



A Deep Convolutional Neural Network for Multi-class Fish Disease Classification using VGGNet-19 Architecture

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ABSTRACT

Background: Accurate fish disease identification is important for ecological research, biodiversity monitoring and conservation. Traditional methods are time-consuming and error-prone. Deep learning provides an automated solution for species classification using image data. Fish disease classification using image-based recognition is an emerging research area, critical for the aquaculture industry. Accurate disease detection is essential for preventing outbreaks, minimizing economic losses and ensuring fish health.

Methods: This study employs the VGGNet-19 architecture to detect fish diseases. The dataset, sourced from Kaggle, contains images of fish affected by various diseases. Images are pre-processed with resizing, normalization and data augmentation techniques, including random flipping, rotation and zoom. The model is trained with an 80%-10%-10% split for training, validation and testing. Performance is evaluated using accuracy, a confusion matrix, a classification report and ROC curves.

Result: The custom model achieved an overall accuracy of 90.96%. It performed well across most disease categories, correctly distinguishing between healthy and infected fish. Some misclassifications were observed between similar diseases, indicating areas for improvement. Despite these challenges, the results demonstrate the effectiveness of deep learning for fish disease classification.

Key words: Aquaculture sustainability, Convolutional neural networks (Cnns), Image-based recognition, Pathogen detection, VGGNet-19 model.

INTRODUCTION

In recent years, global aquaculture production has witnessed significant growth, reaching a record 130.9 million tonnes in 2022, with 94.4 million tonnes consisting of aquatic animals (FAO, 2023). Asia continues to dominate the sector, contributing 91.4% of total production, followed by the Americas (3.5%), Europe (2.8%), Africa (1.9%) and Oceania (0.2%) (WAS, 2023). Furthermore, global fish production increased to 186.6 million metric tons in 2023, reflecting the rising demand for fish and seafood products worldwide (Statista, 2024). This growth highlights the increasing need for effective fish disease detection and management strategies to sustain industry expansion and reduce economic losses.

Fish farming contributes an important part of global food production and provides a substantial source of protein to millions of people worldwide. Due to the rising global demand for protein, fish farming has seen rapid growth. Fish consumption is a vital dietary source of protein, supplying essential nutrients to billions of people globally. In fact, global fish consumption per capita has increased from 9.0 kg in 1961 to 20.2 kg in 2015 and further up to 22.8 kg by 2020 (Coppola *et al.*, 2021). This surge has led to significant advances in aquaculture technologies, enabling increased fish production to meet the growing demand. In 2020, the total annual production of fish and seafood was around 200 million tonnes, including both wild fish catch and farmed fish (FAO, 2020). Over the past two decades, aquaculture production has far outpaced the

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capture fisheries sector, further emphasizing the sector's importance in global food security (Datasource - OurWorldInData.org/fish-and-overfishing).

However, maintaining the health of farmed fish remains a complex and challenging task. Fish diseases can lead to large-scale losses. According to estimates, 20-25% of global fish production is wasted due to factors such as disease outbreaks, delayed transportation and other industrial obstructions (Begum *et al.*, 2024; Zhang *et al.*, 2024). Diseases in fish are particularly concerning in farmed environments, as the confined and contained nature of aquaculture facilitates the rapid spread of pathogens,

much faster than in wild fish populations (Sven *et al.*, 2021).

Traditional methods are time-consuming and prone to human error. As fish farming expands, there is an increasing need for more efficient and automated methods of disease detection and classification. One promising method is the application of artificial intelligence (AI), particularly deep learning techniques such as Convolutional Neural Networks (CNNs). CNNs have demonstrated exceptional performance in various image-based classification tasks, including medical diagnostics and plant disease recognition. Despite their success in other fields, the application of CNNs to fish disease classification has not been extensively explored, presenting an opportunity to improve fish health monitoring systems (AlZubi, 2023, Bagga *et al.*, 2024; Cho, 2024; Hai and Duong, 2024; Maltare *et al.*, 2023).

Islam *et al.* (2024) reviewed modern technologies for managing fish diseases in aquaculture. They highlighted the critical need for early detection of infectious agents such as bacteria and parasites. High-density aquaculture settings accelerated disease spread and could cause up to 100% mortality if untreated. Technologies like IoT sensors, AI and machine learning offer proactive monitoring and early pathogen detection. This approach allowed farmers to address potential outbreaks before they occurred. Vasumathi *et al.* (2024) highlighted the efforts of the Fish4Knowledge project, which created a large library of fish images and videos for training CNN models. A major challenge in this development was the wide variety of fish appearances. These variations depended on factors such as species, age and health. The differences in size, shape, color and pattern made it difficult for AI algorithms to accurately distinguish between healthy and diseased fish. Jiang *et al.* (2024) conducted a study on fish disease detection using big data and deep learning. The researchers collected and labeled data and then extracted key features related to fish diseases. They improved the traditional detection model by incorporating the Akconv network structure and the SimAM attention module into the YOLOv6 model. Experiments showed that the enhanced YOLOv6 model outperformed the original, with an increase in its mean average precision (mAP) by 1.8 percentage points.

Isaac *et al.* (2024) proposed five deep learning models (CNN, DenseNet121, ViT, VGG16 and VGG19) for fish disease detection, evaluating their performance using accuracy. The dataset underwent preprocessing, including resizing, normalization and augmentation, to balance classes. The models were trained and evaluated, with deep transfer learning applied to improve generalization. Nguyen *et al.* (2024) used MobileNet models to automate fish disease classification, aiming to reduce costs and time in aquaculture. The models were trained on the SalmonScan dataset, with MobileNetV1 achieving accuracies of 96.30% and 95.47% with and without data augmentation. The study showed that MobileNet could autonomously learn disease

features, eliminating the need for manual feature extraction and offered more efficient disease detection compared to traditional methods.

This paper proposes a solution to the problem by applying a custom version of the VGGNet-19 architecture to classify fish diseases from image data. VGGNet-19, originally developed for large-scale image classification tasks, has proven to be highly effective in learning rich hierarchical features from images. By customizing and fine-tuning this architecture for the specific application, high classification accuracy is achieved on a diverse dataset of fish images that can improve fish health management systems.

MATERIALS AND METHODS

The model is developed in an Anaconda environment using Jupyter Notebook, with training conducted on a system with 16 GB RAM, Python v3.11 and a TPU-v3:8 setup. The TPU is optimized for machine learning tasks and is supported by TensorFlow. Keras, a high-level neural network API, operates on top of TensorFlow, enabling efficient computation with the 8-core TPU for faster machine learning processing.

Dataset collection

This study utilizes an open-source dataset to develop a fish disease detection model using VGGNet-19-CNN. The dataset includes images of fish affected by seven conditions, categorized into bacterial (Aeromoniasis, Bacterial Gill Disease, Bacterial Red Disease), fungal (Saprolegniasis), parasitic (Parasitic Disease) and viral (White Spot Disease) infections, along with a healthy fish class. Each category contains 250 images, ensuring a balanced dataset for training and evaluation. The dataset was obtained from a publicly available repository on Kaggle (<https://www.kaggle.com/datasets/subirbiswas19/freshwater-fish-disease-aquaculture-in-south-asia?select=SB-FishDisease>) and collected from various sources, including a university agricultural department, an agricultural farm in Odisha, India and agricultural website portals. To ensure effective model training and evaluation, the dataset was divided into three subsets: 80% for training, 10% for validation and 10% for testing. This division was performed using the train-test-split function from the sklearn model selection library, ensuring a fair and randomized distribution across all categories.

Data preprocessing and augmentation

To improve model generalization and avoid overfitting, several preprocessing and augmentation techniques were applied to the dataset. First, image resizing was done to ensure all images had the same dimensions. The VGGNet-19 model requires input images of size 224×224 pixels, so all images in the dataset were resized to match this requirement. This step ensures that the model receives uniform input, which is essential for efficient training.

Next, pixel normalization was applied. The pixel values of each image were scaled to a range of [0, 1]. To further enhance the dataset, data augmentation techniques were used. These techniques artificially increase the size of the training set and make the model more robust. Random rotation was applied to simulate different orientations of the fish. This helps the model recognize diseases from various angles. Horizontal flipping was also used to create mirror images, which accounts for variations in fish orientation. Additionally, random zoom was used to simulate varying distances, allowing the model to focus on different areas of the fish. Random shearing and shifting were applied to introduce slight distortions, increasing the diversity of the training images. These augmentation techniques helped prevent overfitting by providing the model with more varied data and improved its ability to generalize to new, unseen images.

VGGNet-19 Architecture

VGGNet-19 is a deep convolutional neural network (CNN) known for its simplicity and effectiveness in image classification. It consists of 19 layers, including 16 convolutional layers, 3 fully connected layers and 5 max-pooling layers (Fig 1). VGGNet-19 uses 3×3 convolutional filters, which allow the model to capture fine-grained features in the images. The hyperparameters used for modeling are summarized in Table 1.

The model accepts input images of size 224×224×3. This means the input is 224 pixels in height and width, with 3 color channels (RGB). The network has several convolutional blocks, each containing two or three convolutional layers followed by max-pooling layers. These blocks help the model learn hierarchical features, from basic edges to more complex patterns. The convolution operation can be represented mathematically as

$$Y[i,j,k] = \sum_m \sum_n x[i+m, j+n, k] \cdot w[m, n, k]$$

Where,

x = Input image.

w = Convolutional kernel.

y = Resulting feature map.

Max-pooling reduces the spatial dimensions of the feature maps. The operation can be written as

$$Y[i, j, k] = \max_{m,n} x[i+m, j+n, k]$$

After convolutional and pooling layers, the model has two fully connected layers, each with 4096 neurons. These layers help the network make final predictions. The activation function used in the fully connected layers is ReLU.

$$\text{ReLU}(x) = \max(0, x)$$

The final layer is a softmax layer with 7 units, one for each disease category. The softmax function converts the network's output into probabilities.

$$\text{Softmax}(z_i) = \frac{e^{z_i}}{\sum_j e^{z_j}}$$

Where,

z_i = Raw score for class.

i = The softmax function normalizes these scores into a probability distribution.

Dropout is applied to the fully connected layers to prevent overfitting. It randomly disables a fraction of neurons during training. The dropout operation can be expressed as

$$y = x \cdot \text{mask}$$

The model was trained using the Adam optimizer, which is effective for training deep networks. The learning rate was set to 0.0001 to ensure stable convergence. The Adam optimizer updates parameters using

$$\theta_t = \theta_{t-1} - \eta \cdot \frac{m_t}{\sqrt{v_t + \epsilon}}$$

Where,

θ = Parameter at time t.

η = Learning rate.

m_t = First moment estimate.

v_t = Second moment estimate.

The loss function used was Categorical Cross-Entropy. This is appropriate for multi-class classification problems. The formula for categorical cross-entropy is

$$L = - \sum_{i=1}^C y_i \log(y_i)$$

Where,

C = Number of classes.

y_i = True label for class.

i and w_i = Predicted probability for class i.

The model was trained for 100 epochs with early stopping to avoid overfitting. Early stopping halts training if the model's performance on the validation set does not improve after a set number of epochs. The training process used a batch size of 32 images per iteration. This batch size was chosen to balance training speed and model performance. Model checkpoints were saved during training based on the highest validation accuracy. This ensured that the best-performing model was retained. The model's performance was evaluated using the following metrics.

$$\text{Accuracy} = \frac{\text{Number of correct predictions}}{\text{Total number of prediction}}$$

$$\text{Precision percentage (P\%)} = \frac{\text{TP}}{\text{FP} + \text{TP}} \times 100$$

$$\text{Recall percentage (R\%)} = \frac{\text{TP}}{\text{FP} + \text{TP}} \times 100$$

RESULTS AND DISCUSSION

In this part, the results obtained from VGGNet19 model are presented in detail. The training and validation metrics were evaluated for 100 epochs and shown in Fig 2. The VGGNet19 model shows improvement over the 100 epochs, with both training and validation losses steadily decreasing. The training loss starts at 1.8844 and drops to 0.0011 by the end, indicating effective learning on the training data. Similarly, the validation loss decreases but stabilizes around 0.1-0.2 after epoch 60, suggesting the model is not generalizing as well to unseen data. Training accuracy steadily increases from 0.3776 to 0.9964, reflecting better performance on the training set. However, validation accuracy plateaus around 0.93-0.95, indicating that the model's ability to generalize has limitations. The gap between training and validation accuracy points to potential overfitting, where the model fits the training data well but struggles to generalize to the validation set. Despite these fluctuations, the overall trends suggest that with further adjustments, such as regularization, the model's generalization could improve.

The confusion matrix provides useful insights into the model's performance (Fig 3). It shows both true positives (diagonal values) and misclassifications (off-diagonal values). The model performs well for most diseases. For example,

Healthy is correctly classified 24 out of 25 times with only one misclassification to Gill disease. Gill disease is correctly identified in 26 out of 28 instances with two misclassifications. Red disease is correctly classified 25 times, but there are some misclassifications for Aeromoniasis and Saprolegniasis. Aeromoniasis is correctly classified 23 times with minor errors to Saprolegniasis and Healthy.

Some diseases are more challenging. White spot disease has three misclassifications, while Parasitic disease is confused with Red disease and Gill disease. These errors likely occur due to similarities in symptoms. The diagonal values are much higher than the off-diagonal values, showing that the model is generally accurate. However, misclassifications still occur, particularly between diseases with overlapping symptoms. The heatmap presented in Fig 3 highlights the model's strengths and areas that need improvement.

The model performance outputs are summarized in Table 2. The VGGNet19 model performs well across most disease categories. It achieves high precision and recall for Healthy, with an F1 score of 0.9410. Aeromoniasis has the highest precision at 0.9580, but its recall is 0.8850, meaning some cases are missed. Gill disease has good recall at 0.9290, but its precision is 0.8670, leading to some false positives. Saprolegniasis performs well with an F1

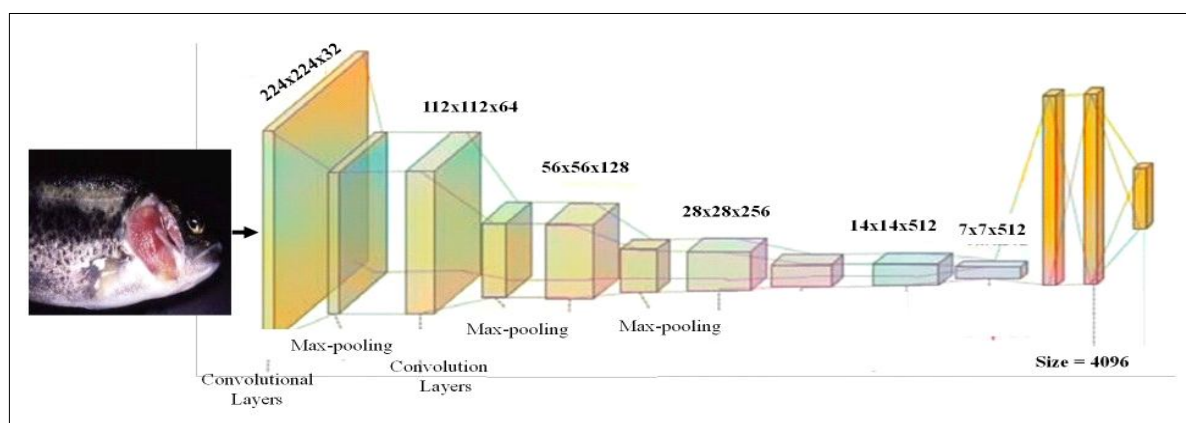


Fig 1: VGGNet-19 modal.

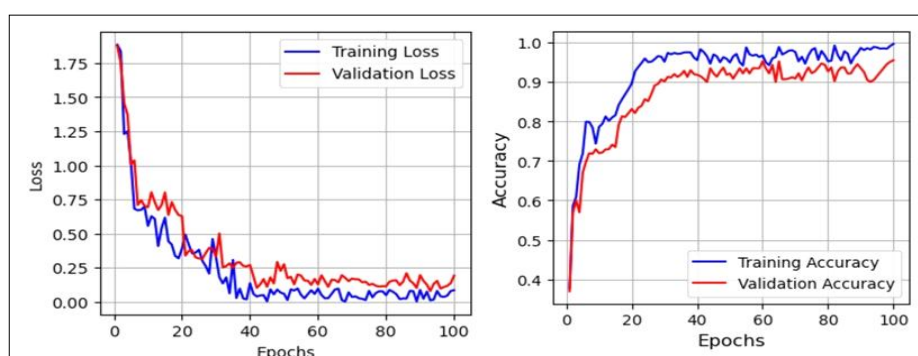


Fig 2: Training and validation outcomes as a function of epochs.

score of 0.8800, but its precision is slightly lower at 0.8460. Parasitic disease has a balanced precision of 0.9570 and recall of 0.9170, with an F1 score of 0.9360. White spot disease shows strong precision (0.9500), but its recall is lower at 0.8640, resulting in missed cases. The overall accuracy of the model is 90.96%. The macro averages for precision, recall and F1 score are around 0.91. The weighted averages are slightly higher due to class distribution. Overall, the model performs well, but misclassifications

still occur. Fine-tuning could improve accuracy, especially for categories like White spot disease.

The ROC AUC scores show different levels of performance across disease categories (Fig 4). The model performs well with Red disease, achieving an AUC of 0.86. Aeromoniasis has an AUC of 0.89, indicating strong classification. Gill disease and Healthy both have excellent AUC scores of 0.91, showing high accuracy. Saprolegniasis has a lower AUC of 0.71, indicating difficulty in distinguishing

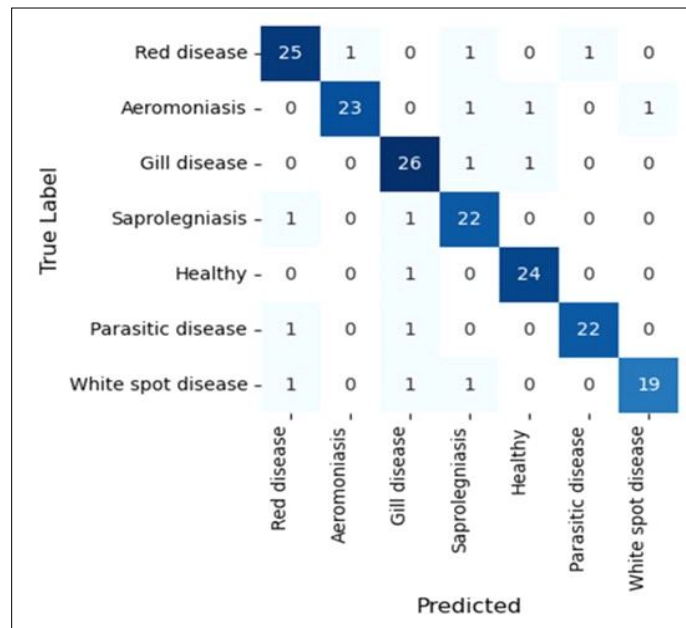


Fig 3: Confusion matrix.

Table 1: summarizes the hyperparameters used in the VGGNet-19 model.

Layer type	Details
Input layer	224×224×3 (Height × Width × Channels)
Convolutional layers	16 convolutional layers, each with 3×3 kernels and ReLU activation
Max-pooling layers	5 max-pooling layers with 2×2 kernel size and stride 2
Fully connected layers	2 layers with 4096 neurons each
Output layer	Softmax layer with 7 units (one for each disease category)
Dropout	0.5 dropout rate applied after fully connected layers

Table 2: Classification matrices.

Class	Precision	Recall	F1 Score	Support
Red disease	0.8930	0.8930	0.8930	28
Aeromoniasis	0.9580	0.8850	0.9200	26
Gill disease	0.8670	0.9290	0.8970	28
Saprolegniasis	0.8460	0.9170	0.8800	24
Healthy	0.9230	0.9600	0.9410	25
Parasitic disease	0.9570	0.9170	0.9360	24
White spot disease	0.9500	0.8640	0.9050	22
Overall accuracy	-	-	0.9096	
macro avg.	0.9130	0.9090	0.9100	177
weighted avg.	0.9120	0.9100	0.9100	177

it from other diseases. Parasitic disease performs reasonably well with an AUC of 0.82. White spot disease has the lowest AUC at 0.67, suggesting the model struggles with this class. Overall, the model is effective for most diseases but needs improvement for Saprolegniasis and White spot disease.

The results obtained from the VGGNet19 model indicate strong classification performance for fish disease detection, with an overall accuracy of 90.96%. The model effectively learns from training data, as shown by the decreasing loss and increasing accuracy over 100 epochs. However, the observed gap between training and validation accuracy suggests potential overfitting. While the training accuracy reaches 99.64%, the validation accuracy stabilizes around 93-95%, indicating that the model struggles with generalization to unseen data. This highlights the need for additional regularization techniques, such as dropout layers or data augmentation, to enhance robustness.

The confusion matrix analysis reveals that most disease classes are correctly classified with high precision and recall. Notably, Healthy samples are accurately identified 96% of the time and Aeromoniasis achieves the highest precision at 95.8%. However, certain disease classes, such as White spot disease and Saprolegniasis, present challenges, as evidenced by their relatively lower recall values of 86.4% and 71%, respectively. These misclassifications likely arise due to visual similarities between disease symptoms, suggesting the need for more discriminative features or the inclusion of additional training samples for these classes.

Despite the overall strong classification performance, some diseases are misclassified more frequently than others. White spot disease, for instance, is often confused with Parasitic disease and Gill disease. This may be due

to overlapping visual symptoms in infected fish. Similarly, Saprolegniasis exhibits a lower AUC score of 0.71, indicating difficulty in distinguishing it from other infections. The model's limitations in these areas suggest that additional feature extraction techniques, such as attention mechanisms or ensemble learning, could help improve classification accuracy for the more challenging disease categories.

The ROC-AUC analysis further supports these findings, showing that most diseases have AUC scores above 0.80, indicating strong classification ability. However, White spot disease has the lowest AUC (0.67), demonstrating the need for improvement in detecting this particular condition. The imbalance in disease recognition performance suggests that additional data preprocessing, such as synthetic data generation or class-balancing techniques, could help mitigate these issues.

Future improvements to the model could involve hyperparameter tuning, employing more advanced architectures such as transformer-based models and leveraging domain-specific augmentation techniques to enhance generalization. Additionally, integrating multi-modal data, such as water quality parameters and behavioral analysis, may further refine disease classification accuracy.

The comparison of results obtained in the presented study highlights the importance of the proposed model. Maruf *et al.* (2024) focused on classifying freshwater fish diseases in Bangladesh using deep learning techniques. The authors proposed two ensemble models: A baseline Averaged Ensemble (AE) model and a novel Performance Metric-Infused Weighted Ensemble (PMIWE) model. The study achieved a testing accuracy of 97.53%, with precision, recall and F1-score all at 97%. To enhance the interpretability and trustworthiness of the model, the authors employed Grad-CAM (Gradient-weighted Class Activation Mapping), an explainable artificial intelligence (XAI) technique. Azhar *et al.* (2024) focused on detecting Protozoan white spot disease, caused by *Cryptocaryon irritans* in saltwater fish, using an intelligent system based on a Convolutional Neural Network (CNN). The study used GoogleNet, a deep learning algorithm, to identify infected fish from raw underwater images. The model achieved an accuracy of 90%, offering a promising solution for early screening of this contagious disease.

Mia *et al.* (2022) aimed to improve fish disease recognition to help remote farmers manage their farms. They developed expert systems using smartphone images for disease identification. A segmentation algorithm is selected to distinguish healthy and diseased areas. In this work, eight classification algorithms are tested and achieved a remarkable accuracy of 88.87% with the Random Forest algorithm. Ahmed *et al.* (2021) conducted a study on fish disease detection using image-based ML techniques in aquaculture. The research had two main phases. The first phase involved image pre-processing and segmentation to reduce noise and enhance image

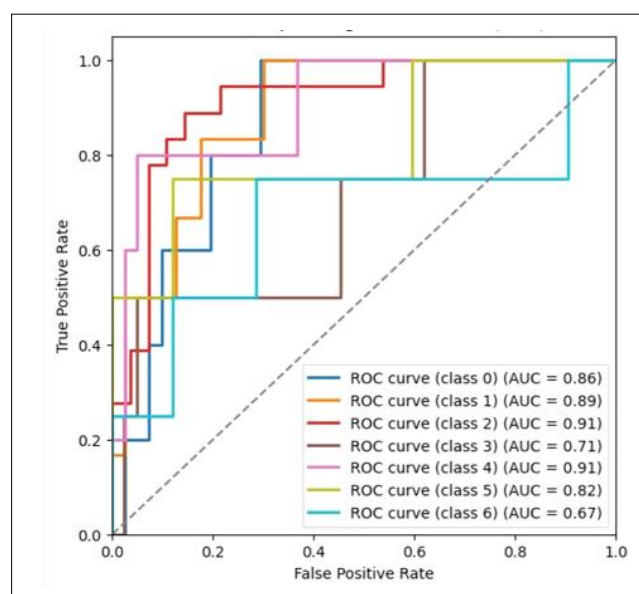


Fig 4: ROC-AUC curve.

quality. The second phase focused on feature extraction for disease classification using a Support Vector Machine (SVM) algorithm with a kernel function. The processed images were tested on a salmon fish dataset, both with and without image augmentation. The SVM model achieved accuracies of 91.42% with augmentation and 94.12% without augmentation, demonstrating its effectiveness in fish disease detection.

In summary, the VGGNet19 model demonstrates high accuracy in fish disease detection, with promising classification performance for most disease categories. However, challenges remain in classifying visually similar diseases, particularly White spot disease and Saprolegniasis. Addressing these limitations through advanced model optimization techniques could further enhance disease detection capabilities and improve practical applicability in aquaculture health monitoring systems.

CONCLUSION

This study proposed a fish disease detection approach using VGGNet-19, achieving 90.96% accuracy across seven disease categories. While the model performed well, it struggled with White Spot and Saprolegniasis, requiring further fine-tuning. The dataset provides a structured representation of specific diseases but does not cover all fish diseases. The flexible VGGNet-19 architecture allows for expansion with more labeled data. Future work will enhance accuracy by exploring ResNet and Inception architectures, using synthetic data and integrating explainable AI. This approach can benefit commercial aquaculture by enabling faster, more accurate disease detection, improving fish health management and reducing economic losses.

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Authors' contributions

All authors contributed toward data analysis, drafting and revising the paper and agreed to be responsible for all the aspects of this work.

Data availability

The data analysed/generated in the present study will be made available from corresponding authors upon reasonable request.

Use of artificial intelligence

Not applicable.

Declarations

Authors declare that all works are original and this manuscript has not been published in any other journal.

Conflict of Interest

Authors declare that they have no conflict of interest.

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