



# Implementing ResNet for Early Detection and Classification of Fish Skin Diseases

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## ABSTRACT

**Background:** Fish diseases pose significant challenges in aquaculture, impacting health and productivity. Timely detection is important for effective management. This study explores the application of a ResNet-20 deep-learning model for classifying various fish skin diseases.

**Methods:** We utilized a dataset sourced from Kaggle, comprising 442 images categorized into seven groups: healthy fish and six disease types. To improve variety, images were scaled up to 224 × 224 pixels. Training (70%), validation (15%) and testing (15%) sets make up the dataset partition.

**Result:** The overall accuracy of the model was 82.35%. Strong performance was shown by classification metrics, especially for healthy fish and Aeromoniasis. For the majority of disease categories, AUC values above 0.9 were found using ROC curves, indicating effective classification. The ResNet-20 model effectively detects fish diseases, showcasing the potential of deep learning in aquaculture applications. This research provides insights into the strengths and limitations of the model. Future work should focus on expanding the dataset and exploring additional neural network architectures to enhance accuracy and generalization.

**Key words:** Aquaculture, Diseases detection, Fish diseases, Skin diseases.

## INTRODUCTION

Aquaculture farming is important for meeting the growing demand for seafood and supporting the livelihoods of millions of people around the world (FAO, 2023). Moreover, the socio-economic impacts of aquaculture are important as well. While it can create jobs, it may also displace local communities and interfere with traditional fishing practices. Aquaculture production has grown rapidly in recent years. In 2022, it reached 130.9 million tonnes, with 94.4 million tonnes consisting of aquatic animals (FAO, 2023). Asia remains the leading producer, accounting for 91.4% of total output. Other regions contribute significantly less: the Americas (3.5%), Europe (2.8%), Africa (1.9%) and Oceania (0.2%) (WAS, 2023).

Fish production continued to rise, reaching 186.6 million metric tons in 2023 (Statista, 2024). This increase reflects the growing global demand for fish and seafood products. It is essential to balance the benefits of aquaculture with its environmental and social costs to ensure sustainability (Ahmed *et al.*, 2021). However, rapid expansion poses challenges, particularly in disease control. Effective fish disease detection and management strategies are essential to sustain industry growth and minimize economic losses.

Fish are significantly threatened by diseases in both natural environments and aquaculture settings. They are often seen as one of the biggest challenges to the success of fish farming. Various infectious organisms, including bacteria, viruses and parasites, are responsible for these diseases (Hasan *et al.*, 2022; AlZubi, 2023; Bagga *et al.*, 2024; Cho, 2024; Hai and Duong, 2024; Maltare *et al.*, 2023). Among these, bacteria are the leading cause of most

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diseases found in farmed fish. In addition, in aquaculture, infectious diseases pose a serious risk due to the high density of fish in confined spaces. When fish are crowded together, it creates an environment that allows diseases to spread rapidly. Stress from overcrowding can weaken the fish's immune systems, making them more susceptible to infections. Additionally, poor water circulation can further facilitate the spread of pathogens among the fish populations (Li *et al.*, 2024; Koike *et al.*, 2023). This combination of factors makes it challenging to maintain healthy fish stocks in aquaculture. Chakravorty (2020) explored DL approach for detecting fish diseases using augmented

reality (AR) and image processing. The study focused on early identification of diseases to prevent their spread, addressing the limitations of existing image processing techniques. Traditional methods do not allow for on-the-spot disease comparison. The proposed AR model enables real-time identification of diseased fish. Images captured using the AR model were processed using HSV operations to enhance accuracy in detecting diseased areas. Li *et al.* (2023) tackled the issue of fish detection under occlusion. They developed a dataset specifically for occluded fish and enhanced the You Only Look Once version 8 (YOLOv8) model. The modified YOLOv8 achieved a mean Average Precision (mAP) of 0.971 on the occlusion dataset, compared to 0.912 for the original YOLOv8. Cunningham (2002) reviewed molecular diagnostic methods for fish and shellfish diseases under European Commission regulations. The research highlighted the ability to identify pathogenic species and discriminate between strains, suggesting that controlling specific pathogenic strains might be more effective than targeting entire groups. Nayan *et al.* (2021) studied early detection of fish diseases by analyzing water quality. They highlighted that changes in factors like pH and oxygen levels can lead to fish health problems. The researchers used machine learning algorithms to predict when water quality might worsen, helping farmers take action before diseases spread. Their experiments showed that the machine learning model accurately detected fish diseases based on real water quality data. Qin *et al.* (2021) aimed to develop an effective method for rapid detection and classification of water states in aquaculture. They created a dataset with four water categories and derived corresponding Hough datasets using the Hough transform. The study compared the performance and spatio-temporal complexity of 12 popular convolutional neural network models for classifying water state images. The results showed that the InceptionResNet model performed the best, while the InceptionV3 model exhibited the lowest spatio-temporal complexity. Both models effectively achieved water state classification. Despite advancements in aquaculture disease detection, gaps still exist. There is a need for better integration of technologies and long-term impact studies. Holistic disease management approaches are lacking. Field validation of techniques and standardized datasets are also essential. More research on diverse aquaculture systems would enhance sustainability and effectiveness.

This work addresses these gaps by using the ResNet-20 architecture on a diverse dataset of fish diseases. This study highlights the potential of deep learning in practical aquaculture settings.

## MATERIALS AND METHODS

### Dataset description

The dataset was sourced from a publicly accessible repository on Kaggle and compiled from various reliable sources. These sources include contributions from a

university agricultural department, an agricultural farm in Odisha, India and multiple agricultural websites. The diverse origins of the dataset ensure a wide range of image variations, contributing to the robustness of the model. The dataset is available on Kaggle (Biswas, 2024). The dataset comprises images depicting fish affected by seven distinct health conditions, encompassing bacterial, fungal, parasitic and viral infections. Specifically, the bacterial infections included in the dataset are Aeromoniasis, Bacterial Gill Disease and Bacterial Red Disease. The fungal infection category consists of Saprolegniasis, while the parasitic infection is represented by Parasitic Disease.

White spot disease can affect both fish and shrimp, but the causative agents are different. In this study, we refer specifically to white spot disease in fish, which is caused by *Ichthyophthirius multifiliis*, a ciliate parasite. This is distinct from the white spot syndrome virus (WSSV) that affects cultured shrimp.

The dataset also includes images of fish affected by the viral infection White Spot Disease. Additionally, a separate class representing healthy fish is incorporated to ensure a comprehensive classification system. Each condition in the dataset contains 250 images, resulting in a well-balanced dataset with an equal representation of different disease categories. Fig 1 presents a few examples of diseased fish from this dataset. This diverse collection of images is invaluable for training and evaluating the RESNET20-CNN algorithm. It enables precise disease detection in aquaculture, which is important for maintaining fish health.

### Data preprocessing

The experimental setup featured an 11th Gen Intel® Core™ i5-11320H processor at 3.20 GHz and 16.0 GB of RAM running on Windows 11 Home Single Language, Version 23H2. The images are resized to a uniform dimension of 224 × 224 pixels. This standardization ensures consistent input for the model. Additionally, images are converted to RGB format to meet the model's requirements. Invalid images, such as unreadable ones or those in the wrong format, are removed using exception handling. This process maintains a high-quality dataset, which is essential for effective model training and evaluation.

This study used the ResNet-20 model to classify fish diseases. This deep learning architecture is known for efficient feature extraction and classification (He *et al.*, 2015). The model was implemented in Python. All tools and frameworks, including TensorFlow and PyTorch, are open-source, ensuring reproducibility and transparency (Abadi *et al.*, 2016; Paszke *et al.*, 2019).

For this proposed study, the images were divided into three parts using a 70:15:15 ratio. Data augmentation techniques are applied using Tensor Flow. These include random horizontal flips, rotations at various angles and zooms. This creates diverse variations of the original image. A vertically flipped version of the image is also

generated. These augmentations increase the dataset's diversity. This, in turn, improves model robustness and performance. Finally, the original, augmented and vertically flipped images are visualized side by side in Fig 2.

### Model architecture

The ResNet-20 model consists of several residual blocks that enhance feature learning through skip connections (Fig 3). Each block includes two convolutional layers, batch normalization and ReLU activation. The output of these layers is added to the input, allowing gradients to flow more easily during training. This structure helps to prevent the

vanishing gradient problem, enabling deeper networks to learn effectively. The architecture starts with a convolutional layer that reduces input dimensions. It is followed by multiple residual blocks where the number of filters increases as the network deepens. This design allows the model to capture more complex features. After processing through the residual blocks, global average pooling reduces the spatial dimensions. A fully connected layer with dropout follows to prevent overfitting. Finally, the output layer uses a softmax activation function to generate class probabilities. The hyperparameters used for training are summarized in Table 1.

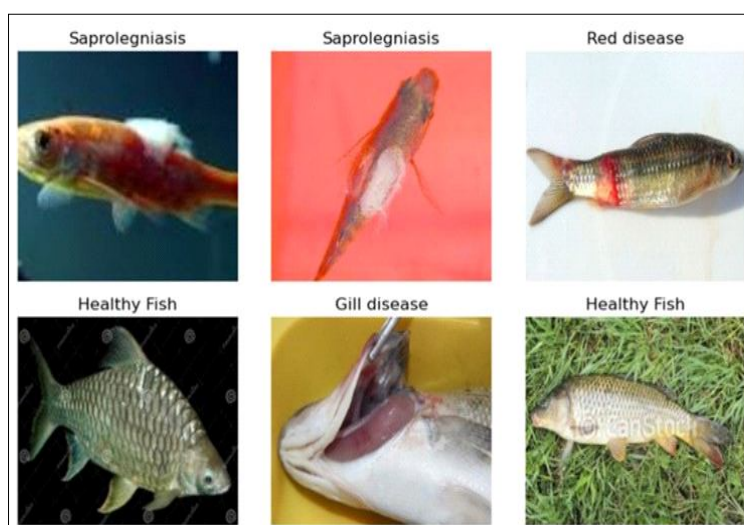


Fig 1: A sample of images from dataset.

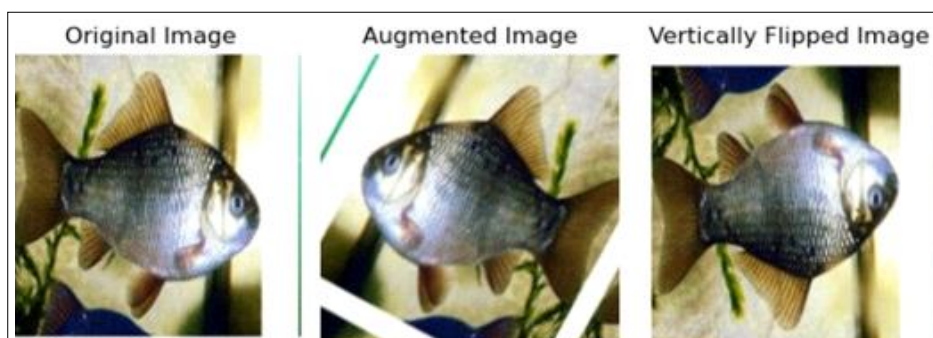


Fig 2: Augmentation of images to increase dataset.

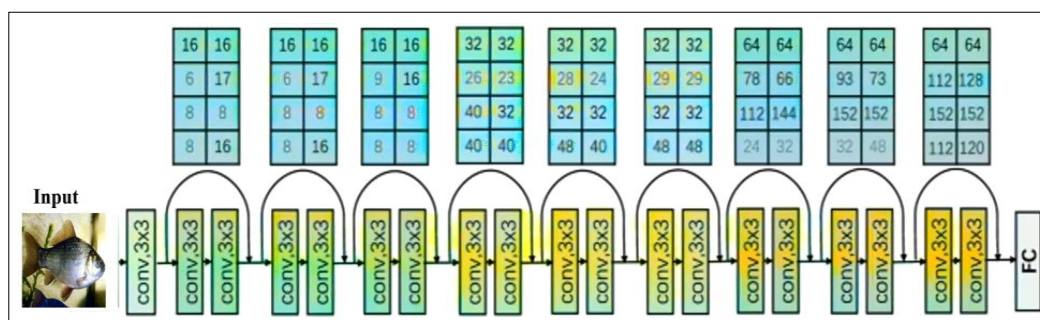


Fig 3: Architecture of RESNET20.

Mathematically, the model's operations can be described in several steps that highlight its structure and function. The convolution operation is defined as follows:

$$\text{Conv}(x) = \text{ReLU} [\text{BatchNorm Conv2D}(x, \text{filters}, \text{kernel Size})]$$

This operation applies a convolutional layer to the input  $x$ , followed by batch normalization to stabilize learning and a ReLU activation function to introduce non-linearity. In a residual block, the output is computed as:

$$\text{Output} = \text{ReLU} [F(x) + x]$$

Where,

$F(x)$  = Two convolutional layers.

This design allows the network to learn residual mappings, which help to preserve important information as it propagates through the layers. The global average pooling operation is given by:

$$\text{GAP}(x) = \frac{1}{H \times W} \sum_{i=1}^H \sum_{j=1}^W x_{i,j}$$

This step reduces the feature map to a single vector, summarizing the spatial information. Finally, the model generates its output using the formula:

$$\text{Output} = \text{Softmax}[W \cdot \text{GAP}(x) + b]$$

Where,

$W$  = Weight matrix that connects the pooled features to the output classes.

$b$  = Bias term.

The softmax function ensures that the output is a probability distribution across the different classes, making it suitable for classification tasks. This mathematical framework underpins the effectiveness of the ResNet-20 architecture in capturing complex patterns in the data. The training process uses categorical cross-entropy loss, optimized with the Adam optimizer. Callbacks like model checkpoints ensure that the best model based on validation accuracy is saved during training. This architecture is designed for effective classification tasks, leveraging the advantages of deep residual networks.

**Table 1:** Hyperparameters used for training.

Hyperparameter	Value
Input shape	(224, 224, 3)
Number of classes	7
Initial filters	16
Filter sizes	(3, 3)
Dropout rate	0.5
Learning rate	0.0001
Batch size	32
Epochs	100
Data augmentation	Yes
Activation function	ReLU
Loss function	Categorical crossentropy

## Evaluation matrices

The performance of the model was assessed using the test dataset to measure its accuracy. Predictions were made and a confusion matrix along with classification reports were generated to analyze the results. Key performance metrics, including accuracy, precision, recall, F1-score and Matthews correlation coefficient (MCC), were calculated using the following formulas:

$$\text{Accuracy} = \frac{TP + TN}{TP + TN + FP + FN}$$

$$\text{Precision (P)} = \frac{TP}{TP + FP}$$

$$\text{Recall (R)} = \frac{TP}{TP + FN}$$

$$\text{F1 - score} = 2 \cdot \frac{P \cdot R}{P + R}$$

$$\text{MCC} = \frac{TP \cdot TN - FP \cdot FN}{\sqrt{(TP + FP)(TP + FN)(TN + FP)(TN + FN)}}$$

Additionally, Receiver Operating Characteristic (ROC) curves were plotted for each class and the Area Under the Curve (AUC) was calculated using the equation:

$$\text{AUC} = \int_0^1 \text{TPR}(\text{FPR}) d\text{FPR}$$

In this equation, TPR represents the True Positive Rate and FPR represents the False Positive Rate.

## RESULTS AND DISCUSSION

The model's performance was evaluated over 100 epochs by examining accuracy and loss metrics (Fig 4). Training accuracy began at around 24.1% in the first epoch and increased to about 96.5% by the end. This shows effective learning. Validation accuracy started at approximately 21.7% and peaked at 99.3%, with some fluctuations in later epochs. This indicates that the model learned well but occasionally struggled to generalize.

Training loss decreased consistently from about 1.52 in the first epoch to around 0.16 by the end. This indicates good fitting to the training data. In contrast, validation loss began at approximately 1.96, decreased initially, but became unstable later, peaking around 0.97. Monitoring both training and validation metrics is important. It ensures that the model performs effectively on unseen data and retains the training data.

The model's classification performance for seven fish disease classes is revealed by the confusion matrix (Fig 5). The projected class is displayed in each column, while the actual class is represented in each row. Proper predictions are indicated by the diagonal elements. For example, Red disease has 10 correct predictions, but 2 were misclassified



as Healthy. For Aeromoniasis, there were 12 correct predictions and 2 misclassifications as Gill disease. Gill disease shows 15 correct predictions, with 3 misclassified as Aeromoniasis and 1 as Healthy. The Healthy class had 25 correct predictions and no misclassifications, indicating strong performance in identifying healthy fish. However, Saprolegniasis had 5 misclassifications, suggesting challenges in accurate identification. Parasitic diseases had 11 correct predictions, with 2 misclassified as Healthy.

Lastly, White spot disease showed 13 correct predictions, with 5 misclassifications as Healthy and 1 as Aeromoniasis.

The classification metrics offer key insights into the model's performance for different fish diseases (Table 2). Precision indicates the accuracy of positive predictions. Red Disease and Parasitic Disease achieved perfect precision at 1.0000. In contrast, Healthy had a precision of 0.6250, showing more false positives. Recall measures the ability to identify all relevant instances. Healthy had a

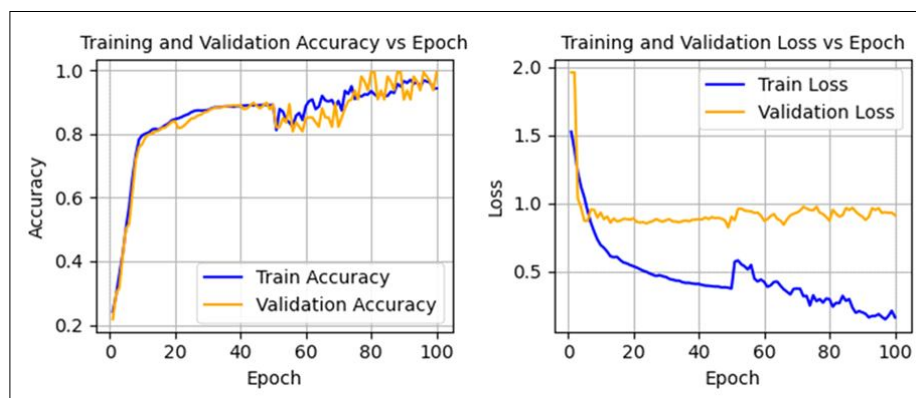


Fig 4: Accuracy and loss measurements.

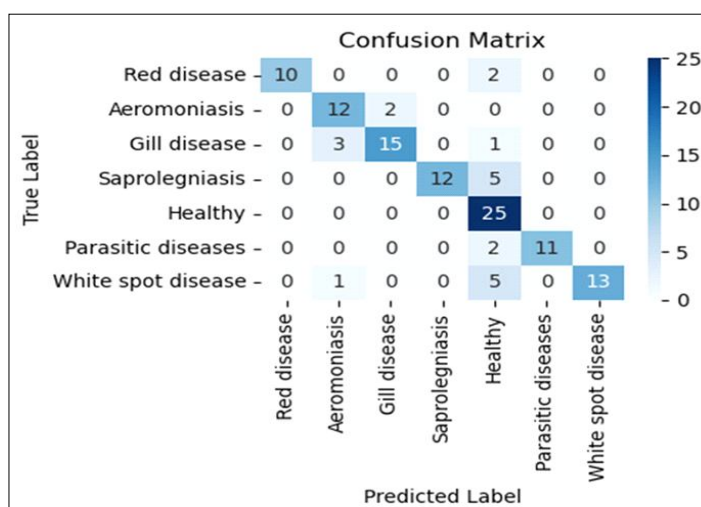


Fig 5: Confusion matrix.

Table 2: Classification matrices.

Class	Precision	Recall	F1 Score	Support
Red disease	1.0000	0.8333	0.9091	12
Aeromoniasis	0.7500	0.8571	0.8000	14
Gill disease	0.8824	0.7895	0.8333	19
Saprolegniasis	1.0000	0.7059	0.8276	17
Healthy	0.6250	1.0000	0.7692	25
Parasitic disease	1.0000	0.8462	0.9167	13
White disease	1.0000	0.6842	0.8125	19
Overall accuracy	0.8235			119
Macro avg.	0.8939	0.8166	0.8383	119
Weighted avg.	0.8730	0.8235	0.8285	119

perfect recall of 1.0000, correctly identifying all healthy cases. However, Saprolegniasis had a lower recall of 0.7059, indicating some misclassifications. F1 Score balances precision and recall. Red Disease excelled with an F1 score of 0.9091. Healthy scored 0.7692, reflecting challenges in precision despite the high recall. The overall accuracy of the model was 0.8235, showing solid performance. The macro average score was 0.8383, treating all classes equally. The weighted average, considering instance numbers, was slightly lower at 0.8285.

The model's predictions show strong confidence in its classifications (Fig 6). For healthy fish, it reported a confidence score of 91.12%. This indicates high certainty in identifying healthy specimens. For cases of Aeromoniasis, the model achieved an impressive confidence score of 99.95%. This near-perfect score reflects its ability to accurately identify this disease.

These confidence scores highlight the ability of the model in distinguishing between healthy fish and those affected by Aeromoniasis, suggesting its practical utility. ROC curve and AUC value provide key insights into the model's performance for each disease category (Fig 7). For Red disease, the AUC is 0.9821, indicating excellent discrimination. Aeromoniasis has an AUC of 0.9833, also showing strong performance. Gill disease achieves a perfect AUC of 1, meaning the model perfectly distinguishes between positive and negative cases. Saprolegniasis scores 0.9833, reflecting strong predictive capability. Healthy fish have an AUC of 0.9875, confirming the model's

effectiveness in identifying healthy specimens. Parasitic disease has a slightly lower AUC of 0.9423, indicating good performance. White spot disease scores 0.9911, showing excellent classification ability. Overall, these AUC values demonstrate the model's strong capacity to differentiate between various fish conditions. Most categories achieve scores above 0.9.

In contrast, current research on fish disease detection shows a variety of methods and results (Table 3). An automatic fish categorization method utilizing a customized deep residual neural network (DRNN) for small-scale underwater photos was presented by Sudhakara *et al.* (2022). Six iterations of the RESNET model were assessed. Layers, iterations, batch size and dropout layers were the main topics of the analysis. Using an untrained benchmark fish dataset, the smaller RESNET model obtained a testing accuracy of 90.26% with a validation loss of 0.0916. Tamou *et al.* (2018) presented a technique that uses the CNN-AlexNet with transfer learning to automatically classify fish species. They used the pretrained AlexNet, both with and without fine-tuning, to extract features from foreground fish photos in an underwater dataset. A linear SVM classifier was used for classification. Their strategy worked, as evidenced by the 99.45% accuracy they obtained on the fish recognition ground-truth dataset. A study on fish disease identification in aquaculture using image-based ML algorithms was carried out by Ahmed *et al.* (2021). There were two sections to the work. Pre-processing and picture segmentation were used in the initial step to improve

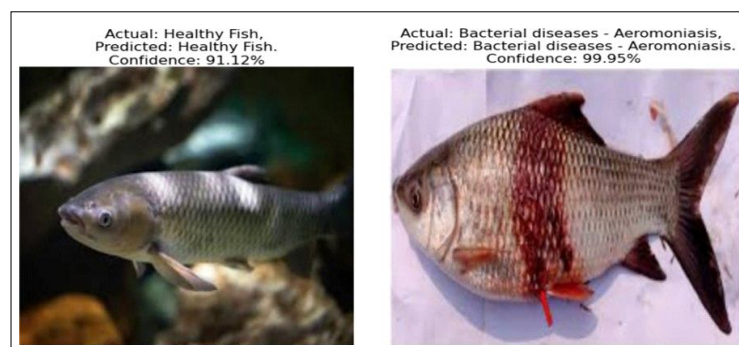


Fig 6: Prediction and true labels of images.

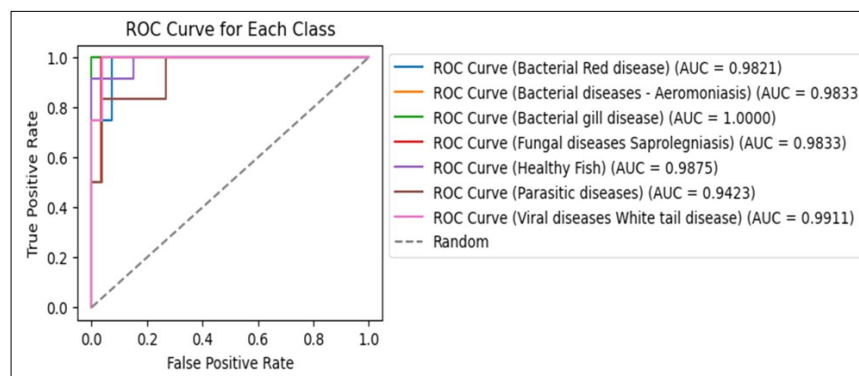


Fig 7: ROC(AUC) curve.

and lower noise in the photos. The second section concentrated on employing a Support Vector Machine (SVM) algorithm with a kernel function to extract features for disease classification. A dataset of salmon fish, comprising both augmented and non-augmented photos, was used to test the processed images. With accuracies of 91.42% with image augmentation and 94.12% without augmentation, the findings demonstrated the SVM's strong performance.

Mia *et al.* (2022) aimed to improve fish disease recognition to support remote farmers in effective fish farming. Early identification of diseased fish can help prevent the spread of diseases. The study involved an in-depth analysis of expert systems that use smartphone-captured images for disease identification. The authors selected two sets of features and employed a segmentation algorithm to differentiate between diseased and healthy areas. They implemented eight classification algorithms to evaluate performance, achieving a notable accuracy of 88.87% with the Random Forest algorithm.

Rachman *et al.* (2023) focused on detecting Epizootic Ulcerative Syndrome (EUS), a disease caused by the pathogenic fungus *Aphanomyces invadans*. The study employed Object Segmentation Inference with MobileNet V2 and image processing techniques. Using HSV thresholding, the researchers identified infected areas on the fish. The object segmentation process distinguished the disease-affected regions from the healthy parts of the fish. The system's performance was evaluated using the F1 score, achieving an average accuracy of 84% from 80 augmented images. Recent studies highlight diverse approaches in fish disease detection. They showcase different models and methodologies with varying outcomes. This work adds to the field by demonstrating the effectiveness of the ResNet-20 architecture. It achieves competitive accuracy and provides insights into its strengths in identifying various fish diseases.

### Application of ResNet-20 model for Co-infection detection

To detect co-infection using the ResNet-20 model, several modifications in dataset preparation, training strategy and classification methods are necessary. Since co-infection involves multiple diseases present in the same fish, a multi-label classification approach must be adopted instead of a traditional single-label classification. This requires modifying the dataset by labeling images with multiple diseases, using sigmoid activation in the output layer instead of softmax and employing binary cross-entropy (BCE) loss to handle multi-label outputs effectively. The BCE loss is given by:

$$L = \frac{1}{N} \sum_{i=1}^N [y_i \log(y_i) + (1 - y_i) \log(1 - y_i)]$$

Where,

$y_i$  = Actual label (0 or 1) for disease presence.

$w_i$  = Predicted probability.

The dataset should include both single and co-infected cases, with data augmentation techniques used to create realistic co-infection scenarios while maintaining class balance to prevent model bias. The ResNet-20 architecture should also be adjusted by modifying the final layer to output multiple probabilities, where each neuron represents a specific disease. The predicted probability for each disease  $d$  in an image  $x$  is computed as:

$$P(d|x) = \frac{1}{1 + e^{-z_d}}$$

Where,

$z_d$  = Raw output (logit) from the model before applying the sigmoid activation function.

Training should be conducted using labeled co-infection data, with performance evaluation metrics to measure the model's effectiveness. Post-processing

**Table 3:** Comparison of presented result with existing literature.

Reference	Model	Results	Remarks
Sudhakara <i>et al.</i> (2022)	Smaller RESNET	90.26% testing accuracy	Enhanced performance with fewer layers
	Standard RESNET	80.56% accuracy on training data	Higher validation loss and more memory intensive
Tamou <i>et al.</i> (2018)	AlexNet with SVM	Accuracy: 99.45%	Effective for automatic fish species classification
Ahmed <i>et al.</i> (2021)	SVM with feature extraction	Accuracy: 91.42% (with augmentation)	Effective for fish disease detection
Mia <i>et al.</i> (2022)	Random forest with segmentation	Accuracy: 88.87%	Effective for early fish disease recognition
Rachman <i>et al.</i> (2023)	MobileNetV2: Object segmentation	Accuracy: 84%	Effective for detecting EUS in fish
This work	RESNET20	Accuracy: 82.35%	Effective for detecting fish diseases

techniques, including probability thresholding and visualization methods like Grad-CAM or SHAP, can help interpret how the model identifies different infection regions in the image. Further enhancements, such as integrating ensemble learning with other CNN models, applying attention mechanisms for improved feature focus and incorporating additional data sources like clinical symptoms and water quality parameters, can improve the accuracy of co-infection detection.

### Study limitations

Despite its promising performance, this study has several limitations. The dataset size and diversity may not cover all fish disease variations across species and environments. Expanding the dataset could improve model robustness. The co-infection detection is also limited. The model was trained for single-disease classification and may not detect multiple infections accurately. A multi-label classification approach is needed in future work.

Both aeromoniasis (caused by *Aeromonas hydrophila*) and epizootic ulcerative syndrome (EUS) (caused by *Aphanomyces invadans*) exhibit similar external clinical signs. Our model relies on image-based feature extraction, which may not fully distinguish between them. While it shows promise in classification, incorporating histopathological characteristics and causative agent analysis could enhance differentiation. Gill infections often require microscopic examination or histopathological analysis for accurate diagnosis. Since our method is image-based, its ability to detect gill diseases is limited.

The real-world applicability of the model is another challenge. It relies only on image-based classification, but integrating clinical symptoms and environmental factors could improve accuracy. Computational requirements remain a concern. Although ResNet-20 is lightweight, deep learning models still demand significant resources. Optimizing for real-time use is necessary.

Further, generalization to different conditions is an issue. Variations in lighting, image quality and fish positioning can reduce accuracy. A more diverse and real-world dataset is required. Future studies will focus on dataset expansion and advanced architectures like Efficient Net (Tan and Le, 2019) and Vision Transformers (Dosovitskiy *et al.*, 2021) to improve performance.

### CONCLUSION

In terms of fish disease classification, the ResNet-20 model performed admirably, attaining an overall accuracy of 82.35%. The model effectively distinguished between healthy fish and those affected by various diseases, particularly Aeromoniasis. Obtained metrics indicate robust classification capabilities, especially for specific diseases. The augmentation techniques employed enhanced the dataset's diversity, contributing to improved model generalization. The AUC values further confirmed the model's effectiveness, with most categories scoring above 0.9. The study highlights the value of DL in aquaculture

and adds important insights to the field of fish disease identification. To further improve detection accuracy, future studies will concentrate on expanding the dataset and investigating other neural network structures.

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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.

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The views and conclusions expressed in this article are solely those of the authors and do not necessarily represent the views of their affiliated institutions. The authors are responsible for the accuracy and completeness of the information provided, but do not accept any liability for any direct or indirect losses resulting from the use of this content.

#### Availability of data and materials

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

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