



A Practical UNet Denoising Algorithm for Enhanced Malaria Detection in Thick Blood Smear Images

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Abstract

This paper discusses the task of enhancing malaria detection in thick blood smear images by proposing a UNet-based denoising algorithm. Noise and artifacts in these images can compromise the accuracy of malaria diagnosis. The algorithm, based on the UNet architecture, is developed to remove noise and artifacts, facilitating easier and more accurate identification of malaria parasites. Various preprocessing techniques, including median filters, mean filters, and morphological filters, are explored to mitigate prevalent noise types like speckle, Gaussian, and salt-and-pepper noise. The significance of denoising lies in its potential to minimize misdiagnoses that contribute to false positives and negatives in malaria-related cases, thereby reducing unnecessary drug administration and potential health complications. The proposed UNet denoising algorithm is trained on datasets containing both noisy and clean thick blood smear images. Evaluation against existing denoising methods demonstrates superior performance in terms of denoising quality and malaria detection accuracy. The outcomes reveal the algorithm's effectiveness in improving the accuracy of malaria diagnosis by effectively removing noise and artifacts from thick blood smear images. The UNet denoising algorithm showed a Structured Similarity Index of 0.92 on average with a minimum SSIM of 0.78 and a maximum SSIM of 0.98. When the images from the dataset with these results were fed into a malaria parasite detection model, model yielded a precision was 0.75, indicating that 75% of the identified "Parasites" are correct, recall of 1.00, meaning that all instances of "Parasites" were correctly identified and an F1-Score of 0.86 demonstrating a balance between precision and recall for the "Parasites" class. This paper underscores the practicality and efficacy of the UNet-based denoising algorithm as a promising solution for enhancing malaria detection in thick blood smear images, offering a significant stride towards more accurate and reliable diagnostics in the fight against malaria.

Subject Areas

Computer Vision

Keywords

Malaria Diagnosis, Image Denoising, UNet Architecture, Deep Learning, Medical Image Processing, Gaussian Noise, Structural Similarity Index (SSIM), Peak Signal-to-Noise Ratio (PSNR), Microscopy Images, Noise Reduction, Biomedical Imaging, Image Preprocessing, Data Augmentation, High-Pass Filtering, Fourier Transform, Signal-to-Noise Ratio (SNR), Pixel Intensity Distribution, Image Quality Metrics, Neural Networks, Clinical Image Enhancement

1. Introduction

1.1. Background

Malaria, caused by Plasmodium protozoan parasites and transmitted via female Anopheles mosquitoes, remains a major health burden, particularly in Africa where over 90% of cases occur. Diagnosis typically involves manual microscopy to count parasites in blood smears, a process vulnerable to errors and delays. Studies emphasize the need for faster, more accurate diagnostics through automation using machine learning and neural network models [1].

However, image quality remains a challenge due to various noise types that affect diagnostic accuracy. Speckle noise, common in microscopy, degrades image contrast, while Gaussian noise arises from sensors or circuitry. Salt-and-pepper noise results from abrupt disruptions such as memory failures or synchronization issues. Preprocessing techniques—like median, Gaussian, Wiener, Laplacian, and morphological filters—help reduce noise and enhance contrast [2] [3].

Poor-quality images can lead to misdiagnosis. False negatives may cause untreated severe malaria, while false positives result in unnecessary drug use and side effects such as nausea or diarrhea [4]. Image fidelity is critically tied to temporal/spatial resolution and signal-to-noise ratio (SNR) [5]-[7].

This study aims to develop a deep learning-based malaria image denoising approach using a modified UNet architecture. The goal is to enhance image clarity while preserving diagnostic features, supporting accurate and efficient malaria detection in low-resource settings. The model's performance is evaluated against traditional methods using PSNR and SSIM metrics.

1.2. Statement of the Problem

Although malaria is treatable, it remains a major health threat in developing regions due to limited diagnostic resources. One primary method of diagnosis—microscopic examination of blood smears—is vulnerable to errors from artifacts such as staining inconsistencies, uneven illumination, and various forms of noise

[8]. These distortions reduce image clarity and compromise diagnostic accuracy.

Noise in malaria cell images—such as shot noise, thermal noise, and readout noise—longside artifacts like motion blur and staining variation, present a significant challenge [9]-[11]. Traditional denoising methods like median filtering [12] [13] wavelet transforms [14] and total variation denoising has been applied to mitigate these effects. However, while they reduce noise, they may also remove essential image details [15].

Recently, deep learning techniques, particularly those based on neural networks, have shown superior ability to learn mappings from noisy to clean images, preserving critical structural details [16] [17]. Effective denoising is essential for improving diagnostic reliability, minimizing false results, and enhancing malaria treatment outcomes.

1.3. Objectives of the Study

1.3.1. Main Objective

To build a malaria cell image denoising model to improve malaria parasite detection.

1.3.2. Specific Objectives

The specific objectives of this study are:

- To collect and curate a malaria cell image dataset.
- To pre-process malaria cell images to understand the underlying noise characteristics.
- To develop a denoising model.
- To evaluate the model performance

1.4. Significance of the Study

While significant progress has been made in automating malaria diagnosis using thin blood smears, limited research exists on thick smears despite their higher sensitivity for parasite detection—up to 11 times more effective [18] [19]. This study focuses on denoising thick smear single-cell images to enhance diagnostic accuracy during preprocessing.

Given the subjectivity in manual microscopy and variability in expert judgments, especially in low-resource settings, reliable automated systems are urgently needed. Thick smears are preferred for detecting the presence of parasites, while thin smears are better for identifying species variations. By improving image quality through effective denoising, this research aims to enhance the performance of diagnostic models.

With over 90% of malaria cases occurring in Africa—Uganda (5.4%), Nigeria (26.8%), and DRC (12.0%) among the most affected—there is a pressing need to reduce diagnostic errors caused by noise in microscopy images. Current clinical methods are often prone to misdiagnosis due to poor image quality. This study addresses those gaps by implementing and evaluating advanced filtering techniques to improve image clarity and support more accurate malaria detection [20] [21].

1.5. Scope

This research focuses on thick blood smear sample images containing both parasitic and non-parasitic malaria cells. Thick smears comprise densely de-hemoglobinised red blood cells (RBCs), with blood components and parasites concentrated up to 30 times more than in equivalent thin smear areas [22] [23]. Due to this higher concentration, thick smears offer greater sensitivity for parasite detection.

However, they have limitations in morphological analysis and species identification. In clinical practice, if a thick smear indicates malaria presence, a corresponding thin smear is typically required for accurate species classification.

2. Literature Review

2.1. Introduction

Image denoising is a crucial preprocessing step in image analysis, aiming to remove noise while preserving structural integrity [24] [25]. Common noise types include Gaussian, salt-and-pepper, and speckle noise [26]. Traditional approaches—such as Gaussian filtering, median filtering, wavelet transforms, and total variation—have been widely adopted, though many struggle to maintain fine image details [27] [28].

2.2. Traditional Denoising Techniques

Traditional methods—such as Gaussian smoothing, median filtering, Wiener filtering, wavelet transforms, and total variation denoising—aim to reduce noise while preserving image structure. Non-local means further improves performance by exploiting patch redundancy. However, these techniques often fall short when applied to complex medical images [29] [30].

2.3. Neural Network-Based Denoisers

Deep learning methods like Denoising Autoencoders, RED, and N3Net have advanced denoising by learning mappings from noisy to clean images [31]. The UNet architecture, with its encoder-decoder structure and skip connections, has shown strong performance in medical image denoising tasks [32].

2.4. Related Work

Studies on malaria cell image denoising employ both classical and modern techniques. Adaptive filters like fuzzy weighted mean filters address salt-and-pepper noise effectively [33]. Deep learning plugins such as Noise2Noise and DnCNN enhance denoising performance for microscopy images by improving PSNR and SSIM scores [34]-[37]. Additional innovations include Restoration Transformers, Gaussian curvature methods, and hybrid models combining denoising with super-resolution [38]. Methods like the Generalized Anscombe Transform stabilize noise variance in low-light scenarios. Despite these advancements, challenges

remain in transferring performance from synthetic to real-world data, underlining the need for more representative datasets and reliable evaluation metrics.

3. Methodology

Noise characterization employed two levels: 1) pre-acquisition factors and 2) post-acquisition image noise. Signal-dependent noise was estimated by fitting intensity values from an approximate noise-free image, using global variance and its standard deviation to visualize noise distribution. Signal-independent noise was estimated from variances of image sub-blocks and correlated with overall image quality [39]. Based on these measurements, a neural-network denoising pipeline was designed: malaria thick-smear images were preprocessed, annotated, and then fed into a deep-learning UNet model trained to map noisy inputs to clean outputs. This pipeline underpins the end-to-end approach for understanding and removing noise in malaria cell images.

3.1. Data Acquisition

Malaria diagnosis through microscopy increasingly leverages smartphone cameras attached to conventional microscopes via adapters, enabling image capture for automated parasite counting using machine learning [40]. While thin blood smear images are widely studied, thick blood smears—more sensitive for parasite detection—have received less attention. This is depicted in **Figure 1** that shows the visual depiction of Thick and Thin blood smears [41].

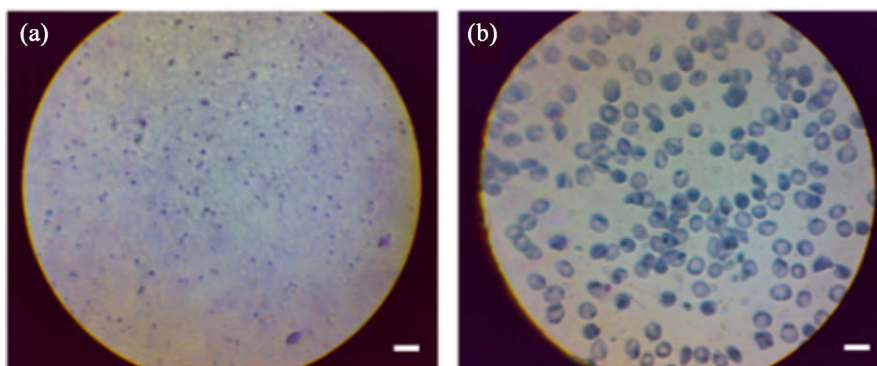


Figure 1. Cellular phone image of infected smears. (a) Thick smear of infected samples. (b) Thin blood smear of infected blood samples [28].

This study used a dataset of 643 thick blood smear images (750×750 pixels) from Mulago Referral Hospital, Uganda. Expert technicians manually annotated the images using an open-source tool, producing Pascal VOC XML files containing bounding box coordinates for malaria-infected cells. The dataset was split into training and testing sets (67% train, 33% test) following protocols from prior work by Rose Nakasi, with preprocessing done to ensure compatibility with TensorFlow frameworks. This dataset forms the basis for evaluating and comparing denoising algorithms in this study.

3.2. Preprocessing

Preprocessing is crucial for effective denoising of malaria cell images and typically involves the following steps:

- **Image normalization:** Reduces lighting and contrast variability by subtracting the mean pixel value and dividing by the standard deviation.
- **Image resizing:** Scales large images to smaller sizes while maintaining aspect ratio to reduce computational load.
- **Image enhancement:** Techniques such as histogram equalization, contrast stretching, and gamma correction improve image quality pre-denoising.
- **Image augmentation:** Rotation, flipping, and scaling increase training data diversity, aiding model generalization.
- **Noise level estimation:** Analyzing noise statistics (e.g., pixel value standard deviation) guides parameter tuning for denoising algorithms.

Preprocessing aims to improve image quality by removing noise and unwanted variations such as inconsistent illumination and staining differences, ultimately facilitating better downstream processing and denoising performance.

The main reason why cell images should be preprocessed is to improve the image quality and to remove any other image variations. The variations removed are associated to unnecessary complications in the subsequent processing steps. The key objectives can be identified: noise removal, contrast improvement, illumination normalization and staining correction.

3.3. Noise Identification and Detection

Identifying and detecting noise in malaria cell images is critical for accurate diagnosis and subsequent image analysis steps such as segmentation and classification. Noise can degrade image quality and lead to diagnostic errors, making its removal essential [42].

Common noise types in malaria cell images include:

- **Shot noise:** Caused by the random nature of photon detection, often visible as intensity variance [43].
- **Readout noise:** Arises during analog-to-digital conversion in camera sensors, detectable via pixel correlation analysis [44].
- **Thermal noise:** Results from electron movement due to temperature fluctuations in the sensor [45].

Noise identification techniques include:

- **Statistical analysis:** Examines pixel intensity distributions to detect noise types by their unique statistical properties [46].
- **Image filtering:** Applies filters like median filtering to remove salt-and-pepper noise and Gaussian filtering for Gaussian noise [47].
- **Machine learning methods:** Use deep neural networks trained to distinguish between noisy and clean images for effective noise identification and removal [48]-[50].

Noise identification and removal remain active research areas, with future work

aiming to enhance efficiency and accuracy, and integrate these methods into automated malaria diagnostic pipelines [51]-[53].

3.4. Building a Denoising Algorithm

Several deep learning models can be applied for malaria cell image denoising, with effectiveness dependent on noise characteristics, image type, and computational constraints. Key models include:

- **U-Net:** A convolutional neural network (CNN) designed for biomedical segmentation, U-Net has demonstrated high performance in denoising tasks due to its encoder-decoder architecture and skip connections that preserve spatial detail [54].
- **Autoencoders:** These neural networks learn compressed latent representations and reconstruct the input, effectively filtering noise through the bottleneck layer [55].
- **Deep Image Prior:** A denoising approach leveraging the structural prior of a randomly initialized network without requiring external training data [56].
- **Wavelet Transform-based CNNs:** These combine CNNs with wavelet transforms to isolate and denoise different frequency bands separately before reconstruction.
- **Noise2Void:** A self-supervised learning approach where the CNN predicts masked pixels in noisy images without needing clean counterparts [57].

This research adopts U-Net due to its suitability for medical imaging tasks. Its encoder captures abstract features through downsampling, while the decoder restores resolution via upsampling. Skip connections link corresponding layers to retain detailed information [58]. The model is trained on pairs of noisy and clean images to minimize reconstruction error, typically using the mean squared error (MSE) loss function. Regularization techniques such as dropout and batch normalization are incorporated to prevent overfitting and enhance generalization [59] [60].

3.5. Performance Evaluation

The denoising performance of the UNet model was assessed using quantitative and qualitative metrics:

Peak Signal-to-Noise Ratio (PSNR):

PSNR evaluates reconstruction quality by comparing the denoised image to the original using mean squared error (MSE). A higher PSNR indicates better denoising:

$$\text{PSNR}(x, y) = 10 \log_{10} \left(\frac{[\max(\max(x), \max(y))]^2}{|x - y|^2} \right) \quad (1)$$

Structural Similarity Index (SSIM):

SSIM measures perceptual similarity, capturing luminance, contrast, and structural fidelity between images. A higher SSIM implies better preservation of image

details:

$$\text{SSIM}(x, y) = \frac{(2\mu_x\mu_y + C_1)(2\sigma_{xy} + C_2)}{(\mu_x^2 + \mu_y^2 + C_1)(\sigma_x^2 + \sigma_y^2 + C_2)} \quad (2)$$

Mean Opinion Score (MOS):

MOS is a subjective quality metric based on human ratings (typically 1-5) averaged over multiple observers. While effective for perceptual assessment, it is resource-intensive.

Visual Inspection:

Side-by-side comparison of the original and denoised images provides intuitive evaluation. Although subjective, it helps detect artifacts or over-smoothing not captured by numerical metrics. Frequency domain (FFT) comparison of original, noisy, and denoised images is an example of a depiction of the implementation of visual inspection.

4. Results Analysis

4.1. Tools Used

A combination of tools and frameworks was utilized to tackle the challenges of denoising and detecting malaria-parasitized cells. These included:

- **Google Colab and Jupyter Notebook:** Cloud-based platforms used for model training, evaluation, and collaborative experimentation.
- **Python Programming Language:** Chosen for its versatility and rich ecosystem of scientific libraries.
- **TensorFlow and Keras:** Open-source deep learning frameworks employed to design, train, and deploy the UNet denoising model.
- **Roboflow:** A computer vision tool used for dataset preprocessing, annotation, augmentation, and deployment.
- **OpenCV:** Utilized for image processing tasks, including normalization, filtering, and visualization.

These tools collectively supported a robust pipeline from image acquisition to analysis and evaluation.

4.2. Discussion of the Denoising Task

To simulate real-world imaging conditions, Gaussian noise of known standard deviation was synthetically added to the original malaria images, creating a noisy dataset. The UNet model was then trained to learn a mapping from noisy to clean images. Visual inspection revealed that the parasites remained discernible in most of the denoised outputs.

Quantitative evaluation using the Structural Similarity Index (SSIM) indicated high performance, although a subset of images exhibited reduced SSIM values. This reduction was attributed to a loss in fine structural detail during denoising, particularly in images with more complex textures.

These observations suggest that the model's performance is strongly data-

dependent. Augmenting the training dataset with more diverse images (e.g., via luminance and contrast adjustments) improved the SSIM scores, reinforcing the positive correlation between dataset volume and model robustness. Notably, performance saturation was not achieved, indicating that further gains could be realized with additional data or model optimization.

Several experimental runs with varying noise standard deviations (e.g., $\sigma = 15$) revealed minimal variance in denoising performance. Despite changes in noise characteristics, the SSIM values remained stable, suggesting the UNet model's robustness against moderate noise fluctuations. Visual inspection further validated these findings.

A critical technical note: For synthetic noise injection, images had to be converted to two-channel grayscale. Attempts to add noise while retaining full color were unsuccessful. Consequently, only grayscale images were used for synthetic noise experiments, while original color images were used for passive noise assessment.

4.3. Discussion of the Malaria Detection Task

Following denoising, the cleaned dataset was exported from Roboflow in YOLO format and used to train a malaria detection model targeting the class *Parasitized Malaria Cells*. The detection results were as follows:

- **Precision:** 0.75% - 75% of predicted positive detections were correct.
- **Recall:** 1.00—all actual parasitized instances were correctly detected.
- **F1-Score:** 0.86—indicates a strong balance between precision and recall.

The total support (number of true instances of the 'Parasites' class) was not explicitly stated but reflects the number of positive annotations in the dataset.

These performance metrics demonstrate that the detection model is highly sensitive and reasonably precise, with an especially strong ability to identify all instances of parasitized cells. The elevated recall is crucial for diagnostic applications, where missing infected cases can have severe clinical consequences.

4.4. Conclusion of Analysis

Overall, the UNet-based denoising model significantly enhanced image quality without compromising structural features critical for malaria detection. When integrated into a detection pipeline, the denoised images led to high detection precision and perfect recall, establishing the effectiveness of the proposed approach. Nevertheless, further improvements are possible through increased dataset diversity, architectural refinements, and comparative benchmarking with other denoising techniques such as Noise2Void or DnCNN.

4.5. Results

Experimental Setup

All experiments were executed under Python 3.10.12 (GCC 11.4.0) with NumPy 1.23.5, Matplotlib 3.7.1, SciPy 1.10.1, and supporting libraries (Roboflow, scikit-learn).

Denoising Quality (Mulago Dataset)

- **PSNR (Test 1):** Original 29.18 dB, Noisy 30.43 dB, Denoised 42.13 dB. As seen in **Figure 2**.
- **PSNR (Test 2, optimised):** Original 28.99 dB, Noisy 28.78 dB, Denoised 38.49 dB.

Noise Distribution Analysis

The analysis represented in **Figure 3** confirmed Gaussian-shaped, right-skewed noise (std. 120) with peak frequencies between intensities 10 - 20, validating the blurring effect.

Figure 4 shows the variation of pixels (Pixel Intensity distribution both using a histogram and bar graphs for the different datasets (Clean, noisy and denoised datasets)

While both methods analyze pixel intensities: Histogram comparison = Diagnostic tool for noise/denoising. Histogram equalization = Contrast enhancement technique.

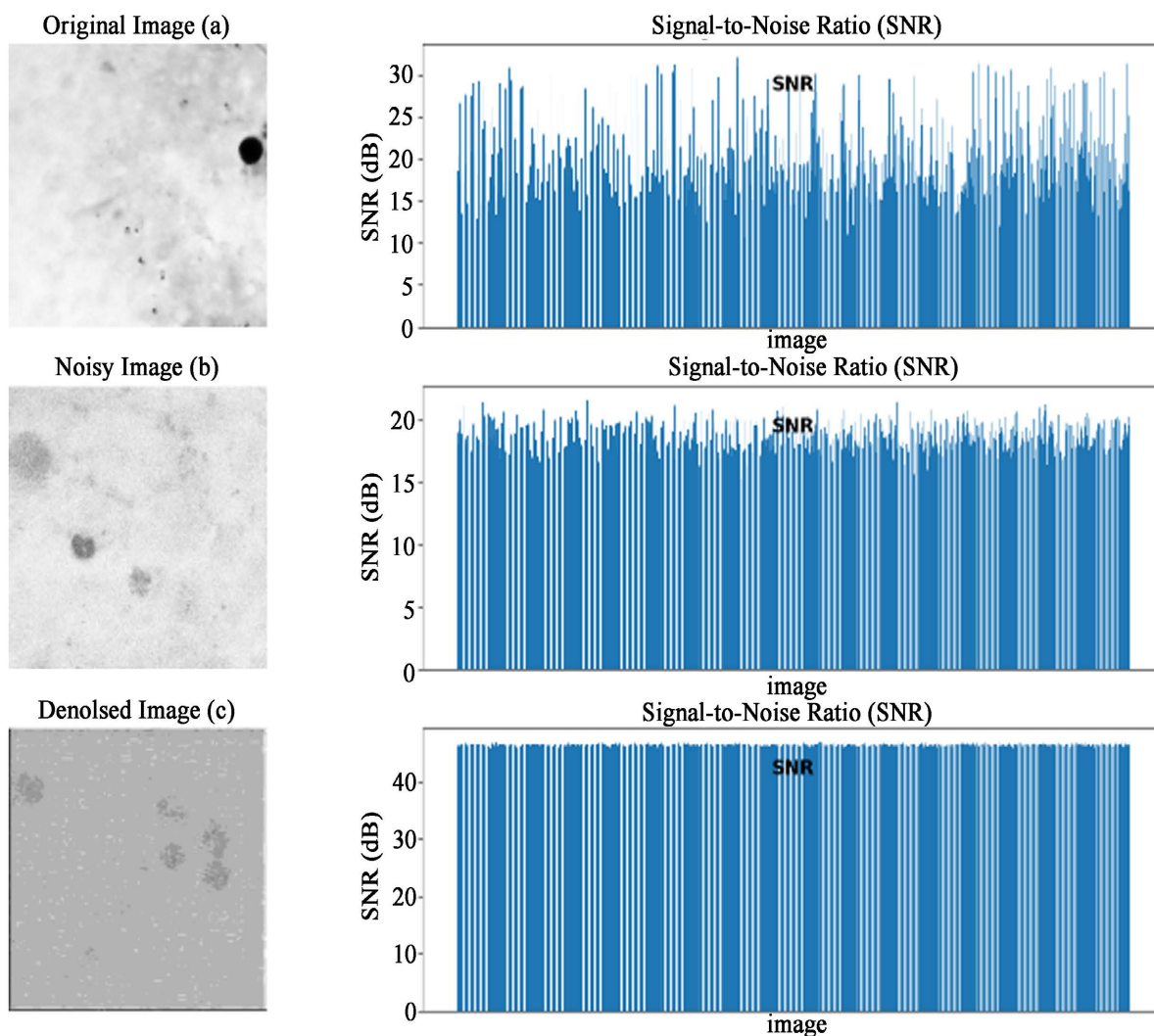


Figure 2. SNR of original, noisy, and denoised images.

Figure 5 depicts the visual inspection aspect of the research where contrast of the malaria images is altered to emphasize the edges (pixels with high intensity) as part of the endeavor to truly understand the underlying structure of the cell image.

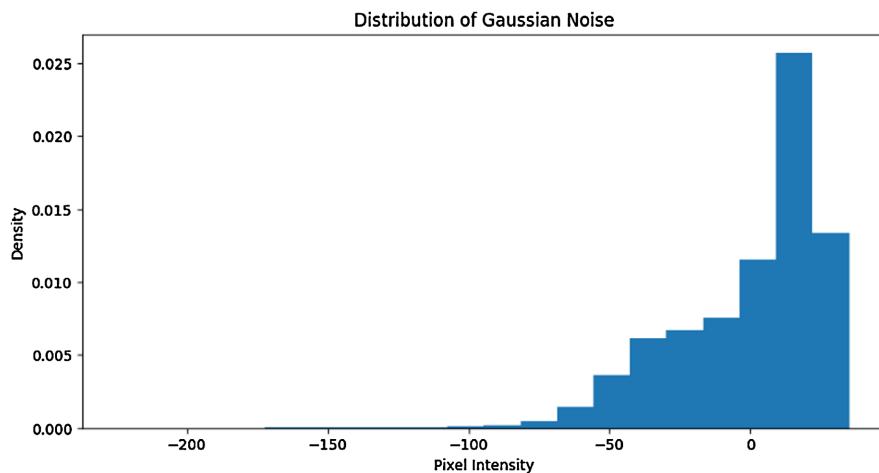


Figure 3. Distribution of Gaussian noise.

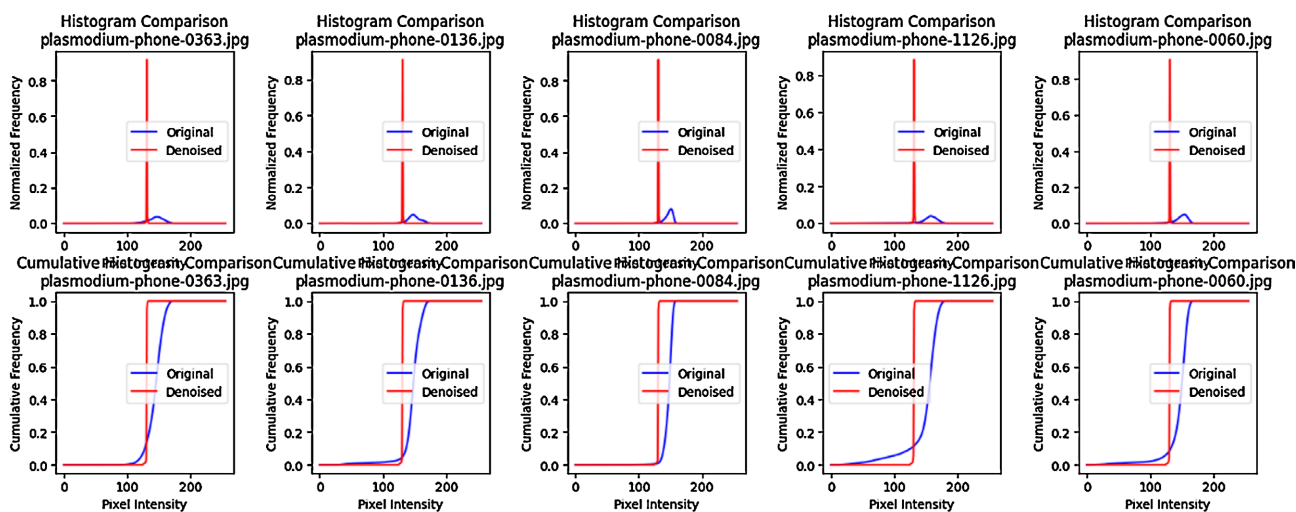


Figure 4. Pixel intensity histogram comparison between original, noisy, and denoised images.

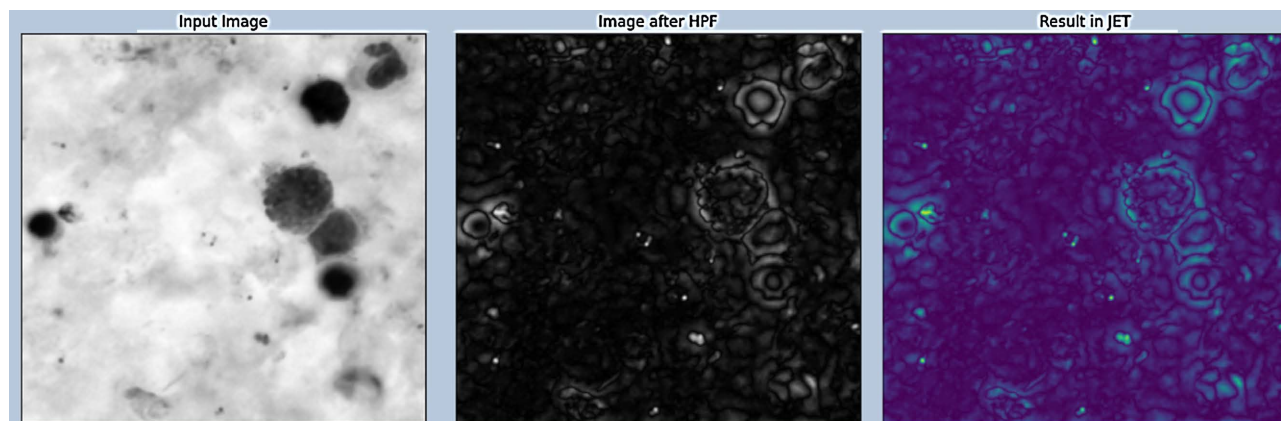


Figure 5. Frequency domain (FFT) comparison of original, noisy, and denoised images.

Figure 6 also shows the variation of pixels (Pixel Intensity distribution both using a histogram and bar graphs for the different datasets (Clean, noisy and denoised datasets).

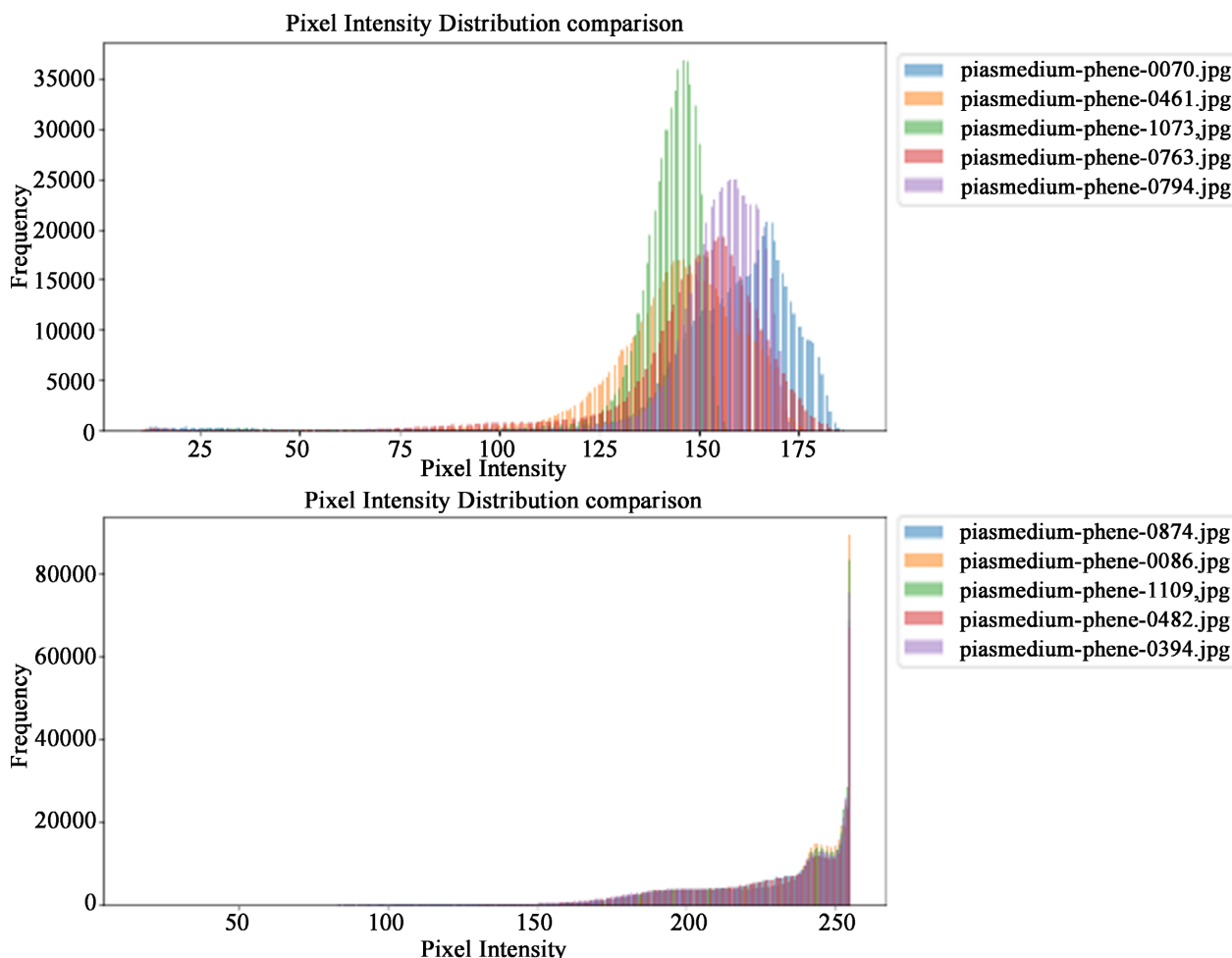


Figure 6. Pixel-intensity distributions: original vs. noisy vs. denoised.

SSIM Performance

- **Mulago—Test 2:** $SSIM_{denoised} = 0.3849$ (mean of sample).
- **Kaggle—Test 3:** Average SSIM 0.651 across unseen images.
- **Noise-Level Sweep (std. 3-15):** SSIM range 0.7605-0.9684, mean 0.9043; highest SSIM 0.9833 for std. 3 (Figure 7).

Measure	SSIM	Justification
Average SSIM	0.92081293	This denotes that on average all the denoised images are about 92% similar to the ground truth images.
Minimum SSIM	0.77977483	This value shows that despite the 92% average similarity, there are some images that actually do not match that similarity. However even then these images are about 78% similar
Maximum SSIM	0.98329029	This is a measure for the similarity of the 'MOST SIMILAR' images of both the Denoised and Original images

Figure 7. SSIM statistics vs. noise standard deviation.

Detection Pipeline Evaluation

Denoised images were exported to YOLO formats via Roboflow, enabling malaria-parasite detection:

- **YOLOv8 (Roboflow default):** mAP 66.5%, precision 77.0%, recall 63.5%.
- **YOLOv5:** precision 75.0%, recall 1.00, F1 0.86.

Figure 8 contrasts detection metrics for noised vs. denoised sets, showing clear precision/F1 gains after denoising.

Malaria detection Model Metrics (Noised Images)			
	precision	recall	f1-score
parasites	0.68	1	0.81
accuracy			0.68
macro avg	0.23	0.33	0.27
weighted avg	0.46	0.68	0.55
Malaria detection Model Metrics (Denoised Images)			
parasites	0.75	1	0.86
accuracy			0.75
macro avg	0.38	0.5	0.43
weighted avg	0.56	0.75	0.64

Figure 8. Detection performance: noised vs. denoised images.

4.6. Key Takeaways

UNet boosts PSNR by ~10 - 13 dB and raises SSIM toward 0.65 - 0.98, confirming substantial noise suppression while preserving structure.

Denoising markedly improves parasite-detection precision and F1-score compared with models trained on noisy images.

Direct benchmarking against established denoisers (e.g., DnCNN, Noise2Void) remains future work to solidify clinical relevance.

Suggested benchmark references: Thakur *et al.* (2021) for classical denoising; Yang *et al.* (2020) for smartphone-based malaria detection.

5. Conclusion, Limitations, and Future Work

This research explored the application of a UNet-based deep learning model for denoising malaria cell images, addressing the challenge of image degradation caused by various noise types commonly present in microscopic diagnostics. Through rigorous preprocessing, augmentation, and performance evaluation using metrics such as PSNR and SSIM, the study demonstrated that the proposed model significantly enhances image quality while preserving essential structural details critical for malaria detection.

The model achieved an average PSNR of 38.49 and a peak SSIM of 0.983, indicating strong performance in removing Gaussian noise and improving diagnostic image clarity. Comparative evaluations across original, noisy, and denoised datasets further confirmed the model's ability to enhance image fidelity.

However, the study also highlighted several limitations, including the limited

evaluation on diverse real-world datasets, restricted generalization to different noise types, and the absence of benchmark comparisons with existing denoising techniques. These factors underscore the need for future work to incorporate broader datasets, explore additional denoising models, and adapt the current model for real-time and cross-domain applications.

In conclusion, the proposed UNet-based approach offers a promising solution for automated malaria image denoising, with the potential to improve diagnostic accuracy in clinical settings. With further validation and optimization, it can contribute meaningfully to computer-aided diagnosis and the broader application of AI in medical imaging.

5.1. Limitations of the Current Work

Despite the promising results, several limitations may impact the broader applicability and robustness of the proposed model:

1) Robustness to Diverse Noise Types:

The model was primarily trained on Gaussian noise. However, medical images often exhibit various types of noise (e.g., salt-and-pepper, Poisson, speckle). The current model's ability to generalize to these noise types remains untested.

2) Handling Complex Noise Patterns:

Non-uniform or mixed noise patterns found in real-world microscopy images may not be well addressed by this approach, which relies on synthetic Gaussian augmentation.

3) Trade-off Between Denoising and Feature Preservation:

While denoising improves clarity, it risks eliminating fine-grained cellular structures crucial for diagnosis.

4) Limited Generalization Across Modalities:

This study focused exclusively on thick smear microscopy images. Generalization to other modalities (e.g., CT, MRI) is yet to be explored.

5) Dataset Bias and Limited Diversity:

The dataset used was relatively limited in size and variation. A broader dataset from multiple labs, devices, and acquisition protocols is needed to improve model generalization.

6) Lack of Benchmark Comparisons:

No direct comparisons were conducted against other state-of-the-art denoising methods, limiting the model's contextual positioning.

7) Real-Time Applicability:

UNet, while effective, is computationally intensive. It is currently not optimized for real-time applications such as point-of-care diagnosis or mobile deployment.

Summary of Limitations and Next Steps

To validate practical efficacy, future research should aim to:

- 1) Evaluate the model on more diverse, real-world clinical datasets.
- 2) Train on and test against various noise types beyond Gaussian.
- 3) Benchmark the UNet model against classical and modern denoising methods.

- 4) Test generalizability to other medical imaging tasks and modalities.
- 5) Optimize the model for deployment on mobile and resource-limited devices.

5.2. Future Recommendations

To expand the scope and impact of this research, future work may explore:

- 1) Standardized Benchmarks: Compare performance against classical techniques (e.g., wavelet denoising) and recent deep learning approaches (e.g., Noise2Void) on public datasets.
- 2) End-to-End Pipelines: Integrate denoising with parasite detection and classification for full diagnostic workflows. Report metrics such as mAP (mean Average Precision).
- 3) Real-World Validation: Test in clinical environments with varied equipment, acquisition protocols, and lighting conditions to ensure robustness.
- 4) Parasite Counting: Extend the detection pipeline to count parasites per image and compute parasitemia. This would aid in grading severity levels automatically.
- 5) Color Image Processing: Explore noise modeling and removal techniques that retain full RGB channels, as grayscale conversion limits biological context.
- 6) Blind Noise Removal: Improve model generalization for "blind denoising," where noise type and level are unknown or mixed.

Conflicts of Interest

The author declares no conflicts of interest.

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