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Course: Machine Learning (CSO7013)

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Mid – Term Assessment

Malaria Cell Detection Using Convolutional Neural
Networks

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Problem & Dataset

Problem Definition -> This project implements a binary classification system to detect malaria infection from microscopic blood cell images. The task classifies thin blood smear images as either:

- Parasitized -> Infected with Plasmodium parasites
- Uninfected -> Healthy cells

Why this matters? Malaria causes over 600 000 deaths annually (National Library of Medicine, 2018), yet diagnosis remains bottlenecked by the scarcity of trained microscopists in endemic regions. Automated screening can assist healthcare workers in high volume clinical settings.

Dataset Details ->

- Source: (Rajaraman, et al., 2018) Platform: [Kaggle](#)
- License: Public Domain (US Government Work)
- Origin: Chittagong Medical College Hospital, Bangladesh

Property	Value
Total Images	27 558
Parasitized	13779 (50%)
Uninfected	13779 (50%)
Image Type	RGB
Original Size	~ 130 x 130 pixels

Pre-processing Pipeline ->

The following preprocessing steps were applied:

1. Resizing -> All images resized to 128x128 pixels for consistent CNN output
2. Normalization -> ImageNet statistics applied (mean = [0.485, 0.456, 0.406], std = [0.229, 0.224, 0.225])
3. Data augmentation ->
 - Random horizontal flip ($p = 0.5$)
 - Random vertical flip ($p = 0.5$)
 - Random rotation (+/-20 degrees)
 - Colour jitter (brightness = 0.2, contrast = 0.2)

Data Splitting ->

Split	Ratio	Images
Training	70%	19 290
Validation	15%	4134
Testing	15%	4134

Reproducibility -> Fixed random seed (42) used throughout

Leakage Prevention -> Data split performed before augmentation to ensure no information leakage between sets.

Model & Training

Architecture Justification -> A Convolutional Neural Network (CNN) was selected over alternative architectures:

Architecture	Considered?	Reason
CNN	✓ Selected	Preserves spatial patterns, ideal for image classification
MLP	✗ Rejected	Flattens images, loses spatial relationships
LSTM	✗ Rejected	Designed for sequential data, not applicable to images

Key advantage -> CNNs learn hierarchical spatial features; from edges and textures to complex parasite morphology patterns, through local receptive fields and weight sharing.

Network Architecture ->

Input: (batch, 3, 128, 128) — RGB images

BLOCK 1: Conv2d(3→32) → BatchNorm → ReLU → MaxPool(2×2)

BLOCK 2: Conv2d(32→64) → BatchNorm → ReLU → MaxPool(2×2) → Dropout(0.25)

BLOCK 3: Conv2d(64→128) → BatchNorm → ReLU → MaxPool(2×2)

BLOCK 4: Conv2d(128→256) → BatchNorm → ReLU → MaxPool(2×2) → Dropout(0.25)

FLATTEN: (batch, 16384)

FC1: Linear(16384→512) → ReLU → Dropout(0.5)

FC2: Linear(512→2) → Output logits

Architecture Summary:

Component	Specification
Convolutional Blocks	4
Filter Progression	[32, 64, 128, 256]
Kernel Size	3x3 with padding = 1
Pooling	MaxPool 2x2
FC Layers	[512, 2]
Total Parameters	~ 8 780 000

Regularization Strategy -> To prevent overfitting, the following techniques were employed:

- Dropout2d (p = 0.25) -> Applied after convolutional blocks 2 and 4

- Dropout ($p = 0.5$) -> Applied before final FC layer
- Data Augmentation -> Artificially expands training diversity
- Early Stopping -> Halts training after 7 epochs without improvement

Training Configuration ->

Parameter	Value	Justification
Loss Function	CrossEntropyLoss	Standard for multi-class classification
Optimizer	Adam	Adaptive learning rates, fast convergence
Learning Rate	0.001	Common default for Adam
LR Scheduler	ReduceLROnPlateau	Reduces LR when validation loss plateaus
Scheduler Patience	3 epochs	Allows time for recovery
Scheduler Factor	0.5	Halves LR on plateau
Early Stopping	7 epochs	Prevents overfitting
Max Epochs	35	Sufficient for convergence
Batch Size	64	Balance of speed and gradient stability

Baseline Model ->

- Model -> Logistics Regression
- Features -> Flattened pixel vectors (49 152 dimensions)
- Preprocessing -> StandardScaler normalization
- Purpose -> By deliberately discarding spatial information, this baseline quantifies the CNNs advantage from spatial feature learning. A meaningful comparison demonstrates the value of the chosen architecture.

Results

Model Performance -> The CNN was evaluated on the held-out test with the following metrics:

Metric	CNN Result	Interpretation
Accuracy	96.42%	Overall correctness
Precision	0.9560	Of predicted positives, how many correct
Recall	0.9749	Of actual positives, how many detected
F1 Score	0.9654	Harmonic mean of precision/recall
ROC-AUC	0.9936	Discrimination ability across thresholds

Note -> High recall is particularly critical in medical diagnosis; missed infections (false negatives) can be fatal if left untreated (World Health Organization, 2023).

Baseline Comparison ->

Model	Accuracy	F1 Score
Logistic Regression (Baseline)	61.96%	0.6380
CNN	96.42%	0.9654
Improvement	+34.46%	+0.3274

This substantial improvement validates the architectural choice: spatial feature hierarchies learned through convolution significantly outperform pixel level linear classification.

Training Analysis (Figure 1) ->

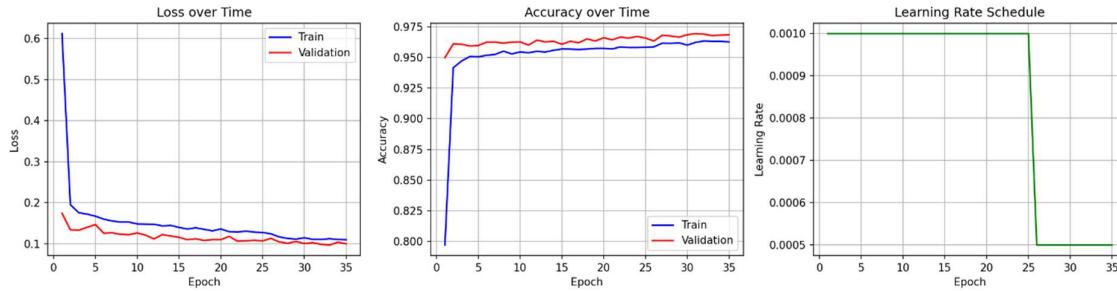
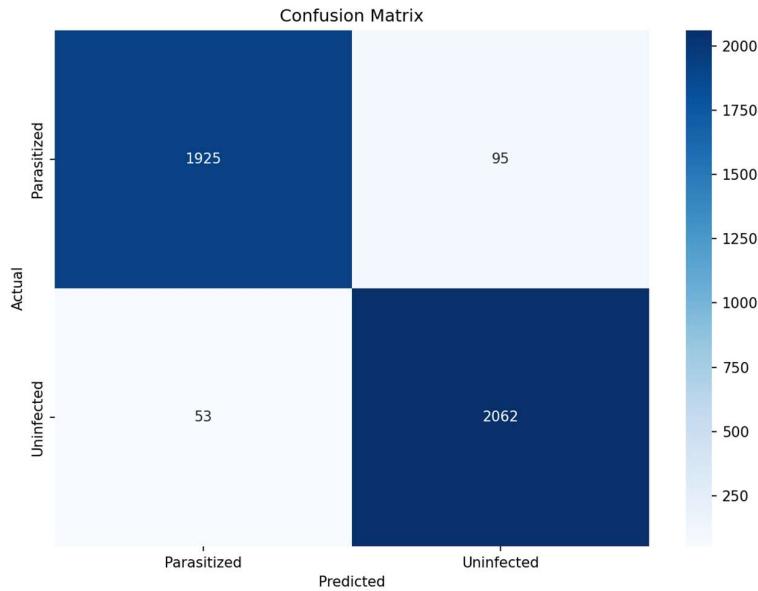


Figure 1: Training and validation metrics over epochs. Left: Loss curves. Center: Accuracy curves. Right: Learning rate schedule.

Observations:

- Both training and validation loss decrease consistently, converging by epoch 27
- The narrow train-validation accuracy gap (96.28% vs 96.85%) indicates minimal overfitting
- Learning rate was reduced when validation loss plateaued
- Best model checkpoint saved at epoch 31 with validation accuracy 96.95%

Confusion Matrix Analysis (Figure 2) ->



Prediction	Parasitized (Actual)	Uninfected (Actual)
Parasitized (Predicted)	1,925 ✅	95
Uninfected (Predicted)	53 ⚠️	2,062 ✅

Error Analysis ->

- True Positives (1,925) -> Correctly identified infections
- True Negatives (2,062) -> Correctly identified healthy cells
- False Positives (95) -> Healthy cells misclassified as infected (causes unnecessary follow-up)
- False Negatives (53) -> **⚠️ Missed infections, clinically dangerous** as untreated malaria can be fatal

In medical screening, **false negatives are more dangerous** than false positives. The model's 51 missed infections (2.5% of actual infections) warrant attention for clinical deployment.

ROC Curve Analysis (Figure 3) ->

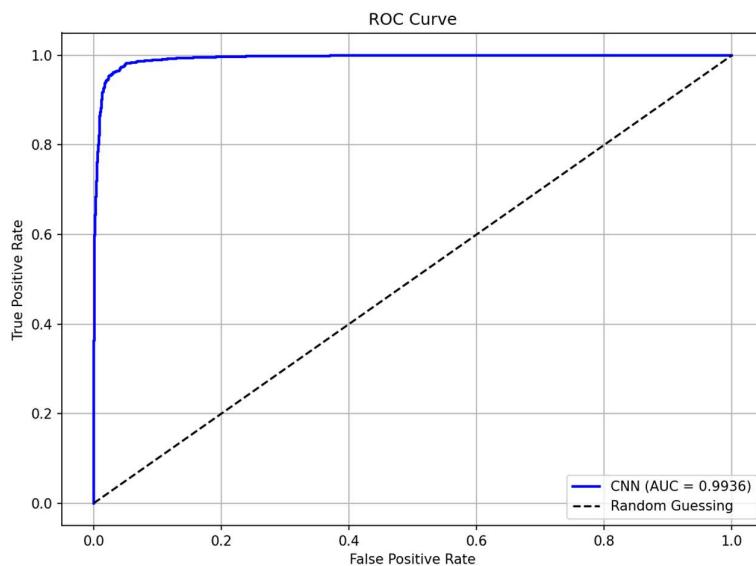


Figure 3: ROC curve showing CNN performance (AUC = 0.9936) versus random baseline (diagonal).

Interpretation:

- **AUC = 0.9936** indicates excellent discriminative ability
- Substantially above random chance (AUC = 0.5)
- The curve's proximity to the top-left corner demonstrates strong true positive rates with low false positive rates across classification thresholds

Discussion & Limitations

What Worked Well ->

The following design choices contributed to strong performance:

- CNN Architecture -> Successfully learned discriminative spatial features, achieving 96.42% accuracy
- Data Augmentation -> Effectively expanded training diversity without additional data collection
- Regularization -> Dropout and early stopping collaborated to prevent overfitting (minimal train-val gap)
- Baseline Comparison -> Demonstrated clear value of spatial feature learning (+34.46% improvement)

Limitations ->

Several limitations warrant consideration

Limitation	Impact
Single Geographic Region	Dataset from Bangladesh only; may not generalize to other populations
Controlled Lab Conditions	Laboratory imaging differs from variable field settings
Binary Classification	Cannot identify Plasmodium species (falciparum, vivax, etc.)
No Severity Quantification	Does not estimate infection severity or parasite count
Single Cell Images	Requires pre-segmented cells; doesn't process full blood smear slides

Generalization Concerns ->

Real-world deployment would require validation across ->

- Different microscope types and magnifications
- Various staining techniques beyond Giemsa
- Diverse patient populations and geographic regions
- Variable image quality and lighting conditions

Ethics & Responsible ML

Key Ethical Considerations ->

Automated malaria screening raises important ethical considerations:

- Human Oversight -> AI should augment -> not replace -> trained medical professionals. Final diagnostic decisions require clinical judgment.
- Consequence of Errors -> False negatives carry severe health consequences -> the 51 missed infections in our test set represent cases that could be fatal without treatment.
- Geographic Bias -> The model may exhibit bias from single-region training data, potentially underperforming for underrepresented populations.
- Data Privacy -> The dataset uses anonymized, public domain images with appropriate consent for research use.

Recommendations ->

For responsible deployment ->

- Require confirmation by trained microscopist before treatment decisions
- Validate on diverse, multi-region datasets before clinical use
- Monitor performance across demographic groups to detect bias
- Provide uncertainty estimates alongside predictions

References

1. National Library of Medicine. (2018). *Malaria Cell Images Dataset*. Retrieved from Kaggle: <https://www.kaggle.com/datasets/iarunava/cell-images-for-detecting-malaria>
2. Rajaraman, S., Antani, S. K., Poostchi, M., Silamut, K., Hossain, M. A., Maude, R. J., . . . Thoma, G. R. (2018). Pre-trained convolutional neural networks as feature extractors toward improved malaria parasite detection in thin blood smear images. *PeerJ*, 6, e4568. Retrieved from <https://doi.org/10.7717/peerj.4568>
3. World Health Organization. (2023). *World Malaria Report 2023*. Retrieved from WHO: <https://www.who.int/teams/global-malaria-programme/reports/world-malaria-report-2023>