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A Convolutional Neural Network Approach for Precision Fish Disease Detection

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Abstract

Background: Detecting and classifying fish diseases is crucial for maintaining the health and sustainability of aquaculture systems. This study employs deep learning techniques, particularly Convolutional Neural Networks (CNNs), to automate the detection of various fish diseases using image data. Methods: The study utilizes a carefully curated dataset sourced from the Kaggle database, comprising images representing seven distinct types of fish diseases, along with images of healthy fish. Data preprocessing techniques, including resizing, rescaling, denoising, sharpening, and smoothing, are applied to enhance image quality and facilitate accurate disease detection. Data augmentation is employed to increase the model's ability to generalize to unseen data. The CNN architecture is designed with cascading convolutional layers, ReLU activation functions, and pooling operations to extract high-level features associated with fish infections. The model architecture, implemented using the Keras Sequential API, includes convolutional layers, max pooling layers, and densely connected layers for classification. Results: Experimental results demonstrated promising performance across various disease categories, with high accuracy and balanced precision and recall values for most classes. The study also discussed the impact of climate change on fish disease incidence and underscores the importance of effective monitoring and management practices facilitated by technological innovations such as Big Data, IoT, sensors, and robotics in ensuring sustainable fisheries management.

Keywords: Fish Diseases, Deep Learning, Convolutional Neural Networks, Classifying.

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1. Introduction

Fishes are among the most important sources of protein, consequently resulting in a substantial increase in fish farming or aquaculture, and has become the fastest-growing animal food sector. It is expected to rise to 30 % by 2030 to meet the increasing population in the Asia-Pacific region (Mohd-Aris et al., 2019). Fish farming includes the process of rearing and raising fish for commercial purposes. This sudden and extreme proliferation in fish farming businesses has produced apprehension regarding fish health, with disease emergence constituting a paramount concern. Diseases are one of the reasons for anticipating the slowing of aquaculture production growth rate by 2032 along with factors such as environmental regulations and limited availability of suitable production locations (OECD and FAO, 2023). Studies indicate that fish disease has been responsible for approximately 50% of overall production losses (Liet al., 2022). The quick spread of these diseases can cause the mass extinction of local fish species in a short amount of time, resulting in substantial water contamination and posing a threat to other aquatic animals and human health through contact with diseased fish (Aziz & Abdullah, 2021). Several bacterial, viral, fungal, and parasitic diseases have been described by researchers (Crane& Hyatt, 2011; Novoslavskij et al., 2016; Bohara et al., 2022; Irshath, et al., 2023). Diseases such as Red spot disease, Aeromoniasis, Bacterial Gill Disease, Saprolegniasis, White spot disease, and some viral diseases are a few of them. Table 1 provides a short description of these diseases along with their causal organisms and physical symptoms. These pathogens infect fish when stressed, injured, or living in poor water quality conditions (Winton, 2001).

Table 1: Different diseases of fishes

DISEASES	PATHOGEN/AGENT	CHARACTERISTICS
BACTERIAL RED DISEASE	Genus Vibrio (Vibrio anguillarum)	Bloody lesions in the musculature of infected fish (Takahashi et al., 2017).
AEROMONIASIS	Aeromonas hydrophila	Causes small surface lesions, haemorrhagic septicemia, ulcers, fin and tail rot; affects carps, eel, channel catfish, tilapia, trout, and ayu (Zaheen et al., 2022)
BACTERIAL GILL DISEASE	Flavobacterium branchiophila	Loss of appetite, mortality of 20-50% in 24 hours, extensive clubbing of gill filaments in the microscopic examination, lethargy, gasping for air, the proliferation of epithelium causing clubbing and fusing (Singh, 1989; Starliper, 2012)
SAPROLEGNIASIS	Genus Saprolegnia (S. parasitica)	Manifests as white or grey patches of filamentous mycelium on the body or fins of infected fish; prevalent in the salmon fish-farming industry (Phillips et al., 2008)
WHITE SPOT DISEASE	Ichyophthiriusmultifilis	Attaches to fish, moves under the skin, feeds on cells and body fluids; identified by changes in behaviour (rubbing against stones, swimming disorientation), tightly folded fins, small white cysts (Faruk,2018).

The identification of fish diseases can be done by physical examination as the changes caused due to diseases are reflected in morphological changes in organs and impairment of their functions, for instance, the changes in the morphology of gills may indicate the health of fish and level of pollution (Noga, 2010). Traditional diagnostic methods including the dissection of fish tissues under laboratory setups are time-consuming and expensive. However, in situ diagnosis of diseases can help in very early detection of diseases allowing timely interventions, but necessitates sophisticated technological infrastructure. Moreover, the manifold nature and heterogeneity of fish diseases exacerbate diagnostic challenges, compounded by the limited diagnostic accuracy of conventional physiological indicators. Aquaculture has seen notable technological advancements recently, allowing the industry to increase current production levels to meet the growing demand for aquatic products. The increased growth in this sector has resulted in the accumulation of huge amounts of data and has led to the embracing of smart AI-based technologies such as machine learning and data mining to achieve sustainable aquaculture production. The present study aims to develop a method for disease detection by using a machine-learning technique using fish images. The next section provides a brief description of how AI and machine learning are being utilized in aquaculture to enhance productivity.

2. Review of Literature

Artificial intelligence (AI) and machine learning (ML) have found applications in animal tracking (Alzubi, 2023), disease detection based on their behavior (Kavlak et al., 2023), quality assessment of processed meat (Huang & Gu, 2022) and many more. They have also been explored in fisheries too, and utilized in many endeavors including population tracking, disease detection, automated feeding systems, behavior analysis, species identification etc.

Gómez-Vargas et al. (2023) suggested tracking population changes of fishes, particularly in species with conservation concerns, like marine organisms such as the undulate skate. To address the difficulty of accessing these organisms and obtaining sufficient training samples for photo identification, the researchers proposed using deep learning techniques. They specifically developed a Siamese neural network methodology to overcome the challenge of having limited training data. Their approach yielded promising results, correctly identifying 70% of individuals in the test set, including recaptures. Likewise, Jenrette et al. (2022) developed a Shark Detector tool for the classification of sharks using videos and images with the application of transfer learning and convolutional neural networks (CNNs) and achieved impressive accuracies. The tool was capable of classifying 47 species of sharks, achieving high accuracy in locating sharks in baited remote camera footage and YouTube videos (89%), as well as in classifying them to the species level (69%). The study emphasized the significance of media-based remote monitoring in shark observation. Notably, the authors suggested that the inclusion of more images in the training dataset would improve the prediction accuracy, highlighting its adaptability and potential for further improvement.

The application of ML in aquaculture and capture fisheries was discussed in an elaborative manner by Gladju, Kamalam & Kanagaraj (2022). Capture fisheries refers to the harvesting of fish from wild populations. Data on fish catch, sightings, and environmental conditions can be used to create models that estimate fish stock sizes and predict future trends (Rosenberg et al., 2014; Bastardie et al., 2014; Sheaves et al., 2020). This information can be used to set sustainable fishing quotas. Machine learning can be used to analyze sonar data to identify fish schools and optimize fishing gear and strategies. It can also be used to monitor fishing activity and ensure regulation compliance. Cossa et al. (2023) utilized drones and machine learning to develop a monitoring method to identify dugong feeding trails and seagrass beds accurately. Results indicated a significant overlap between dugong foraging areas and gillnet fishing grounds, with higher fishing activity correlating with increased dugong feeding trails. Particularly, the study emphasized the potential of drones and machine learning in studying animal behavior in remote areas and highlighted the need for effective management strategies to mitigate the accidental bycatch of dugongs, suggesting tighter restrictions on the use of gillnet as a crucial step in marine conservation efforts.

Data on fish populations, other marine life, and environmental conditions can be used to create models that assess the health of marine ecosystems. This information can be used to develop strategies to protect ecosystems and ensure sustainable fishing practices. Hu et al. (2020) explored the application of machine learning techniques to understand the complex relationships between environmental factors and fish communities in river ecosystems, aiming to facilitate sustainable ecosystem management. Machine learning methods were employed to analyze diverse datasets by identifying critical environmental variables, and an adaptive network-based fuzzy inference system (ANFIS) was utilized to estimate fish biodiversity. Strong correlation between model estimations and biodiversity indices, with certain environmental factors such as biochemical oxygen demand (BOD), water temperature, total phosphorus (TP), and nitrate-nitrogen (NO3–N) was revealed. In addition, ML can be used to improve post-harvest processes, quality assurance, and marketing in the fish production industry (Nimbkar et al., 2023; Kaur et al., 2023).

In the domain of aquaculture, data mining and ML are used in water quality and rearing environment control. Sensors can monitor water quality parameters like pH, oxygen levels, and ammonia. Machine learning algorithms can then be used to adjust feeding, aeration, and other parameters to keep these levels within optimal ranges. For example, Lee et al. (2000) applied a Fuzzy logic-based expert system in the bioreactors for controlling the process of denitrification which is a process of converting nitrate (NO_3^-) produced as a toxic by-product by fish into Nitrogen gas which helps in maintaining the water quality. The use of fuzzy logic in control systems is ideal for managing complex systems. It is a rule-based approach that involves a process of inference to determine the significance of a problem or the urgency of a control action (Liu, 2004).

Utilizing machine learning, data about fish growth can be analyzed, feed intake can be tailored according to the need, minimizing waste and maximizing the growth of the fish. Adegboye et al. (2020) introduced an intelligent fish-feeding system meant for measuring fish feed intake by predicting fish activities. It utilized fish behavioral vibration analysis and artificial neural networks (ANN) to use data from various sensors. A new Chain Code generator algorithm was employed to extract activity vectors, which were then processed using DFT (Discrete Fourier Transform) and evaluated by an artificial neural network (ANN). They achieved an accuracy of 100% outperforming the accuracy of 35.60% achieved with direct acceleration and angular velocity data, hence proving the system as a viable solution for automated fish feeding based on fish behavior analysis.

Tracking fish growth, movement, and behavior can also help in detecting signs of stress or diseases allowing farmers to take early action and machine learning algorithms can prove extremely efficient in doing the task. Li et al. (2022) proposed a method of recognizing abnormal behavior where image processing was used to extract the information about the moving object and its position which was enhanced using mosaic image fusion. Finally, by adding three new features to YOLOv5, i.e. BCS-YOLOv5 was developed which produced as average accuracy of 96.69 % at 45 frames per second across four typical behavior datasets. Proving to be an appropriate method for extraction of location information and detecting similar anomalous behavior helping in real-time tracking of fish abnormal behavior.

In recent years, image-based disease-diagnostic techniques have garnered widespread adoption for the assessment and identification of fish diseases. AI algorithms and ML methods have been extensively used for decision-making and classification tasks. These intelligent algorithms can learn the correct classification from the parameter space of the system using real image datasets, enabling the identification of deviations from selected configurations with high accuracy. Mamun et al. (2023) employed an image segmentation technique to first locate the diseased areas on fishes and then employed several pre-trained deep learning algorithms (VGG-16, VGG-19, ResNet 50 etc.) of Convolutional Neural Networks for classification. In addition, they used an ensemble model in which a combination of various pre-trained models was applied. They found that the ensemble model (VGG-16 + VGG-19 ensemble models) was able to differentiate three classes of diseases of fish namely Red Spot, White Spot, and Black Spot from the Healthy fish with the highest accuracy of 99.64%. Similarly, Barik et al. (2023) attempted to classify the lesion areas present in fishes with the Red Spot, White Spot, and Black Spot diseases. They utilized edge-based segmentation, grey threshold-based segmentation, hue saturation, and value-based color segmentation employing k-means clustering to fish sampling for the spontaneous detection of lesion regions.

Malik et al. (2017) proposed a method based on image processing which included segmentation and edge detection to recognize the Epizootic Ulcerative Syndrome (EUS) disease in fish. The FAST (Features from Accelerated Segment Test) feature extractor was employed to extract features from the fish images with symptoms of the disease. Principle Component Analysis (PCA) was employed to reduce the dimensions and retain usefult information from the extracted features. A Neural Network machine learning algorithm was subsequently was used which provided a high in the classification of EUS-infected and non-infected fish images.

Recently, Pauzi et al. (2021) presented a review paper on fish disease detection using image processing techniques which included rule-based expert systems, machine learning, deep learning, statistical methods, and hybrid methods.. They discussed the performance of these methods and their suitability for other domain applications and highlighted the need for improvement in image processing approaches to further enhance performance in fish disease detection. They concluded that image processing can provide a more reliable and efficient alternative to manual techniques conducted by fish experts, allowing for early detection and prevention of diseases. The development of image processing techniques can contribute to more advanced and automated detection methods with higher accuracy.

In the present paper a new algorithm is proposed to detect 6 fish diseases and separate them from the healthy fishes by using Convolutional Neural Network.

3. Methodology

3.1 Dataset selection

The Kaggle database is used to collect the dataset. It was chosen with care to create a deep learning model that would recognize fish skin diseases. It is divided into seven groups, each of which stands for a distinct type of fish disease. The count of associated images for diseases is as follows: Bacterial diseases - Aeromoniasis (51 images), Bacterial gill disease (58 images), Bacterial Red spot disease (55 images), Fungal diseases - Saprolegniasis (49 images), Healthy Fish (220 images), Parasitic diseases (40 images), and Viral diseases - White spot (48 images). The few diseased fish images from the dataset are presented in Figure 1. This diverse dataset serves as a valuable resource for training and evaluating Convolutional Neural Network algorithms, enabling precise disease detection in aquaculture. Images are split into 80:10:10 ratios for training, validation, and testing in this proposed study. These ratios are used to evaluate the classification performance according to training and testing accuracy.


Bacterial diseases Aeromoniasis

Fungal diseases Saprolegnias

Bacterial gill disease

Figure 1. Diseased fish images.

3.2 Data Preprocessing

Within a deep learning model, the resize and rescale components are the first step of the preprocessing stage. This step is essential to ensure that the images of input data are in the same sizes. Improving image quality for disease detection in fish by eliminating unwanted elements or noise is an important task. Image pre-processing must be carried out before sending the data for training in the CNN model. Effective pre-processing improves image segmentation, detection, recognition, and classification, which identify fish diseases more accurately. In aquaculture, various techniques such as minimizing noise, sharpening, and smoothing, are frequently used for image pre-processing. Image quality can be effectively maintained by denoising techniques such as the combination of Haar wavelet transform and histogram equalization (Atteya et al., 2016). Creating an algorithm that handles light absorption, dispersion, and noise is a big challenge. A variety of research needs could be satisfied by intelligent image-noise reduction, which combines artificial intelligence and decision-support methods to reduce noise and enhance image quality. Images must be sharpened to enhance contours and edges. It can be carried out by high-pass filtering. Many techniques have been proposed for image sharpening, including Laplacian sharpening, histogram equalization, and filtering in the transform domain. However, preventing ringing around edges and noise augmentation is a significant difficulty. In comparison to sharpening, image smoothing minimizes unexpected changes, increases overall image quality, and gradually modifies brightness. When disease identification does not depend on edge information, smoothing is useful even though it may soften edges. Various techniques have been used, such as the Savitzky-Golay algorithm for multispectral images and the two-dimensional exponential smoothing for echo fish images. By boosting the accuracy of subsequent detection, these approaches set up images for feature extraction.

3.3 Data Augmentation

The data augmentation technique adds a variety of original images to the training dataset to increase the model's ability to fit previously unknown data. By adding controlled randomization to the model through data flipping and rotation, overfitting is reduced. In the present work, the first of two sequential layers, RandomFlip (horizontal and vertical), flips input images horizontally and vertically to introduce randomness. Simulating real-world variability adds a variety of viewpoints and orientations to the training dataset. RandomRotation(0.2), the second layer, gives each image a random rotation of up to 0.2 radians. By rotating the dataset, this rotation exposes the model to more variances in object angles.

3.4 Feature Extraction

The main objective of the proposed CNN is to recognize the high-level features associated with the infections in Fish that are depicted in the image. The CNN architecture makes use of multiple cascading convolutional layers. Non-linear convolution and activation functions are incorporated into each convolutional layer design through the use of ReLU and pooling methods. The CNN's input consists of training and test images with a height and width of 256 x 256 pixels.

the output (y) of the convolutional layers is given by the expression

$$y = f\left(a^{l} + \sum_{x}^{X}\sum_{y}^{Y} g_{x,y}^{l} h_{x,y}^{l-1}\right) \qquad (1)$$

The variables X, Y denote the size of the filters (height and width), while a^{l} denotes the convolutional layer's bias. The output of preceding convolutional layers is represented by h^{l-1}, g^{l} denotes the weight of the convolutional layer. The non-linear ReLU function f(y) is defined as

$$f(y) = \mathrm{ReLU}\ (y) = \begin{cases} y, y > 0, \\ 0, y \leq 0. \end{cases} \qquad (2)$$

With the specific training set, the parameter δ could be calculated by utilizing the highest estimate. It is described as

$$E(\delta) = \prod_{n=1}^{N} f(y)\delta_{n} \qquad (3)$$

In equation 3, E(δ) is called highest estimation parameter. In this corresponds the vector value is calculated using equation 4.

$$w^n = \sum_{j=1}^{n} w_j^n \qquad (4)$$

The next step is pooling, which makes the feature maps smaller in size and less computationally demanding on the network. The convolutional layer generates features that are precisely located for subsequent operations. In the output of the Max-pooling layer, several pooling techniques, such as the Max-pooling method, are available to choose the most important features from the previous feature map. The retention of features and patterns is not compromised in the process of this pooling-based reduction. After a sequence of convolution layers, ReLU activation, and pooling operations, flattening is the next step. This process creates a feature vector from the 2D feature matrix, which is then fed into a classifier model. Providing the classifier with the flattened vectors is the main objective of the fully connected process. The flow chart of process used in this study is presented in the Figure 2.

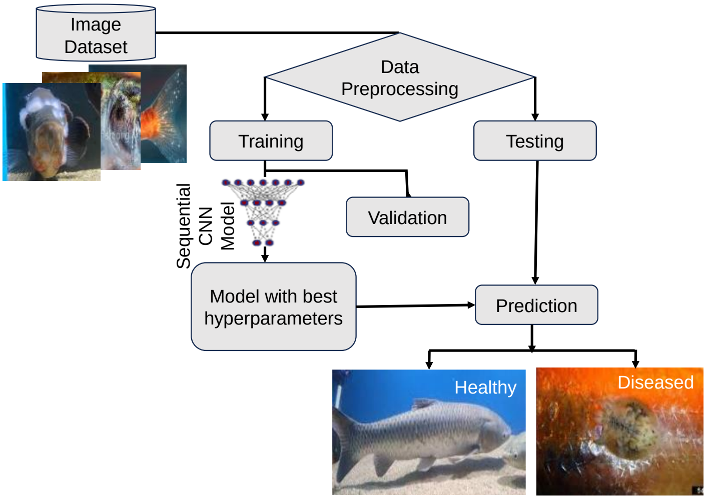


Figure 2. Flow chart of proposed CNN model.

3.5 Algorithm of Proposed System

Using the Keras Sequential API, a neural network architecture is used in the proposed approach. The convolutional layers and tightly coupled layers of the model implied healthy and diseased image categorization. There are several convolutional layers in the architecture. The first convolutional layer (conv2d) starts the sequence with 64x3x3 filters and uses an activation function called a Rectified Linear Unit (ReLU) on input data with dimensions of (256, 256, 3). Convolutional Layers 2 through 6 (conv2d_1 to conv2d_5) are the next layers that add more filters and their matching ReLU activations. Max pooling layers, MaxPooling Layers 1 through 6 (max_pooling2d_1 to max_pooling2d_5), are used in between these convolutional layers to slowly decrease spatial dimensions. The 2D output is converted into a 1D array with 2048 items by a Flatten Layer (flatten), which comes after the convolutional and max pooling layers. Dense Layer 1 (dense) and Dense Layer 2 (dense_1), which are fully connected layers, perform the same task. Dense Layer 2 is the output layer, containing 7 neurons that represent the number of classes in the classification work, whereas Dense Layer 1 consists of 64 neurons with ReLU activation. This layer creates class probabilities using a softmax activation function. There are 2,125,191 trainable parameters in all, according to the model summary, which also reveals the number of parameters in each layer. All things considered, the architecture is optimized for image classification tasks, using fully connected layers to make predictions and convolutional operations to extract structured features (Figure 3).

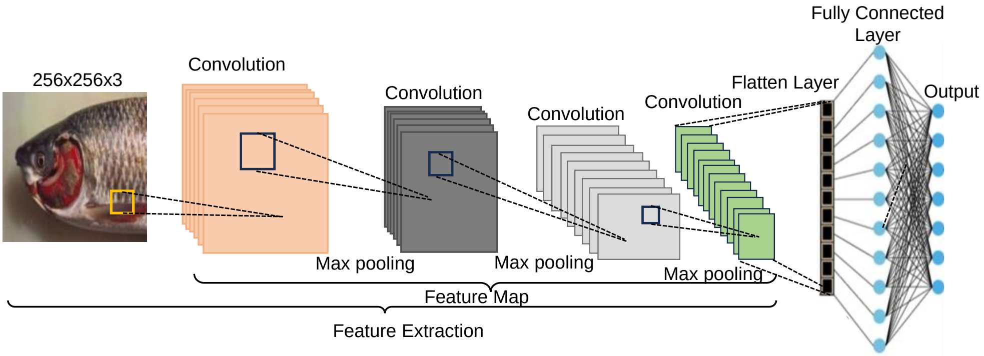


Figure 3. Architecture of CNN model used for classification of healthy and diseased fishes.

3.6 Performance Evaluation Method

Accuracy in classifying the dataset serves as a measure for the detection and classification model developed in this study. The CNN model measures the performance in terms of true and false classifications. All classifiers are evaluated using statistical metrics, such as accuracy, precision, recall, F1-Score and error rates. Within the test data model, a confusion matrix table displays the counts of instances that were correctly and incorrectly identified. The percentages of correctly identified sample images to all sample images are used to calculate recognition and classification accuracy. The equation describes the accuracy of identification and classification process.

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

$$\text{Precision} = \frac{\text{TP}}{\text{TP} + \text{FP}}$$

$$\text{Recall} = \frac{\text{TP}}{\text{TP} + \text{FN}}$$

$$\text{F1} - \text{Score} = \frac{2 \times \text{Precision} \times \text{Recall}}{\text{Precision} + \text{Recall}}$$

4. Results and Discussion

The PYTHON programming language was used to evaluate fish disease detection and classification. The experiment included seven categories of images and was designed to demonstrate the proposed image classification method. During the experimentation phase, the suggested Convolutional Neural Network (CNN) was utilized by the proposed system to extract relevant image features from the received image data. The loss and accuracy of the model over epochs are presented in Figure 4. It took 100 epochs to complete the training process, where each epoch represents one iteration through the training dataset. The reported training loss is 0.3818, while the validation loss is represented by the value 0.5629. Significantly, the training loss quantifies the error on the training dataset, whereas the validation loss evaluates the model's performance on a separate validation dataset. A reduced loss value suggests that the model is performing better. Additionally, the accuracy metrics are provided, indicating a validation accuracy of 0.8438 and a training accuracy of 0.8338. Higher accuracy values denote better model performance as measured by the percentage of correctly classified instances during both training and validation.

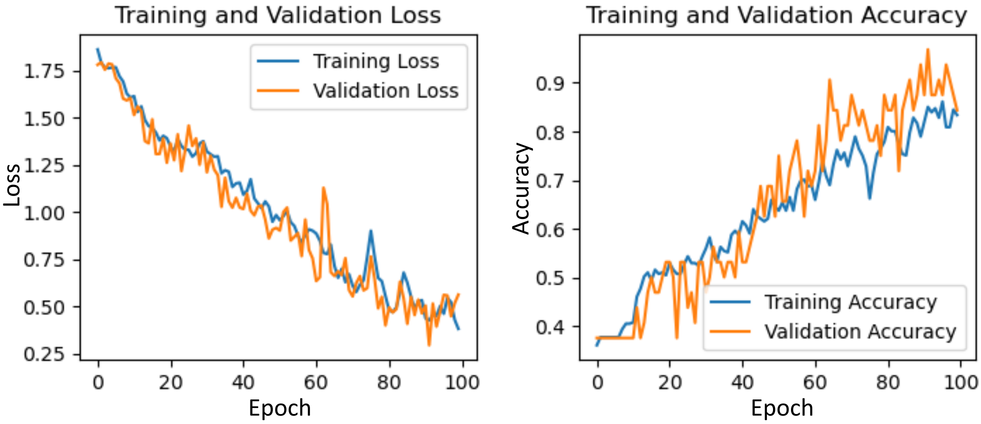
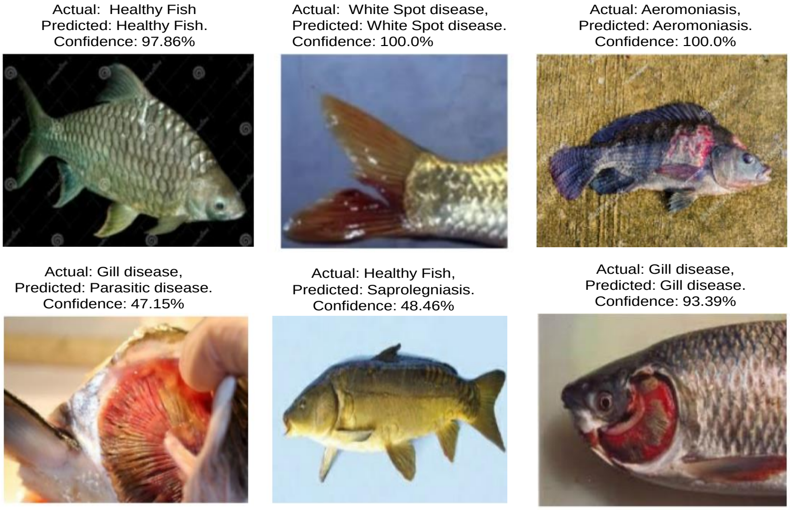


Figure 4. Loss and Accuracy measurements of training and validation datasets.

The model's predictions and confidence scores are displayed for each of the multiple instances in the provided classification results. The model correctly identified classes like Healthy Fish, White Spot disease, and Aeromoniasis with confidence scores of 97.86%, 100.0%, and 100.0% (Figure 5).



Actual: Healthy Fish
Predicted: Healthy Fish.
Confidence: 97.86%

Actual: White Spot disease,
Predicted: White Spot disease.
Confidence: 100.0%

Actual: Aeromoniasis,
Predicted: Aeromoniasis.
Confidence: 100.0%

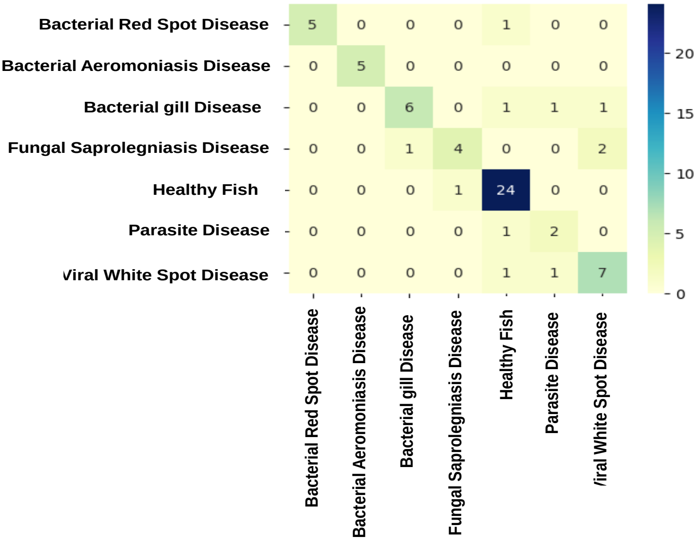
Actual: Gill disease,
Predicted: Parasitic disease.
Confidence: 47.15%

Actual: Healthy Fish,
Predicted: Saprolegniasis.
Confidence: 48.46%

Actual: Gill disease,
Predicted: Gill disease.
Confidence: 93.39%

Figure 5. Confidence score of actual and predicting healthy and diseased fishes.

In most cases, the model has high confidence levels and makes accurate predictions. Misclassifications happen occasionally, as evidenced by the predictions for Healthy Fish (48.46% confidence) as Saprolegniasis and Gill disease (47.15% confidence) as Parasitic disease. The model consistently performs well in correctly identifying a number of fish diseases in spite of these misclassifications, demonstrating its efficacy in the classification task.



	Bacterial Red Spot Disease	Bacterial Aeromoniasis Disease	Bacterial gill Disease	Fungal Saprolegniasis Disease	Healthy Fish	Parasite Disease	iral White Spot Disease
Bacterial Red Spot Disease	5	0	0	0	1	0	0
Bacterial Aeromoniasis Disease	0	5	0	0	0	0	0
Bacterial gill Disease	0	0	6	0	1	1	1
Fungal Saprolegniasis Disease	0	0	1	4	0	0	2
Healthy Fish	0	0	0	1	24	0	0
Parasite Disease	0	0	0	0	1	2	0
iral White Spot Disease	0	0	0	0	1	1	7

Figure 6. Confusion matrix for healthy and diseased categorization.

The confusion matrix summarizes the performance of model across various classes (Figure 6). The predicted classes are represented by each column, and the actual classes are indicated by each row. The diagonal elements represent the accuracy of the model for each class by denoting the number of correct predictions. The model accurately detects, 24 cases of Healthy Fish, 7 cases of Viral White spot disease, and 6 cases of Bacterial gill disease. Some cases of Bacterial red spot disease have been misclassified as Funagal Saprolegniasis disease, and one instance of Funagal Saprolegniasis disease has been misclassified as Viral White spot disease. All things considered, the confusion matrix offers a thorough assessment of the functionality of model, highlighting both accurate classifications and areas that might require improvements.

Table 2. Performance matrices.

Labeling	Precision	Recall	F1-Score	Support
Bacterial Red Spot disease	1.0000	0.8333	0.9091	6
Bacterial Aeromoniasis disease	1.0000	1.0000	1.0000	5
Bacterial gill disease	0.8571	0.6667	0.7500	9
Fungal Saprolegniasis disease	0.8000	0.5714	0.6667	7
Healthy Fish	0.8571	0.9600	0.9057	25
Parasitic disease	0.5000	0.6667	0.5714	3
Viral White Spot disease	0.7000	0.7778	0.7368	9
accuracy			0.8281	64
macro avg	0.8163	0.7823	0.7914	64
weighted avg	0.8366	0.8281	0.8259	64

Table 2 presents classification metrics that provide a thorough evaluation of the model's performance across various disease categories. The disease known as bacterial aeromoniasis show recall and precision, with an F1-Score of 100%. Additionally, Bacterial Red Spot disease exhibits a balanced F1-Score of 90.91% and precision of 100%, demonstrating the model's efficacy in correctly identifying cases of these diseases. Another class that shows promise is Healthy Fish, with a well-balanced F1-Score of 90.57%, recall (96.00%), and precision (85.71%). However, the F1-Score, recall, and precision values for parasitic disease are lower at 50.00%, 66.67%, and 57.14%, respectively. The performance of viral white spot disease is balanced, showing a good F1-Score of 73.68%, recall of 77.78%, and precision of 70.00%. Overall, the model shows different levels of ability in different classes, highlighting the significance of taking particular metrics into account for every disease category during the evaluation process.

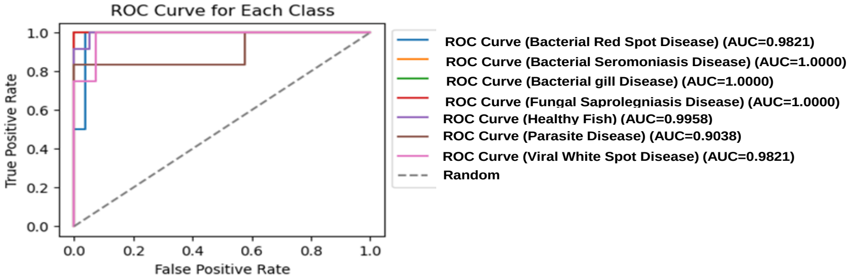


Figure 7. ROC curve with AUC values.

Comparing various disease categories using ROC curves and AUC values demonstrates the binary classification performance of the model (Figure 7). Specifically, significant discrimination is indicated by AUC values of 1.0000 for Bacterial Gill Disease and Bacterial Aeromoniasis Disease. By comparison, Parasite Disease exhibits good discriminatory ability (AUC=0.9038), but introduces a small trade-off between True Positive and False Positive Rates. Viral White Spot Disease and Bacterial Red Spot Disease both have AUCs of 0.9821, indicating arbitrary behavior. The model distinguishes between Healthy Fish with remarkable accuracy, as evidenced by its high True Positive Rate and low False Positive Rate, as well as its high AUC of 0.9958. Fungal Saprolegniasis Disease also shows perfect discrimination, with an AUC of 1.0000. Finally, this comparative analysis demonstrates the complex performance of model, demonstrating differing levels of discriminative capacity across various disease classes. This information is important for evaluating the efficacy of proposed model under various diagnostic conditions.

The incidence of diseases in fish influenced by changing climate has been increasing. The changing temperature due to climate change affects the vulnerability of fish to pathogens, making them more susceptible to diseases. Warmer conditions may even facilitate the establishment of exotic diseases as rising temperatures accelerate the replication rate, virulence, and transmission of pathogens among various species (Maulu et al., 2021; King et al. 2023). Likewise, increased rainfall may lead to the infiltration of invasive species and a decline in water quality due to the mixing of pond water with wild environments (Havel et al., 2015). In addition, the emergence of fish diseases in aquaculture can be associated with the storage processes, handling practices, and environmental factors which can influence microbial composition (Novoslavskij et al., 2016). This underscores the need for effective monitoring and management practices to detect and mitigate changes in microbial flora to prevent fish diseases in aquaculture setups. Innovations such as Big Data, the Internet of Things (IoT), sensors, and robotics have enabled the development of more efficient and precise monitoring equipment. These technologies are becoming increasingly compact and affordable, fostering their widespread adoption. However, their broader utilization is impeded by challenges including initial costs, complex data requirements, issues with data sharing among fisheries management authorities, and a shortage of individuals trained to operate these tools effectively. Addressing these challenges is crucial to fully leverage the potential of technological innovations in ensuring sustainable fisheries management practices.

5. Conclusion

The use sequential CNN model involving image processing technology in aquaculture is examined in this article, with a focus on the use of image analysis for fish disease detection. With a focus on deep learning systems and automatic image-based diagnostic techniques, it provides a summary of important technical approaches. Because of a particular sequential process, CNN model can detect disease in fish with high accuracy based on information or images, but their diagnostic speed and capacity to identify unknown diseases are limited. The Python programming language is used to evaluate CNN's ability to extract important characteristics from fish in seven different disease categories. After 100 training epochs, the model's reported overall accuracy was 82.81%. The resulting analysis showed that, even with a few rare misclassifications, the model had a significant confidence score and accurate predictions for a variety of diseases. Confusion matrix, ROC curves, and AUC values are used to investigate a comparative analysis of disease categories to demonstrate the capacity of the model to make distinctions.

6. Limitations and Future Work

Standardized and common datasets for fish diseases must be created, and current automatic feature-extraction techniques like convolutional neural networks (CNN) must be enhanced. Standardizing disease criteria in the dataset and integrating the Internet's human-machine interface to enable social sharing of the dataset is essential for diagnosing a wide range of diseases on a large scale in the future. To analyze unique features linked to various diseases and provide a dependable and accurate diagnostic approach, deep learning is essential. Additionally, the application of data fusion techniques, including data layer information fusion, feature layer information fusion, and decision layer information fusion, can be advantageous in a range of situations. Integrating information from various sensors increases the precision of diagnosis by simultaneously identifying internal tissues, behavior, and the exterior of the body. This approach ensures a more secure and efficient diagnostic process by advancing a comprehensive understanding of fish health.

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