

Cervical Cancer Screening: Improving Pap Smear Cell Classification

Charlize Sow
Emerging Diagnostic and Investigative Technologies, Department of Pathology, Dartmouth Hitchcock Medical Center

ABSTRACT

- Cervical cancer is the fourth **most common cancer in women**, with ~350,000 deaths yearly; ~90% of deaths occur in underserved regions.
- **Early detection saves lives**, but access to pathologists is limited in many regions.
- This project explores **deep learning (ResNet-18)** with **data augmentation and preprocessing** to classify Pap smear cells.
- **Light and enhanced augmentation strategies** were tested and compared to the original model, evaluated by accuracy, F1, ROC-AUC, and interpretability
- Results show **enhanced augmentation improved Precancer detection (F1 = 0.84, ROC-AUC = 0.978)** while maintaining interpretability (focus on nuclei).
- **Takeaway:** Careful augmentation boosts reliability of AI for cervical cancer screening, with potential impact in underserved regions

INTRODUCTION

- Cervical cancer:
 - Highly **preventable** and **treatable** when **caught early**.
 - Mortality is concentrated LMICs.
- Problem:
 - Pap smears depend on human interpretation, which is **expert-intensive** and **vulnerable to variability** (e.g., stains, illumination, cell morphology).
 - Shortage of pathologists leads to late diagnoses and worst outcomes.
- Why use AI?
 - Convolutional Neural Networks (CNNs) can recognize cell features (nucleus, cytoplasm).
 - An effective cell-level classifier will prioritize suspicious fields for pathologist review to **reduce missed lesions and speed triage**.
 - However, models often fail to generalize due to **staining/brightness/morphology/variability**.
- Goal of this Project:
 - Test augmentation and preprocessing strategies to **improve accuracy** and **minority-class detection** (Precancer)
 - Provide insights into what augmentations help vs. hurt in medical imaging

METHODS

- Dataset: 3,127 Pap smear cell images, labeled (Normal vs Precancer).
- Preprocessing: resize (256x256), normalization, train/validation split (stratified)
- Model: ResNet-18 CNN, trained with weighted cross-entropy loss to balance Normal vs. Precancer (some types appear less).
- Augmentation Strategies Tested:
 - Original (baseline model): resize, normalization, random flips (H/V), random rotation (+90 degrees, -90 degrees), random crop

METHODS

- Light Augmentation: resize, normalization, random flips, gentle rotation (+10 degrees, -10 degrees), random crop
- Enhanced Augmentation: same as Light Augmentation, with additional mild color jitter (brightness/contrast/saturation) and slightly larger rotation (+15 degrees, -15 degrees)
- Evaluation:
 - Metrics: Accuracy, macro-F1, per-class F1; ROC-AUC (how well model tells apart Normal vs. Precancer cells across thresholds)
 - Interpretability: Captum (integrated gradients, NoiseTunnel) to visualize model focus

RESULTS

- Performance Across Augmentation Strategies:
 - Original (baseline model) achieved macro-F1 = 0.867, with a weaker performance on the minority Precancer class (F1 = 0.779).
 - Light augmentation improved generalization (macro-F1 = 0.887, Precancer F1 = 0.840).
 - **Enhanced augmentation yielded the best results** (macro-F1 = **0.905**, Precancer F1 = **0.840**)
- ROC-AUC for the Enhanced augmentation model was **0.978**, indicating excellent separation between Normal and Precancer cell types.
- Attribution maps confirmed the model focused on the nucleus and nuclear-cytoplasmic boundary, **consistent with cytological features**.

run	acc	macro_f1	f1_Normal	f1_Precancer
1 original	0.9249201277955271	0.8670534596736661	0.9547641963426372	0.7793427230046949
2 light	0.9361022364217252	0.8872742333387356	0.9614643545279383	0.8130841121495327
3 enhanced	0.9488817891373802	0.9047908745247148	0.9695817490494296	0.84

Table 1: Classification performance of three augmentation strategies on Pap smear cell images, evaluated by Accuracy, Macro-F1, and per-class F1 scores.

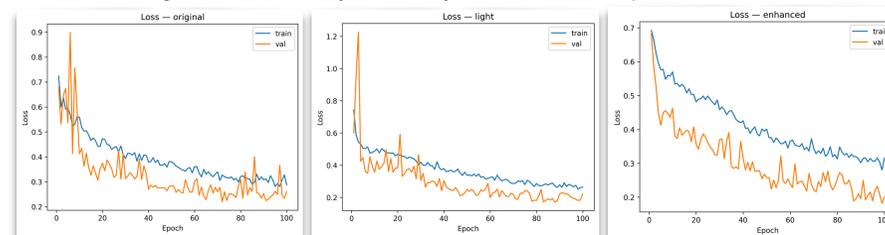


Figure 1: Training and validation loss curves for the original model, light, and enhanced augmentation runs (100 epochs).

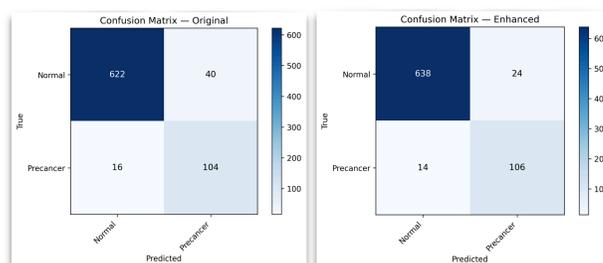


Figure 2: Confusion matrices for Original vs. Enhanced runs, showing reduction in false negatives for the Precancer class after augmentation.

RESULTS

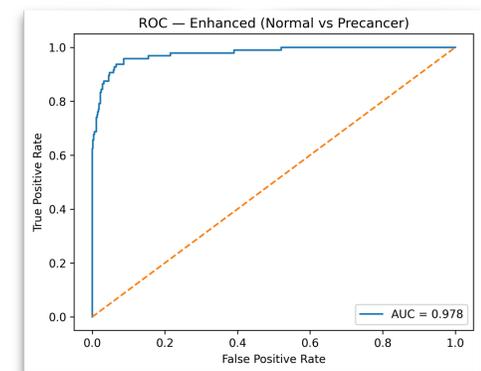


Figure 3: ROC curve for the Enhanced Augmentation run, with ROC-AUC = 0.978, demonstrating strong separation of Normal versus Precancer cases.

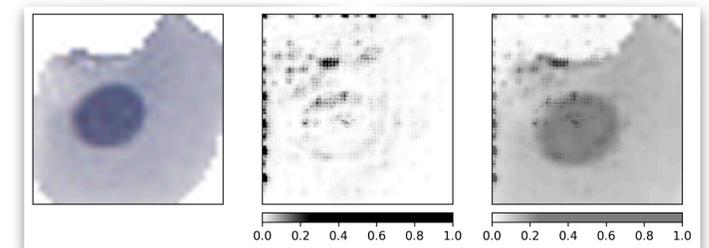


Figure 4: Captum attribution maps (NoiseTunnel, Integrated Gradients) for a Precancer example.

CONCLUSION

- Data augmentation strategies **improved the performance of a CNN classifier** for Pap smear cell images.
- Enhanced augmentation (rotation + mild color jitter) yielded the best results: Macro-F1 = 0.905, Precancer F1 = 0.840, ROC-AUC = 0.978
- Interpretability analysis confirmed the model focused on nuclei and nuclear-cytoplasmic boundaries aligning with established cytological features.
- Potential for Clinical Impact:
 - AI-based Pap smear screening could **expand access** to early cervical cancer detection in **low-resource regions** where cytopathologists are scarce.
 - Improved detection of Precancerous cells may **reduce false negatives**, enabling earlier intervention and better patient outcomes.
- Limitations and Future Directions:
 - Dataset was relatively small and limited to two classes (Normal vs. Precancer).
 - Augmentation strategies tested were basic; further work could explore stain normalization, domain adaptation, or transfer learning
 - Validation was limited to a single dataset. Multi-site, multi-population testing is required for clinical translation.
 - Future goal: integration into a web-based tool for global screening access.

