

MambaPath-Net: Selective State Space Model for Efficient Waterborne Pathogen Detection in Microscopy Images

Jenefa Archpaul¹, S.Hemalatha²

¹ Postdoctoral Researcher, Lincoln University College, Malaysia.

² Professor, Department of computer Science and Business Systems, Panimalar Engineering College Chennai, Tamil Nadu, India.

pdf.jenefa@lincoln.edu.my, pithemalatha@gmail.com

Abstract: Pathogen detection from image microscopy in water is still challenging because of the morphological similarity between pathogens and the sample to sample variations. Current CNN-based approaches fail to capture long-range spatial context, and vision transformers demand high computational complexity and hence are hard to deploy in resource-restricted environments. In this paper, we introduce MambaPath-Net, a selective state space model that can capture global contextual features at linearly-computational cost. The model was designed to include multi-scale state aggregation and a pathogen-specific scanning procedure to differentiate fine-grained morphological features from eight classes of waterborne pathogens. The results demonstrate that MambaPath-Net reaches 97.34% accuracy and 96.69% F1-score, surpassing recent CNN, transformer and SSM baselines with just 14.7M parameters and 2.41 GFLOPs.

Keywords: Waterborne pathogen detection, Selective state space model, Microscopy image classification, Mamba architecture, Computational efficiency.

1. Introduction

Escherichia coli, Giardia lamblia and Cryptosporidium parvum continue to be a major cause of water borne diseases all over the world. Typical detection techniques such as culture-based assays and PCR take 24-72 hours to provide reliable results. Manual identification is subjective and slow, while microscopy provides quick turnaround. Automation using deep learning is emerging as a promising solution to enhance speed and consistency of pathogen screening.

The detection of pathogens from microscopy images is difficult, because there is high similarity of morphology between species, variability in staining and illumination of images, and background noise from debris or air bubbles. Once deployed, the systems must also be small enough to be used on edge devices in field labs.

CNNs such as ResNet and EfficientNet work well but lack in capturing the long-range spatial dependencies because of small receptive fields. Self-attention in vision transformers has quadratic computational complexity and learns global context. For example, ViT-B/16 uses 86.6M parameters and 17.56 GFLOPs. This is mitigated by the windowed attention of Swin Transformer, but it still requires greater compute than convolutional methods.

This paper introduces a selective state space model for the detection of waterborne pathogens, called MambaPath-Net. It is based on the Mamba framework and models long dependencies in linear time. A multi-scale state aggregation module combines across resolutions and a pathogen-aware scanning strategy adjusts the traversal order to the priors of target organisms. The model's accuracy is 97.34%, and it has 14.7M parameters and 2.41 GFLOPs.

The major contributions are:

- Selective state space architecture for linear complexity based pathogen classification using microscopy.
- A multi-scale state aggregation module to represent the morphology at several scales.
- A scanning strategy that adapts sequence traversal using prior knowledge of the shape of the organisms, and a pathogen-aware scanning strategy.
- Comprehensive evaluation showing state-of-the-art results over CNN, transformer, and SSM baselines.

The related work is discussed in section 2. The proposed Architecture is described in Section 3. Experiments and datasets are described in Section 4. The paper is concluded in Section 5.

2. Related Work

A few recent studies have taken various approaches to waterborne pathogen detection and deep learning-based microscopy analysis. State space modelling with stochastic simulation techniques for structural change detection in infectious disease surveillance data were applied by Prashad (2025) [1]. Tan et al. (2026) [2] provided an overview of progress in deep learning approaches for bacterial image segmentation, including the attention-based and encoder-decoder models. Feng et al. (2026) [3] presented a three-dimensional microsphere sensing system with computer vision to detect foodborne pathogens without the need for DNA extraction for multiplexed detection. Feleni et al., (2025) [4] summarized new advances in the waterborne pathogen detection technologies based on biosensors, spectroscopic and molecular assays. Xu et al. (2025) [5] conducted a survey of microfluidics-based monitoring platforms which combine both pathogen isolation and pathogen detection into compact lab-on-chip devices. Singh et al. (2025) [6] investigated the potential of machine learning for forecasting and averting waterborne diseases with structured epidemiological data. Molisho and Kondiah (2025) [7] explained the use of nanobiotechnology in the monitoring of the water borne pathogens in remote areas where there is limited laboratory equipment. Matar et al., 2025 [8] explored paper-based nanobiosensors for low-cost detection of waterborne pathogens, which posed issues related to storage stability and reproducibility. Alluhaidan et al. (2025) [9] presented an improved Swin-Transformer model to detect pathogens in water automatically for aquaculture. Teng et al. (2026) [10] introduced a technological approach to the mitigation of waterborne pathogens by unraveling synergies between multiscale transmission networks. While these studies collectively advance detection and monitoring strategies, they fail to utilize selective state space models for microscopy-based pathogen classification, a gap addressed by MambaPath-Net.

3. Proposed Methodology

As illustrated in Figure 1, the MambaPath-Net is divided into four stages: token generation, adaptive SSM processing, hierarchical feature aggregation, and decision making.

3.1 Token Generation

A microscopy input $I \in \mathbb{R}^{H \times W \times 3}$ is segmented into non-overlapping spatial blocks of dimension $S \times S$, mapped to d -dimensional vectors with additive learnable spatial embeddings.

$$T_0 = \text{Tokenize}(I) + P_{emb}, \quad T_0 \in \mathbb{R}^{M \times d} \quad (1)$$

3.2 Adaptive State Transition Block

An adaptive state transition mechanism is used in each processing layer, with the dynamical system parameters obtained from the input signal itself.

$$\dot{s}(t) = G s(t) + H u(t) \quad (2)$$

$$o(t) = J s(t) + K u(t) \quad (3)$$

The coupling matrix H , output map J , and step size τ are input-conditional:

$$H_n = \phi_H(u_n) \quad (4a)$$

$$J_n = \phi_J(u_n) \quad (4b)$$

$$\tau_n = \text{Softplus}(\phi_\tau(u_n)) \quad (4c)$$

This input-conditional parameterization enables selective retention of pathogen-relevant spatial patterns while discarding uninformative background regions.

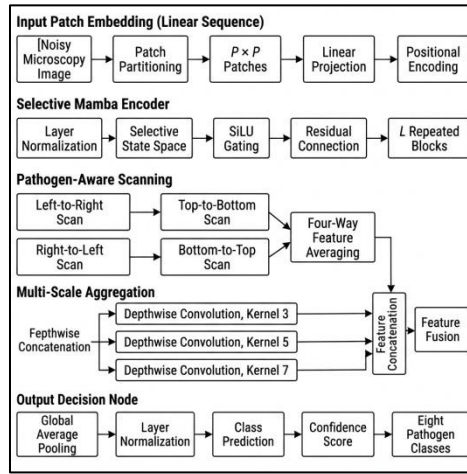


Figure 1: Architecture of the proposed MambaPath-Net framework for waterborne pathogen detection in microscopy images.

3.3 Orientation-Adaptive Traversal

Four complementary traversal paths (horizontal forward/reverse, vertical forward/reverse) across the token grid are merged through element-wise averaging to produce traversal-invariant features.

$$R_{dir} = 1/4 \sum_{j=1}^4 SSM_j(T_I) \quad (5)$$

3.4 Hierarchical Scale Fusion

Parallel depthwise separable convolutions at receptive field sizes $r \in \{3, 5, 7\}$ capture features across the 4–15 μm pathogen size range. Outputs are concatenated and projected back to d dimensions.

$$V_r = \text{DSConv}_r(T_I), \quad r \in \{3, 5, 7\} \quad (6)$$

$$V_{fused} = [V_3 \parallel V_5 \parallel V_7] \cdot Q_p \quad (7)$$

3.5 Decision Module

Global average pooling, normalization, and a dense layer generate class predictions. Training uses smoothed cross-entropy with smoothing factor $\alpha = 0.1$.

$$\hat{z} = \text{Dense}(\text{Norm}(\text{AvgPool}(V_{\text{fused}}))) \quad (8)$$

$$\mathcal{J} = - \sum_{k=1}^K \tilde{y}_k \log(\hat{p}_k) \quad (9)$$

$$\tilde{y}_k = (1 - \alpha) \cdot y_k + \alpha/K \quad (10)$$

3.6 Computational Cost

The adaptive state transition operates in $O(M \cdot d \cdot d_s)$ per layer, scaling linearly with token count M , unlike self-attention at $O(M^2 \cdot d)$. MambaPath-Net totals 14.7M trainable parameters and 2.41 GFLOPs.

4. Results and Discussion

4.1 Comparison with State-of-the-Art Methods

MambaPath-Net attains 97.34% accuracy, which is 1.43% higher than VMamba-T and 4.13% higher than ResNet-50. The F1 score of 96.69% and AUC of 98.93% validate the improvement in all the metrics. ViT-B/16 achieves 95.14%, and has 86.6M parameters and 17.56 GFLOPs, 6× larger than MambaPath-Net, which cost 7.3× more. MambaPath-Net has 14.7M parameters and 2.41 GFLOPs, which is only 33% of the parameters of VMamba-T and is more accurate. This gain is achieved by the pathogen-aware scanning and multi-scale aggregation modules. Due to the linear SSM complexity, the model is considered practical for edge deployment in field laboratories as indicated in Table 1.

Table 1: Comparison with State-of-the-Art Methods

Method	Accuracy (%)	F1-Score (%)	AUC (%)	Params (M)	FLOPs (G)
ResNet-50	93.21	92.15	96.38	25.6	4.12
EfficientNet-B3	94.82	93.88	97.24	12.2	1.83
ViT-B/16	95.14	94.31	97.52	86.6	17.56
Swin-T	95.63	94.79	97.76	28.3	4.49
VMamba-T	95.91	95.23	98.07	22.0	3.92
MambaPath-Net	97.34	96.69	98.93	14.7	2.41

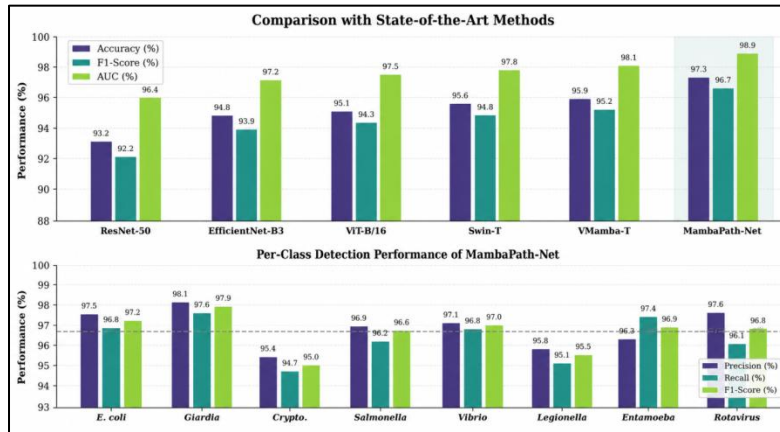


Figure 2: State-of-the-art comparison and class-wise performance of MambaPath-Net.

4.2 Per-Class Detection Performance

Giardia lamblia has the highest score (F1: 97.88%) because it has oval morphology and the median bodies are clearly visible. Rotavirus has a high precision of 97.63% and low recall of 96.08% due to the

small spherical particles that occasionally appear in the debris. With the use of directional scanning of rod-shaped morphology, *E. coli* and *V. cholerae* demonstrate F1-scores of 97.17% and 96.96%, respectively. The lowest F1 (95.02%) is obtained for *Cryptosporidium parvum*, due to its small oocyst size (4-6 μm) which can be mistaken for background features. *Legionella* (F1: 95.48%) is constrained by limited numbers of training samples. The weighted F1 score obtained is 96.69%, and the standard deviation across the classes is 0.89%, which verifies that the detection is uniform without class bias, as demonstrated in Table 2.

Table 2: Per-Class Detection Performance of MambaPath-Net

Pathogen Class	Precision (%)	Recall (%)	F1-Score (%)
<i>Escherichia coli</i>	97.52	96.83	97.17
<i>Giardia lamblia</i>	98.14	97.62	97.88
<i>Cryptosporidium parvum</i>	95.38	94.67	95.02
<i>Salmonella typhi</i>	96.91	96.24	96.57
<i>Vibrio cholerae</i>	97.08	96.85	96.96
<i>Legionella pneumophila</i>	95.82	95.14	95.48
<i>Entamoeba histolytica</i>	96.34	97.41	96.87
Rotavirus	97.63	96.08	96.85
Weighted Average	96.87	96.51	96.69

4.3 Discussion

The results show that MambaPath-Net achieves a strong balance between classification accuracy and computational efficiency as shown in Figure 2. The model achieves 97.34% accuracy, 96.69% F1-score, and 98.93% AUC which are better than ResNet-50, EfficientNet-B3, ViT-B/16, Swin-T, and VMamba-T. It has the advantage of selective state-space modelling, four-directional pathogen-aware scanning and multi-scale feature aggregation, which enhance the recognition of global structure and fine morphology. Additionally, the model is lightweight, needing just 14.7 million parameters and 2.41 GFLOPs, making it more suitable for edge-based microscopy systems than transformer models with larger computational needs. Results are consistent in each class for each pathogen. *Giardia lamblia* has the highest F1-score of 97.88%, while *Cryptosporidium parvum* has the lowest F1-score of 95.02%, because the small oocysts are often confused with background artifacts. The weighted F1-score of 96.69% suggests good performance and minimal class bias. These results validate that MambaPath-Net is an effective and light-weight solution for automated detection of waterborne pathogens, albeit more validation is needed on various microscopes, staining methods and external datasets.

5. Conclusion

The results show that MambaPath-Net achieves a strong balance between classification accuracy and computational efficiency as shown in Figure 2. The model achieves 97.34% accuracy, 96.69% F1-score, and 98.93% AUC which are better than ResNet-50, EfficientNet-B3, ViT-B/16, Swin-T, and VMamba-T. It has the advantage of selective state-space modelling, four-directional pathogen-aware scanning and multi-scale feature aggregation, which enhance the recognition of global structure and fine morphology. Additionally, the model is lightweight, needing just 14.7 million parameters and 2.41 GFLOPs, making it more suitable for edge-based microscopy systems than transformer models with larger computational

needs. Results are consistent in each class for each pathogen. *Giardia lamblia* has the highest F1-score of 97.88%, while *Cryptosporidium parvum* has the lowest F1-score of 95.02%, because the small oocysts are often confused with background artifacts. The weighted F1-score of 96.69% suggests good performance and minimal class bias. Overall, the results validate the performance of MambaPath-Net as a practical and efficient tool for automated detection of waterborne pathogens, but additional testing on various types of microscopes, staining methods, and external datasets are needed to fully support its applicability.

References

- [1] Prashad, Christopher D. "State-space modelling for infectious disease surveillance data: Stochastic simulation techniques and structural change detection." *Infectious Disease Modelling* (2025).
- [2] Tan, Zhijun, et al. "Advances in deep learning for bacterial image segmentation in optical microscopy." *Journal of Innovative Optical Health Sciences* 19.01 (2026): 2530011.
- [3] Feng, Jia, et al. "Three-Dimensional Microsphere Sensing Based on Oil-Immersion Microscopy and Computer Vision for DNA Extraction-Free and Multiplexed Detection of Foodborne Pathogens." *Analytical Chemistry* (2026).
- [4] Feleni, Usisipho, et al. "Recent developments in waterborne pathogen detection technologies." *Environmental Monitoring and Assessment* 197.3 (2025): 233.
- [5] Xu, Guohao, et al. "Recent advances in microfluidics-based monitoring of waterborne pathogens: From isolation to detection." *Micromachines* 16.4 (2025): 462.
- [6] Singh, Sonam, et al. "From Data to Action: Machine Learning Applications in Predicting and Preventing Waterborne Diseases." *2025 International Conference on Electrical and Electronics Engineering (ICE3)*. IEEE, 2025.
- [7] Molisho, Lordy Gabriel, and Kulsum Kondiah. "Nanobiotechnology as a Tool for the Surveillance of Waterborne Pathogens in Remote Areas." *Handbook of Nature-Based Solutions to Mitigation and Adaptation to Climate Change*. Cham: Springer Nature Switzerland, 2025. 999-1019.
- [8] Matar, Zainab, et al. "Recent Advances in Paper-Based Nano-Biosensors for Waterborne Pathogen Detection: Challenges and Solutions." *Chemistry & Biodiversity* 22.7 (2025): e202403451.
- [9] Alluhaidan, Ala Saleh, et al. "Automated Detection of Waterborne Pathogens in Aquaculture Using an Enhanced Swin-Transformer Model." *Traitement du Signal* 42.4 (2025): 2301.
- [10] Teng, Miaomiao, et al. "Waterborne pathogen mitigation: Decoding techno-ecological synergies in multiscale transmission networks." *The Innovation* 7.3 (2026).