p. 35, 2018.

METHODOLOGICAL DUEL

SYMBOLIC VS. CONNECTIONIST

Data Source
NIH Malaria Cell Images Dataset
27,558 Images
50% Parasitized / 50% Uninfected
80% Training / 20% Validation

Method A: Symbolic AI (The Baseline)

- Pipeline: HOG (Histogram of Oriented Gradients) + Random Forest.
- The Math: We explicitly calculate gradient magnitude (M) and orientation (θ) for every pixel (x,y) to detect edges:

$$M(x,y) = \sqrt{g_x^2 + g_y^2}$$

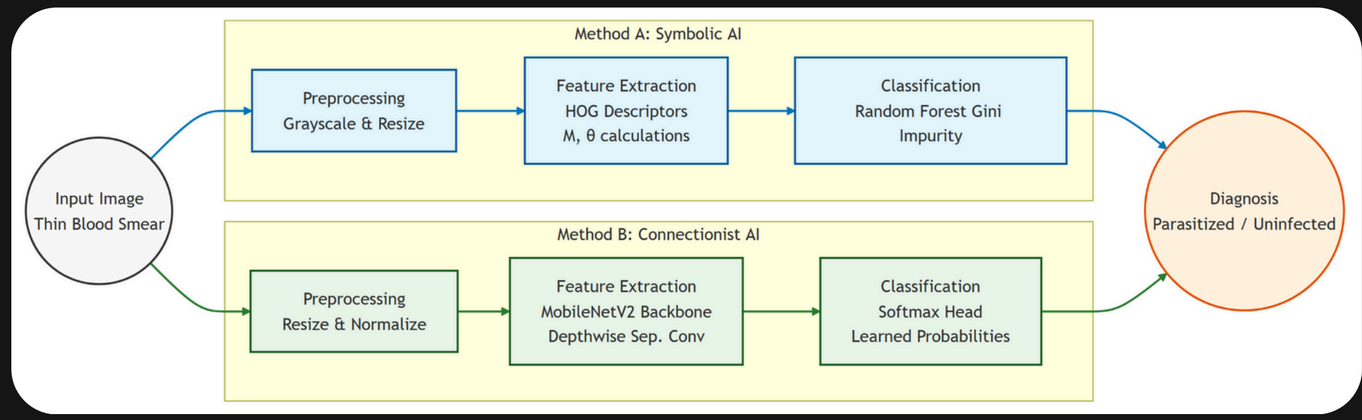
$$\theta(x,y) = arctan\frac{g_y}{g_x}$$

- Classification: Random Forest splits trees by minimizing Gini Impurity:

$$I_G(t) = 1 - \sum_{i=1}^{C} p\,(i|t)^2$$

Method B: Connectionist AI (The Challenger)

- Pipeline: Transfer Learning with MobileNetV2.
- Philosophy: Features are learned implicitly via backpropagation.



Pipelines

DEEP LEARNING ARCHITECTURE

The Constraint

Deployment on edge devices requires low computational cost.

The Efficiency Formula

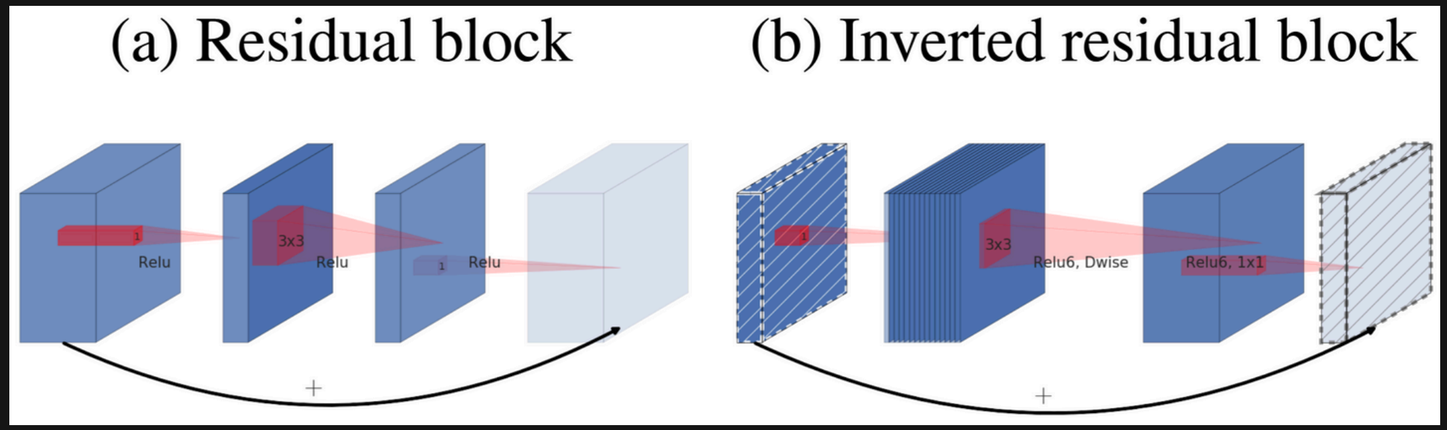
The computational cost reduction factor compared to standard convolution is :

$$\text{Reduction} \approx \frac{1}{N} + \frac{1}{D_K^2}$$

Where N is output channels and DK is kernel size.
Result: With a 3×3 kernel, this yields ≈8–9x less computation.

The Solution: MobileNetV2 & Depthwise Separable Convolutions.

Splits standard convolution into Depthwise and Pointwise layers.



Inverted Residual Block diagram [3]

[3] M. Sandler, A. Howard, M. Zhu, A. Zhmoginov, and L. Chen, "MobileNetV2: Inverted Residuals and Linear Bottlenecks," in Proceedings of the IEEE Conference on Computer Vision and Pattern Recognition (CVPR), 2018, pp. 4510-4520.

THE "EFFICIENCY PARADOX" (RESULTS)

Accuracy

Method B (93%) > Method A (83%).

Inference Speed

- Method A: ~6.6 ms/image (Bottleneck: CPU Feature Extraction).
- Method B: 1.06 ms/image (GPU Accelerated)

Key Finding

Deep Learning is 6x Faster and 10% More Accurate.

Metric	Classical (HOG + RF)	Deep Learning (MobileNetV2)
Accuracy	83.07%	93.00%
False Negatives	379	166
Total Training Time	570s	255s
Inference Speed	6.6 ms/image	1.06 ms/image

Results table

CLINICAL SAFETY

Ethical Question: Is 93% accuracy sufficient when 166 cases are still missed?

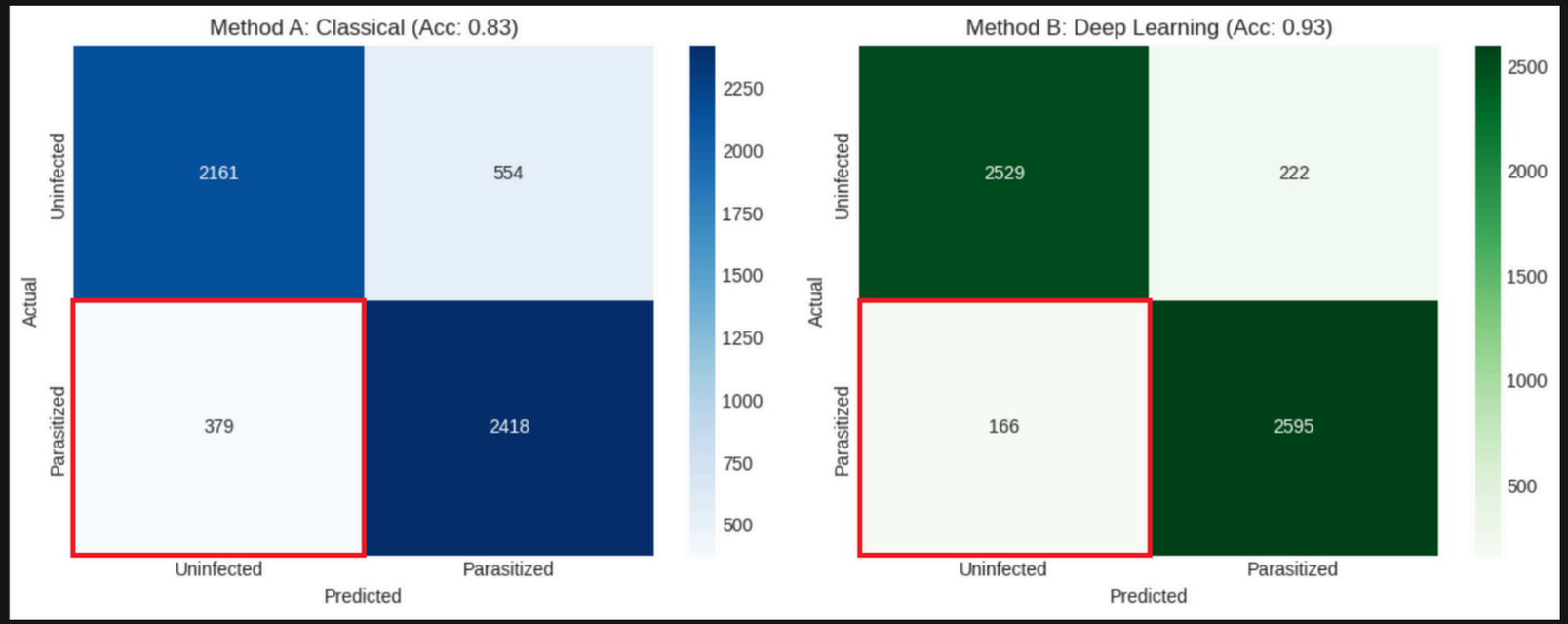
The Critical Metric: **False Negatives** (Missed Infections).

Method A

379 Missed Cases

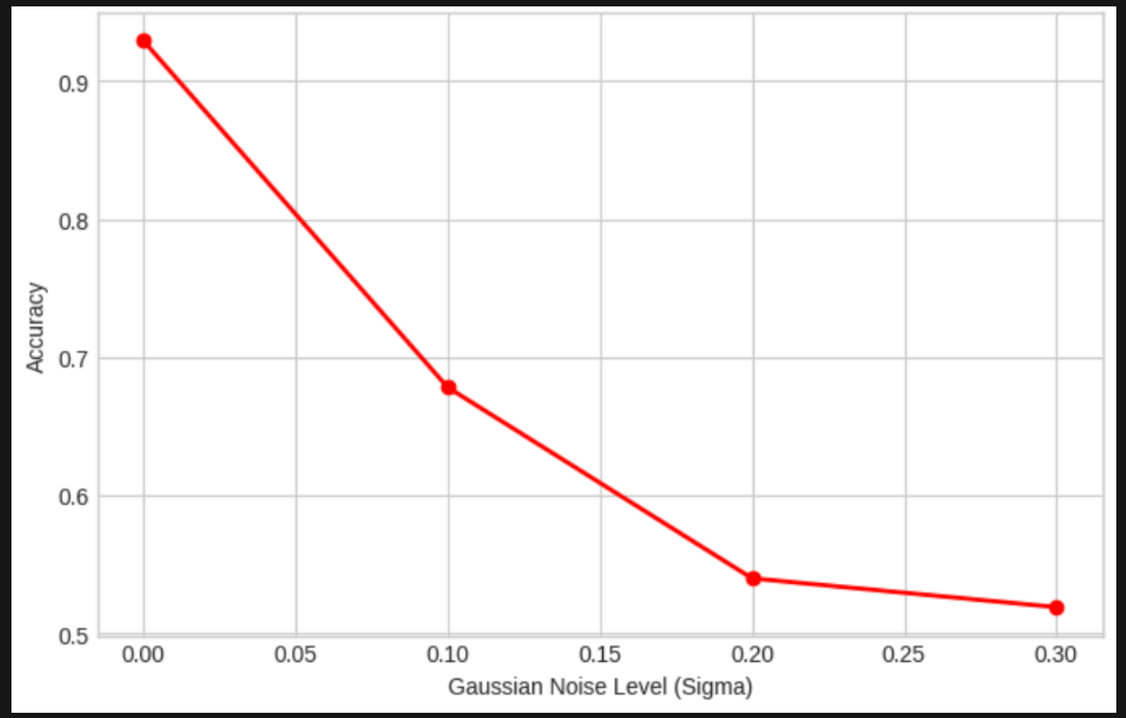
Method B

166 Missed Cases (56% Reduction)



Confusion Matrices

CRITICAL ANALYSIS
THE ROBUSTNESS BARRIER



Model Robustness Analysis Chart

The Test

Gaussian Noise Injection (σ=0.0→0.3).

The Reality Check

- Clean Data: 93% Accuracy.
- Noisy Data (σ=0.3): ~52% Accuracy (Random Guessing).

Implication: The model lacks **"Input Invariance."** It is brittle to sensor dust or poor focus.

AUDITING TRUST

Technique: Grad-CAM (Gradient-weighted Class Activation Mapping)

The Mechanism

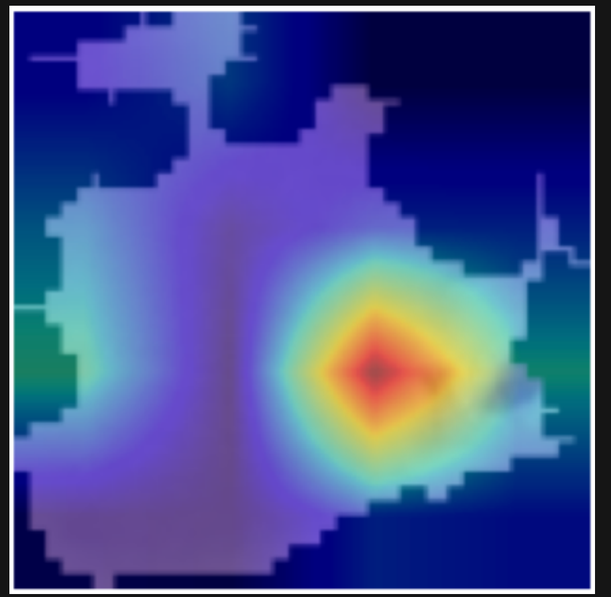
1. Compute gradients of the target class score with respect to feature maps.
2. Calculate neuron importance weights.
3. The Localization Map Equation:

$$L^c_{Grad-CAM} = ReLU(\sum_k \alpha^c_k A^k)$$

Interpretation: The ReLU ensures we only visualize pixels that have a positive influence on the "Parasitized" prediction.

$$\alpha^c_k = \frac{1}{Z}\sum_i \sum_j \frac{\partial y^c}{\partial A^k_{ij}}$$

Grad-CAM Explainability



CONCLUSIONS & FUTURE WORK

- Verdict: MobileNetV2 is the superior candidate (Faster, Safer, More Accurate).
- Limitations:
  - Brittleness: Sensitive to image noise.
  - Domain Bias: Results valid for NIH dataset; risk of Domain Shift in new labs.
- Future Roadmap:
  - Multi-Center Validation: Test on data from different countries to ensure equity.
  - Generative Restoration Pipeline: Implement Diffusion Models (e.g., VADiffusion) to denoise and restore low-quality microscopy images prior to classification, ensuring the model always receives 'clean' inputs regardless of hardware quality.

THANK YOU