Domain-Aware Self-Supervised Learning for Cell-Level Malaria Classification

Label Efficiency, Cross-Dataset Generalization, and Clinical Interpretability

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ABSTRACT

Accurate malaria diagnosis requires expert microscopy skills that are critically scarce where disease burden is highest. While supervised deep learning shows promise for automated cell classification, it demands large annotated datasets that are costly to create. We address this through contrastive self-supervised learning using an enhanced SimCLR framework. Our approach achieves **96.3% accuracy using only 10% of labeled data**, reducing annotation requirements by 90% while maintaining performance within 0.7% of full supervision. The method demonstrates superior cross-dataset generalization (AUC = 0.777 on BBBC041) and provides efficient interpretability through systematic evaluation of eight attribution methods.

Keywords: Self-supervised learning, SimCLR, Malaria, Label efficiency, Interpretability

1. BACKGROUND

Global Malaria Crisis

- 249M cases, 608K deaths (2023)
- 95% burden in Sub-Saharan Africa
- Requires expert microscopy
- Critical shortage of microscopists

The Annotation Problem

- DL needs thousands of labels
- Expert annotation scarce
- Deployment barrier

Research Question

Can SSL reduce annotation needs while maintaining accuracy?

2. METHODOLOGY

Pipeline Overview

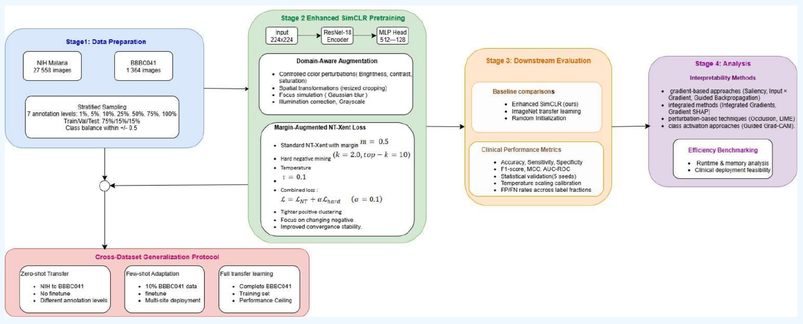

Figure 1. SSL pipeline

SimCLR Framework

- ResNet-18 + 2-layer MLP
- Margin-augmented NT-Xent (m=0.5)
- Hard negative mining
- Domain-aware augmentations

Datasets

- **NIH:** 27,558 cells
- **BBBC041:** 1,364 cells
- Labels: 1%, 5%, 10%, 25%, 50%, 75%, 100%

3. REPRESENTATION QUALITY

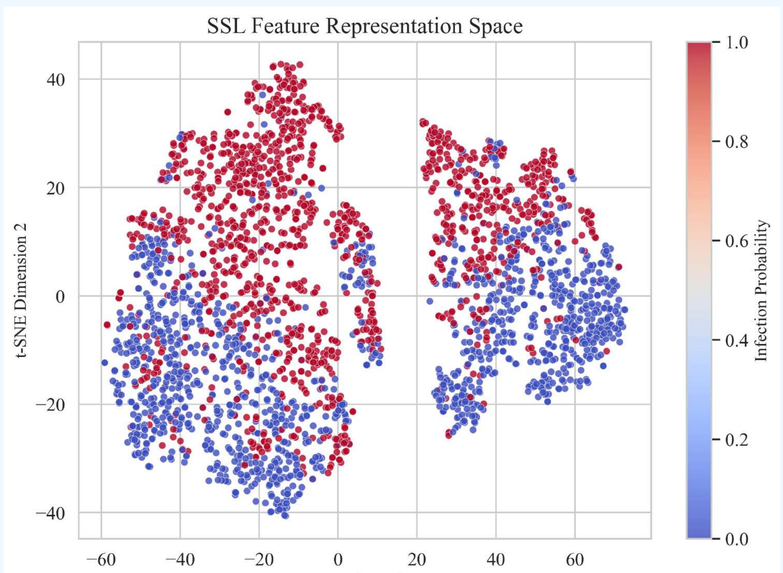

Figure 2. t-SNE visualization

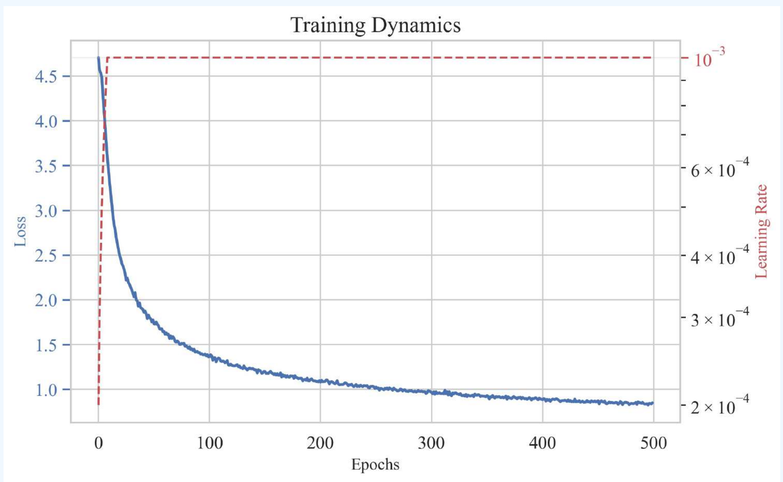

Figure 3. Training convergence

4. LABEL EFFICIENCY

Performance vs. Annotation Level

Method	1%	10%	100%
Random	62.3	95.2	96.7
ImageNet	93.0	94.9	97.1
SimCLR	**91.8**	**96.3**	**97.0**

Table 1. Accuracy (%)

Key Finding

90% annotation reduction with 96.3% accuracy at 10% labels. Only 0.7% below full supervision.

Confusion Matrix (10% Labels)

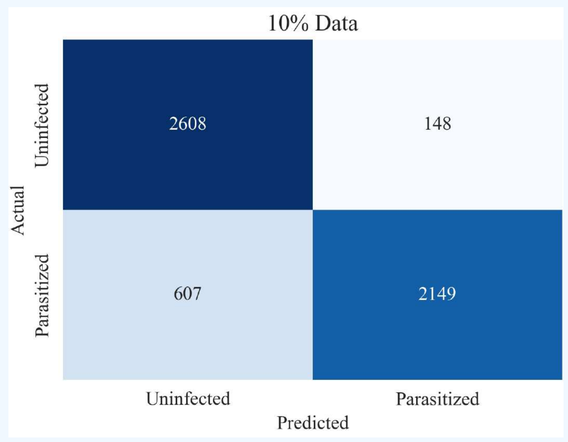

Figure 4. High precision

Clinical Metrics

- Sensitivity: 94.6%
- Specificity: 78.0%
- F1 Score: 95.4%

5. COMPARISON WITH SSL METHODS

Recent SSL Approaches for Malaria

Metric	Ours	M-M	Fu
Method	SimCLR+	SimSiam	BYOL
Dataset	27.5K	15.3K	30K
10% Acc	**96.3**	—	—
Peak Acc	97.0	89.0	**97.8**
X-Dataset	**0.777**	Limited	—
Deploy	**Yes**	Partial	No

Table 2A. SSL comparison (M-M = Mancebo-Martín)

Key Differentiators

- **Label efficiency:** Only work evaluating systematic annotation reduction
- **Cross-dataset:** Rigorous external validation
- **Deployment focus:** Calibration + interpretability + efficiency

Clinical Translation

90% annotation reduction exceeds prior SSL work, directly addressing expert scarcity in endemic regions.

6. CROSS-DATASET RESULTS

BBBC041 External Validation

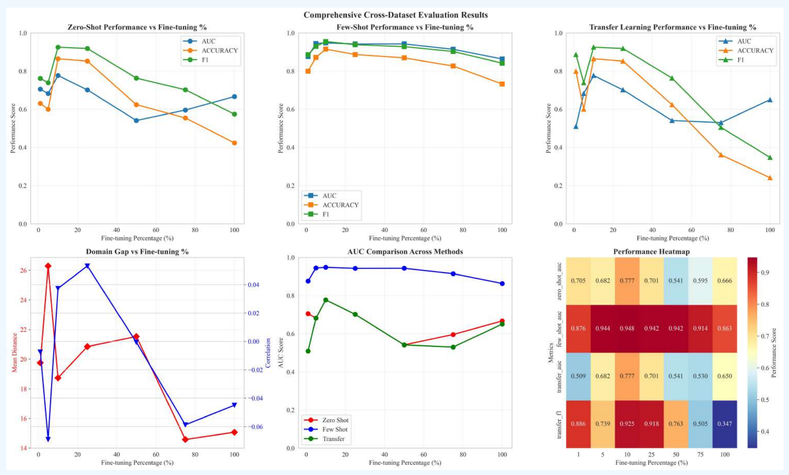

Figure 5. Transfer performance

Train	Zero	Few	Full
1%	0.705	0.876	79.8
10%	**0.777**	**0.948**	**86.4**
25%	0.701	0.942	85.2
100%	0.666	0.863	24.1

Table 2B. AUC (Zero/Few) & Acc (%)

Key Insight

10–25% training prevents overfitting. **10% outperforms full supervision** on external data.

7. INTERPRETABILITY

XAI Method Comparison

Method	Time	Corr	Clin
Saliency	0.03	-0.05	Poor
G-SHAP	**0.15**	**0.01**	**Good**
Guided BP	0.09	0.01	Fair
InputXG	0.09	-0.02	Fair
Int. Grad	0.47	0.83	Excl
Occlusion	10.8	0.01	Good

Table 3. Time (s) & correlation

Visual Examples

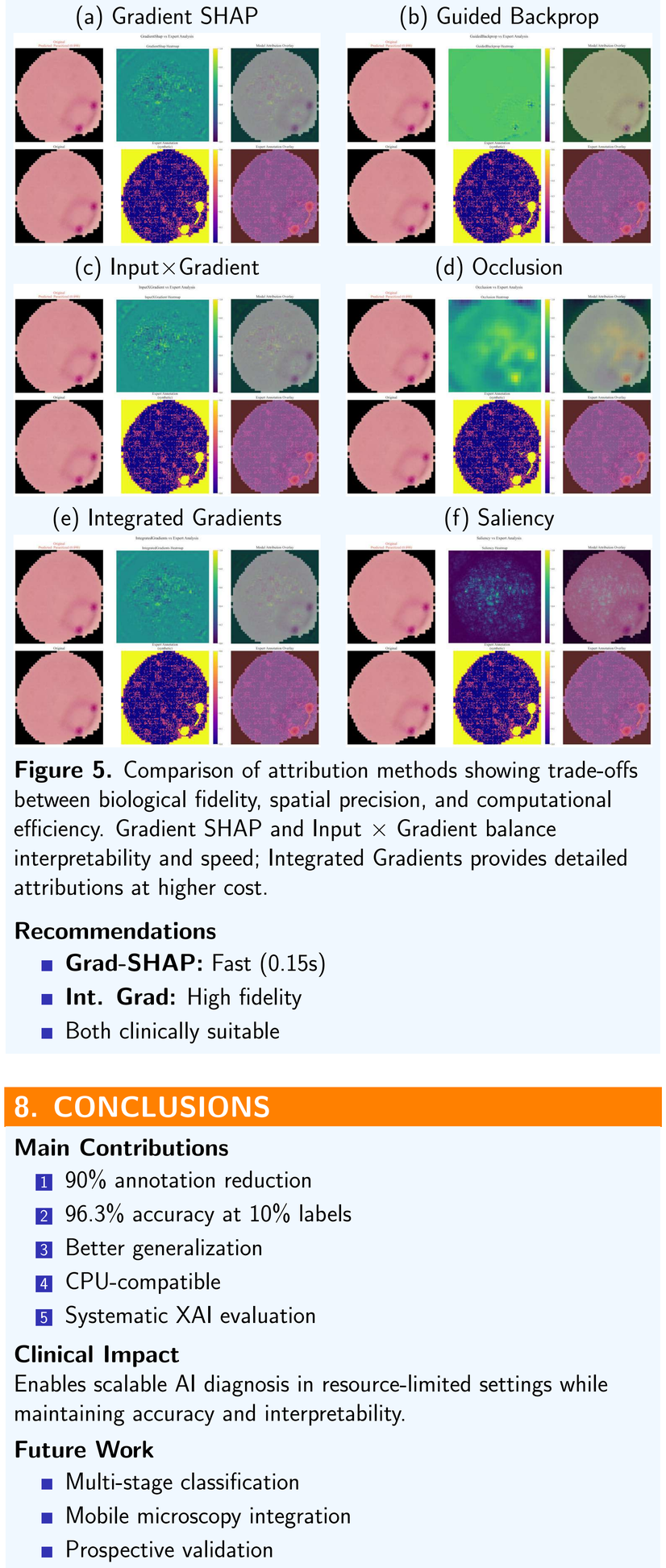

Figure 5. Comparison of attribution methods showing trade-offs between biological fidelity, spatial precision, and computational efficiency. Gradient SHAP and Input × Gradient balance interpretability and speed; Integrated Gradients provides detailed attributions at higher cost.

Recommendations

- **Grad-SHAP:** Fast (0.15s)
- **Int. Grad:** High fidelity
- Both clinically suitable

8. CONCLUSIONS

Main Contributions

1. 90% annotation reduction
2. 96.3% accuracy at 10% labels
3. Better generalization
4. CPU-compatible
5. Systematic XAI evaluation

Clinical Impact

Enables scalable AI diagnosis in resource-limited settings while maintaining accuracy and interpretability.

Future Work

- Multi-stage classification
- Mobile microscopy integration
- Prospective validation

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Code & Paper Repository

github.com/briceket23/ssl_malaria

Scan for full paper & code