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Efficient Fish Disease Classification Using Fine-Tuned MobileNetV3Large for Mobile-Based Aquaculture Diagnosis

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Abstract: Fish diseases represent a major challenge in the aquaculture industry as this phenomenon frequently leads to significant economic losses. Manual disease identification requires specialized expertise and is time-consuming in the field. Therefore, this study aims to implement the MobileNetV3Large Deep Learning architecture to automatically identify eight types of fish conditions. This research dataset utilizes 2,400 digital images distributed evenly across eight fish condition categories. Each class consists of 300 image samples, including Bacterial Red disease, Aeromoniasis, Bacterial gill disease, EUS Disease, Fungal diseases Saprolegniasis, Parasitic diseases, White tail disease, and a Healthy Fish group. The dataset was sourced from https://www.kaggle.com/datasets/irfanulhuda/fish-disease-detection-dataset. These conditions include bacterial, fungal, viral, and parasitic infections, as well as healthy fish conditions. The research methodology applies Transfer Learning techniques combined with Fine-Tuning optimization on the last 70 layers. The methodology applies a transfer learning strategy with a data split of 80% for training, 10% for validation, and 10% for testing. This step was taken to adapt the model's weights to the visual characteristics of the fish disease images. The process was evaluated using the Adam optimization function and the Categorical Cross-Entropy loss function. Experimental results demonstrate highly superior model performance on the test data. The MobileNetV3Large model successfully achieved a test accuracy of 92.92% with a loss value of 0.2099. Furthermore, evaluation through the Confusion Matrix and ROC curves yielded an average AUC value of 1.00 across the majority of classes. This figure indicates that the model possesses exceptionally high discrimination capacity and sensitivity. In conclusion, the computational efficiency of the MobileNetV3Large architecture makes this system a highly potential solution. Researchers can implement this model on mobile devices to assist fish farmers in diagnosing diseases quickly and accurately directly at the aquaculture sites.

Keyword: Automated Identification, MobileNetV3Large, Fish Disease, Transfer Learning, Fine-Tuning.

INTRODUCTION

The aquaculture sector represents a vital pillar in maintaining global food security and enhancing the economy of coastal communities (Jayasekara et al., 2025). However, productivity in this sector is frequently hindered by outbreaks of various pathogenic agents that cause diseases in fish, ranging from bacterial and fungal to viral infections (Iqbal et al., 2023). Delays in detecting clinical symptoms in the field often lead to mass mortality within fish populations, resulting in significant financial losses for farmers (Sajid et al., 2024). The conventional process of identifying fish diseases still relies heavily on manual visual observations by experts or through laboratory testing, both of which are time-consuming and costly (Ahmed et al., 2022). Furthermore, the limited number of experts available in remote areas poses a major obstacle to the rapid management of fish diseases (Mohammed,

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2024). Therefore, a technological solution capable of performing automated, fast, and accurate disease classification utilizing visual data is urgently required (Cheng et al., 2025).

The utilization of Deep Learning-based Computer Vision technology, specifically Convolutional Neural Networks (CNN), has demonstrated remarkable success in various image classification tasks across the agricultural and fisheries sectors (Thu et al., 2021). Several previous studies have successfully developed fish disease classification models using heavy architectures such as ResNet and DenseNet, which achieve high accuracy but require massive computational resources and lack portability for edge devices. Conversely, while light architectures like MobileNetV2 or newer models like EfficientNet offer alternative solutions, MobileNetV2 often suffers from performance degradation on complex biological disease patterns, whereas EfficientNet demands relatively higher latency during real-time inference on low-specification mobile devices.

Consequently, there remains a critical gap in finding a balanced solution that maintains state-of-the-art accuracy while operating within strict computational and memory constraints. To bridge this gap, one state-of-the-art architecture developed for high efficiency on resource-constrained devices is MobileNetV3Large (Qian, 2021). Compared to its predecessors and heavier counterparts, MobileNetV3Large provides a superior trade-off by utilizing a redesigned inverted bottleneck structure and hard-swish activation functions, making it explicitly more suitable for real-time mobile aquaculture diagnosis without sacrificing the model's depth needed to capture subtle fish disease lesions. This architecture employs Hardware-Aware Architecture Search and NetAdapt mechanisms to achieve optimal performance while remaining lightweight to execute (Norouzi et al., 2021).

This study implements the Transfer Learning technique to overcome dataset limitations by leveraging pre-trained weights from ImageNet (Yu & Xiu, 2022). Additionally, a Fine-Tuning strategy is applied to the last 70 layers of the model to enhance feature sensitivity toward the specific characteristics of fish diseases, such as lesion patterns, skin discoloration, and fungal growth (Vrbančič & Member, 2020). Through this approach, the model is expected to deliver precise identification results and be successfully deployed into a mobile-based, real-time fish health monitoring system (Eghbal-zadeh et al., 2024).

LITERATURE REVIEW

To establish a solid theoretical foundation and position this study within the existing body of research, this section reviews relevant literature on automated fish disease diagnosis. The discussion begins with an analysis of prior attempts in fish disease classification using various Convolutional Neural Network (CNN) architectures and highlights their respective limitations. Subsequently, this section explores the evolution of efficient deep learning models, specifically focusing on the MobileNetV3Large architecture. Finally, the theoretical concepts and mechanical advantages of Transfer Learning, Fine-Tuning strategies, and data augmentation techniques are elaborated to justify the methodological choices implemented in this research.

Prior Research on Fish Disease Classification

Efforts to automate fish disease diagnosis have been conducted by various researchers utilizing diverse Convolutional Neural Network (CNN) architectures, moving away from conventional qualitative methods toward data-driven insights. A study by (Kheriji & Kouadri, 2025) employed a simple, custom CNN architecture to detect diseases in freshwater fish; however, that study noted severe accuracy limitations when confronted with complex pond background variations, turbid water conditions, and inconsistent lighting. This indicates that shallow networks often lack the capacity to extract high-level abstract features under noisy field conditions.

Conversely, (Gao, 2024) utilized Transfer Learning on the heavy-weight ResNet50 model for fish disease identification, which yielded a significant increase in classification accuracy due to its deeper residual blocks. Nevertheless, the model possessed an exceptionally large parameter size and high computational complexity. A similar limitation is found in DenseNet architectures, which, despite their excellent feature reuse capabilities through dense connectivity, suffer from extremely high memory footprints due to concatenated feature maps. This structural bulkiness poses a significant bottleneck, making it highly impractical to implement on resource-constrained mobile devices or edge computing hardware typically deployed at remote aquaculture sites.

Model Efficiency and MobileNet

In the development of efficient deep learning architectures suitable for real-time mobile deployment, (Choompol et al., 2025) introduced MobileNetV3, which optimizes the delicate balance between latency and accuracy through Hardware-Aware Architecture Search (NAS) and the NetAdapt algorithm. While newer state-of-the-art scaling models like EfficientNet offer strong competitive accuracy by uniformly scaling depth, width, and resolution, they often introduce complex compound scaling operations that lead to higher floating-point operations (FLOPs) and inference latency on low-end mobile CPUs compared to MobileNet. A study conducted by (Qian, 2021) demonstrated that MobileNetV3Large is capable of outperforming its predecessor models (V1 and V2) in terms of classifying small, low-contrast, and highly textured object images. This capability is highly relevant to the visual characteristics of early-stage lesions, subtle skin discolorations, or localized fungi on fish

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bodies. Furthermore, research by (Yasin et al., 2023) also confirmed that the incorporation of Squeeze-and-Excitation (SE) attention mechanisms features in MobileNet helps the model dynamically recalibrate channel-wise feature responses. This attention block essentially forces the network to focus more on crucial infection areas in fish imagery, thereby effectively reducing background noise originating from muddy aquatic environments, reflections, and floating debris.

The Role of Transfer Learning and Fine-Tuning

The use of Transfer Learning has become the undisputed gold standard in medical and biological image classification where data scarcity is a persistent issue. (Odel et al., 2021) explained that leveraging pre-trained weights from massive source datasets like ImageNet assists the model in recognizing foundational low-level features such as edges, textures, and geometric shapes, which are essential in subsequent pathology detection tasks. More specifically, (Rangkuti et al., 2025) in his study on Fine-Tuning strategies found that keeping the base layers frozen while unfreezing the top layers progressively provides the necessary flexibility for the model to adapt and learn high-level features specific to the target dataset. This operational philosophy aligns perfectly with the strategy implemented in this study, where the last 70 layers are unfrozen to fine-tune the network parameters. This precise adjustment adapts the model to 8 different fish disease classes, which according to (Tao & Zhong, 2025) is the primary methodological key to overcoming high inter-class similarity and low intra-class variance commonly found between distinct bacterial and viral diseases.

Data Augmentation and Generalization

The primary challenge in applying deep learning to fish disease classification is the limited availability of high-quality, balanced datasets, as gathering infected fish samples in controlled environments is both labor-intensive and unpredictable. To mitigate this risk, (Antwi et al., 2024) proved that geometric and photometric augmentation techniques, such as rotation, flipping, and scaling, dramatically expand the synthetic size of the training pool, which in turn enhances the model's generalization capability and prevents catastrophic overfitting. This is strongly supported by (Shan et al., 2024), who stated that models trained with aggressively augmented data exhibit superior mathematical robustness against environmental variations. In practical aquaculture scenarios, this translates to stable classification performance despite shifts in daily outdoor lighting, variable turbidities, and diverse shooting angles captured by fish farmers using standard smartphone cameras within pond or aquarium environments.

METHOD

The methodology in this study is designed to develop an efficient and accurate fish disease identification system by utilizing Deep Learning techniques. Broadly outlined, the stages of this research initiate from dataset management and augmentation processes to enhance data variability, leading to the implementation of a two-phase training strategy (Phase Training) that encompasses layer freezing and fine-tuning(Helmud et al., 2024).

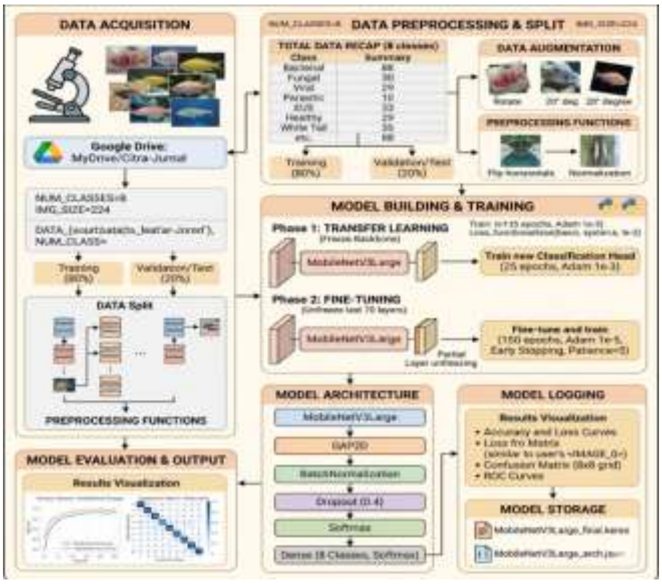

Fig. 1 Research Stages (Developed by the authors)

Figure 1 shows the visual diagram of the research stages conducted in this study. It is important to note that the entire logical workflow, experimental design, and technical parameters—such as the data split, augmentation

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methods, and the two-phase training strategy—were completely and independently designed within this study. Artificial Intelligence was used only as a visual tool to convert the research plan into a clear flowchart for better presentation. The entire process aims to produce a model capable of generalizing effectively across eight different fish condition classes. These stages are explained in detail as follows :

1. Image Preprocessing and Augmentation

The initial stage of the research begins with data preparation to meet the input standards of the MobileNetV3Large architecture. The original images are resized to 224 X 224 pixels. To increase data variability and prevent overfitting, augmentation techniques such as rotation and horizontal flipping are applied. Furthermore, each image pixel is normalized using the v3_pre function, which mathematically maps the pixel intensity value x ε [0,225] into a range more optimal for the neural network(Adeeba, 2025) .

$$x^1 = \frac{x-\mu}{\sigma} \qquad (1)$$

where μ is the mean and σ is the standard deviation of the ImageNet dataset.

2. MobileNetV3Large Architecture and Computational Efficiency

This model was selected due to its superiority in efficiency without significantly compromising accuracy. The core of this efficiency lies in the utilization of Depthwise Separable Convolution(Beyza et al., 2024). Unlike standard convolution, which computes channel and spatial dimensions simultaneously, this technique divides the process into two distinct stages: depthwise and pointwise.

The computational efficiency of this model can be expressed through its cost ratio relative to standard convolution

$$Efficiency = \frac{1}{N} + \frac{1}{D_k^2} \qquad (2)$$

Where D_k is the kernel size (3 or 5) and N is the number of output filters. Furthermore, to accelerate hardware processing, the Hard-Swish activation function is utilized

$$\mathrm{h-swish(x) = x\,.\frac{ReLU6(x+3)}{6}} \qquad (3)$$

3. Training Strategy: Transfer Learning and Fine-Tuning

Training is conducted in two strategic phases to obtain optimal weights for the eight fish disease classes:

- Phase 1 (Transfer Learning): All backbone layers are frozen. Training is focused solely on the newly added classification head layer. In this phase, a learning rate (n) of 10^{-3} is utilized.
- Phase 2 (Fine-Tuning): The last 70 layers of MobileNetV3Large are unfrozen for retraining. This aims to allow the model to learn highly specific microscopic features of fish disease lesions or patches. A lower learning rate 10^{-5} is used to ensure that weight adjustments occur smoothly.

$$A_{new} = \omega_{old} - n\,.\nabla L\,(w) \qquad (4)$$

where $\nabla L(\omega)$ is the gradient of the loss function with respect to the weights.

4. Model Evaluation Stages

The evaluation stage is a crucial step to measure the extent to which the MobileNetV3Large model can generalize to unseen data. The evaluation process is conducted using a testing dataset consisting of 240 images evenly distributed across eight fish disease classes. The evaluation parameters used include:

- Confusion Matrix
  This method is used to map the model's prediction results against the actual labels in detail. From this matrix, it is possible to identify which classes have a high accuracy rate and which classes frequently experience misclassification(Markoulidakis, 2024). Systematically, this evaluation is based on four primary parameters: True Positive (TP), True Negative (TN), False Positive (FP), and False Negative (FN).
- Performance Metrics (Precision, Recall, and F1-Score)
  To obtain a more comprehensive overview of the performance, the Precision, Recall, and F1-Score values are calculated for each fish disease class.

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Precision measures the model's exactness in predicting the positive class:

$$Precision = \frac{TP}{TP+FP} \quad (5)$$

Recall measures the model's ability to retrieve all samples from a specific class:

$$Recall = \frac{TP}{TP+FN} \quad (6)$$

F1-Score represents the harmonic mean of Precision and Recall, providing an overview of the model's performance balance:

$$F1 - Score = 2. \frac{Precision \,.\, Recall}{Precision + Recall} \quad (7)$$

5. ROC Curve and AUC

The evaluation also involves utilizing the Receiver Operating Characteristic (ROC) curve to plot the True Positive Rate against the False Positive Rate across various classification thresholds. The Area Under the Curve (AUC) is used as an indicator of the model's discrimination capacity. An AUC value approaching 1.00 indicates that the model possesses an excellent capability to distinguish between one type of fish disease and another(Helmud et al., 2026).

6. Training Performance Visualization

During the training process, the Accuracy and Loss curves for both the Training and Validation data are strictly monitored. This is conducted to ensure that the Fine-Tuning process runs optimally and that there are no indications of overfitting or underfitting before the final model is saved in .keras and .json formats.

RESULT

The results of the model stability analysis during the training process are presented through the accuracy and loss curves, followed by generalization testing on unseen data using standard evaluation metrics such as the confusion matrix and ROC curves. This analysis aims to demonstrate the effectiveness of using a lightweight deep learning model that maintains high precision in automatically diagnosing fish diseases.

1. Training Process Performance

In the initial stage, the evaluation was conducted on the stability of the model during the training process, which encompasses both the transfer learning and fine-tuning phases(Helmud et al., 2025).

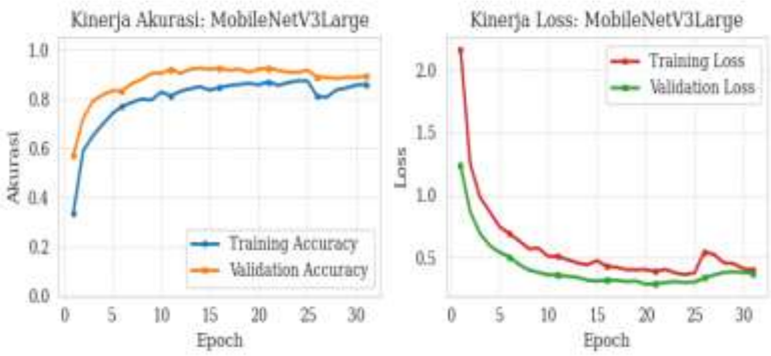

Fig. 2 Accuracy and Loss Curves during the Training and Validation Phases.

Based on Figure 2, the accuracy curves display a stable upward trend as the number of epochs increases. The model achieves a favorable convergence point without significant indications of overfitting, where the validation accuracy remains consistently above or aligned with the training accuracy throughout most of the process. In the loss chart, a sharp decline in error values is observed from above 2.0 down to below 0.5, proving that the Adam optimization function successfully updated the model weights effectively.

2. Global Performance on Testing Data

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Upon the completion of the training phase, the model was evaluated using an independent dataset (test set) that had not been seen previously to measure its generalization capability.

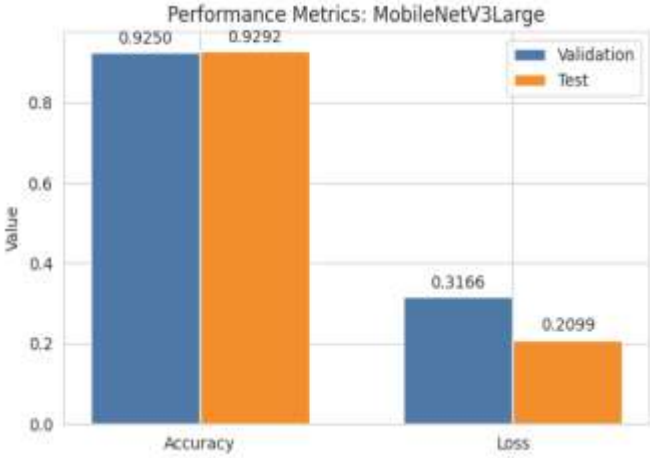

Fig. 3 Comparison of Accuracy and Loss Metrics on Validation and Testing Data.

Figure 3 represents the final performance of the model. MobileNetV3Large yielded a testing accuracy of 92.92% with a loss value of 0.2099. This result is slightly higher than the validation accuracy (92.50%), indicating that the model possesses a highly robust generalization capability and does not merely memorize the training data.

3. Class-by-Class Classification Analysis (Confusion Matrix)

To understand the detailed accuracy across each of the eight fish disease classes, an analysis was performed using a Confusion Matrix.

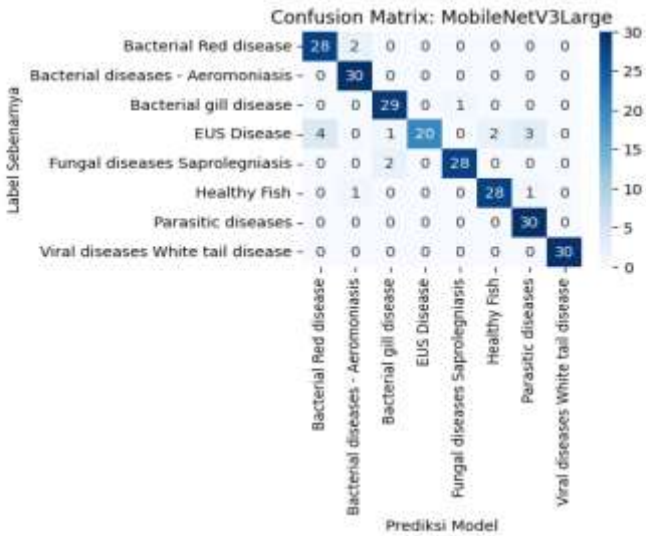

Fig. 4 Confusion Matrix for the 8-Class Fish Disease Classification.

Based on Figure 4, the model is capable of identifying the *Parasitic diseases* and *Viral diseases White tail* classes with perfect accuracy (30/30). However, a challenge arises within the *EUS Disease* class, where 4 samples were misclassified as *Bacterial Red disease*. Clinically, this is caused by the morphological similarities of the lesions on the fish bodies between the EUS fungal infection and the bacterial infection, both of which produce reddish patches, thereby resulting in highly similar extracted visual features.

4. Model Discrimination Capability (ROC Curve)

The model's quality in distinguishing between different classes was further evaluated using ROC curves.

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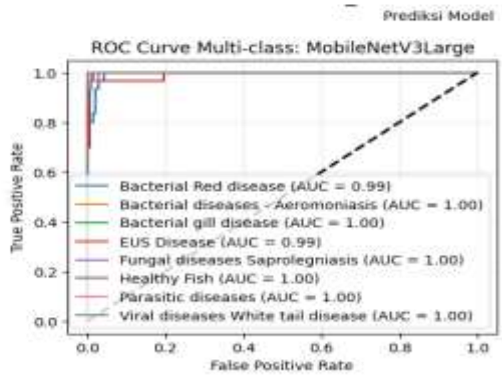

Statistik Performa MobileNetV3Large:

	precision	recall	f1-score	support
Bacterial Red disease	0.88	0.93	0.90	30
Bacterial diseases - Aeromoniasis	0.91	1.00	0.95	30
Bacterial gill disease	0.91	0.97	0.94	30
EUS Disease	1.00	0.67	0.80	30
Fungal diseases Saprolegniasis	0.97	0.93	0.95	30
Healthy Fish	0.93	0.93	0.93	30
Parasitic diseases	0.88	1.00	0.94	30
Viral diseases White tail disease	1.00	1.00	1.00	30
accuracy			0.93	240
macro avg	0.93	0.93	0.93	240
weighted avg	0.93	0.93	0.93	240

Fig. 5 ROC Curves and AUC Values for Each Class.

Figure 5 shows that almost all classes achieved an Area Under the Curve (AUC) value of 1.00, except for the EUS Disease class, which achieved 0.99. To ensure that these exceptionally high AUC metrics were not artifacts of experimental errors, a rigorous data integrity audit was conducted. First, the test dataset was strictly isolated as an independent evaluation set before any data preprocessing occurred. Data augmentation techniques—such as rotation, flipping, and scaling—were applied exclusively to the training set; the test set remained completely unaugmented to preserve raw, unseen visual profiles. Second, a comprehensive deduplication check was performed across the entire dataset to ensure zero duplicate images existed between the splits. Third, the data partition was executed with strict isolation to prevent any fish-level leakage, ensuring that no frames or viewpoints of the exact same fish sample were shared between the training and testing phases.

To provide a comprehensive evaluation of the model's multi-class discrimination power, both micro-average and macro-average AUC metrics were computed. The model yielded a micro-average AUC of 1.00 and a macro-average AUC of 1.00. These aggregate metrics suggest that under the current experimental setting, the model establishes highly stable separation thresholds across all eight categories, minimizing the risk of misdiagnosis or false-positive outcomes. Nevertheless, these near-perfect results must be interpreted with caution. While the statistical evidence confirms optimal performance on this benchmark dataset, the high accuracy may also indicate that the curated images contain distinct, high-contrast pathological features that are relatively straightforward for a fine-tuned deep network to separate. Consequently, these boundaries must be further validated using noisy, uncurated field images captured directly from real-world aquaculture environments to confirm true operational robustness.

DISCUSSIONS

The experimental results demonstrate that the proposed MobileNetV3Large model achieves a high level of efficacy in identifying fish diseases under controlled laboratory conditions. The model attained a classification accuracy of 92.92% on the independent test dataset. This performance indicates that a lightweight convolutional neural network can extract intricate pathological features without requiring massive computational resources. The implementation of the two-phase training strategy contributed to this accuracy. In the first phase, the transfer learning approach preserved the feature extractors from the ImageNet weights. In the second phase, the fine-tuning of the last 70 layers allowed the model to adapt its deeper weights to the unique visual characteristics of fish lesions, discoloration, and tissue abnormalities. The decrease in the categorical cross-entropy loss to 0.2099 indicates that the Adam optimizer updated the network parameters toward convergence, although a risk of minor overfitting remains due to the relatively small size of the target dataset. A deeper analysis of the confusion matrix reveals important insights regarding the misclassifications. The model achieved a 100% accuracy for Bacterial diseases - Aeromoniasis, Parasitic diseases, and Viral diseases White tail disease. However, the system encountered challenges when distinguishing EUS Disease from Bacterial Red disease. In aquaculture pathology, both Epizootic Ulcerative Syndrome (EUS) and severe bacterial infections produce highly similar clinical

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symptoms, such as red necrotizing ulcers on the skin of the fish. Because these two distinct pathogens cause overlapping visual phenotypes, the model extracted highly correlated spatial features, which occasionally led to prediction errors.

Furthermore, the multi-class Receiver Operating Characteristic (ROC) curve validates the discriminative capacity of the model. The system generated an Area Under Curve (AUC) value of 1.00 for seven out of the eight classes, while the EUS Disease class maintained an AUC of 0.99. These AUC metrics suggest that the model establishes defined decision boundaries among the different disease categories, indicating high sensitivity under the current experimental setting. However, these near-perfect values must be interpreted with caution. The evaluation was performed on a clean, balanced benchmark dataset, which may not fully reflect the unpredictable environmental noise of active fish ponds. When compared to prior research, the accuracy achieved in this study (92.92%) aligns closely with the performance of heavier architectures reported in literature. For instance, traditional deep models often struggle with high parameter bulkiness when deployed in real-time environments. However, a major limitation of the current study is the reliance on curated digital imagery. In a real-world aquaculture environment, factors such as water turbidity, varying camera angles, and inconsistent outdoor lighting could severely degrade the model's feature extraction capability. Furthermore, this study lack actual field validation, meaning that the practical feasibility of this framework remains localized to the dataset scope. Therefore, while this efficient deep learning framework shows strong potential for deployment on resource-constrained devices, its actual performance in live mobile-based aquaculture diagnostics is still a theoretical possibility that requires real-time on-site validation in future works.

CONLUSION?

This study successfully addresses the critical need for automated aquaculture diagnostics. The optimized MobileNetV3Large Deep Learning architecture was effectively implemented to classify eight distinct fish conditions. By applying a precise 70-layer fine-tuning strategy, the model successfully captured subtle biological anomalies. The system achieved a remarkable test accuracy of 92.92%. It also recorded a low loss value of 0.2099. Furthermore, the model demonstrated exceptional discrimination capacity with an average AUC of 1.00. This high sensitivity is vital for early disease detection. The architectural efficiency of MobileNetV3Large minimizes computational and memory footprints. Consequently, this system offers a standalone, high-performance solution for edge computing. Future work will focus on embedding this model into a real-time mobile application. This deployment will directly assist fish farmers with fast on-site diagnoses.

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