Indian Journal of Geo Marine Sciences
Vol. 53 (07), July 2024, pp. 509-517
DOI: 10.56042/ijms.v53i07.11740

Research Article

Convolutional neural network modelling and image analysis techniques for the detection of fish diseases

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Received 11 April 2024; revised 05 July 2024

Fish rearing or pisciculture holds the key to food security and economic well-being for several countries across the globe. Diseases in fish are the biggest threat due to their rapid spread rate and high calamity, leading to a sharp decrease in fish yield. Deep learning techniques such as Convoluted Neural Networks (CNNs) hold an extremely promising impact on disease detection and raising the predictability of production amount. In this paper, the sequential CNN model indicates rigour and high reliability. The experimental setup consists of a model based on TensorFlow, Keras and 8-core TPU to accelerate computational Machine Learning (ML) tasks. The dataset obtained from Kaggle consists of 457 files depicting seven distinct classes (one healthy and six diseased classes), including all major fish diseases. Image data preprocessing is done by resizing and rescaling to train the optimised model. Image augmentation is done to expand the available data set and resolve overfitting issues within the CNN model. Modelling involves multiclass classification with a convolutional layer to extract features, keeping non-linearity in the model by an activation function. By transfer learning, inadequacies of the dataset are minimised. The proposed CNN model architecture efficaciously classifies various fish diseases. Identification and categorisation are done using Python, and the algorithm's learning efficiency is predicted to be quite high. The model makes reasonably accurate predictions with an accuracy close to 91 %. A good pattern of learning during the training of the model is observed. These observations indicate the model's remarkable capacity to correctly identify the diseases.

[**Keywords**: Aquaculture, Convolutional Neural Network (CNN), Deep Learning, Fish diseases]

Introduction

The coastal communities and developing countries profoundly depend on fish rearing and aquaculture. The dependence of the nation's economy on aquaculture is on the rise. To work for the hunger of the people and raise the nation's per capita income, aquaculture or fish rearing appears to be very promising. It is considered to be one of the sustainable approaches to food security and a step towards ensuring a balanced diet for all. Aquaculture is also regarded as contributing to the global economy and social stability worldwide[1]. With the rise in the economic status of countries over the last five decades, the consumption of fish has gained considerable growth. A large population depends on aquatic food for protein needs. Fish is a vital protein source providing essential nutrients to billions of people across the world. With economic stability[2] and awareness of diets with high protein content, the world 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. Several stakeholders including the industry, national and international policymakers, non-government organisations and consumers, are gaining focus on enhancing the well-being of aquatic environments for the growth of fish and other seafood. The current production of fish and seafood is around 200 million tons annually throughout the globe[1]. This includes wild fish catch as well as fish farming. Over the last two decades, aquaculture production has largely outnumbered capture fisheries production[2]. Though the production has shown considerable growth, around 20 – 25 % of the production gets wasted due to several factors. Some of the factors affecting the production include disease outbreaks, limitations of transportation at the right time leading to wastage of food and other industrial obstructions[3]. To continue securing the growth within this sector, the health and well-being of the aquatic organisms is extremely crucial[4]. The spread rate of diseases in fish farming is observed to be much more rapid than in wild fish catch due to the confinement and contained environment. Thus, diseases in fish become a primary constraint to the net production of fish farming. The outer layer of aquatic organisms, especially fish, together with their gills and gut, are the primary mucosal barriers. The role of these mucosal barriers is to protect the organism from external infections in the form of bacteria, fungi and viruses[5]. Any kind of pathogen attack or some internal abnormality can lead to a change in the structure and appearance of the outer layers of the skin[6-9].

The common diseases in fish vary depending on the species and the environment in which they inhabit, but some of the diseases that are commonly prevalent include white rot disease, fin rot, cotton wool disease, dropsy, swim bladder infection, and other fungal and parasitic infections. These diseases are of great concern for the aquatic yield, which is sharply affected by mass deaths. The traditional methods of disease detection involving fishermen and other manual techniques are very limiting and time-consuming. These methods often lead to misleading and inaccurate information due to humanistic limitations[9]. Minimising human intervention and shifting towards machine-based measurements to limit human errors and amplify the process timing for corrective actions is inevitable. This will lead to unbiased results and the possibility of reproducing data in multiple situations with great accuracy. Human observation and analysis cannot be completely ignored, especially when providing insights into new features like typical morphology and disease patterns. Nevertheless, Machine Learning (ML) techniques have contributed immensely to classification and segmentation[10-13]. Many machine learning techniques, each with specific advantages and applications, may be used to identify fish diseases. Convolutional Neural Networks (CNNs) are a strong contender for identifying signs linked to fish diseases because of their expertise in image classification[14,15]. Using the simple K-Nearest Neighbour (KNN) method, diseased fish images can be categorised. Support Vector Machines (SVMs) may use recovered data to distinguish between fish in excellent health and those in poor health in high-dimensional feature spaces. A large data set may be needed for the accurate training of the model, but the requirement is often mitigated by employing methods like data augmentation or customising layers, etc.[14]. Krizhevsky *et al.*[15] adopted CNN to accomplish the classification of images. The accuracy measured was much higher than that of the classical algorithms. Heaton *et al.*[16] pioneered simple deep-learning models called deep feed forward where information is only propagated in one direction using neurons. Aquatic systems pose challenges for image capture at high speeds and extreme mobilities. Malik *et al.*[17] worked on a particular fish disease called Epizootic Ulcerative Syndrome (EUS) detection. They reported that the accuracy of the model was 86 % and 63.3 %, respectively. Several algorithms like backpropagation, and recurrent neural networks are utilised for monitoring and identifying the images by training the computational models[18,19]. Fish disease detection is comparatively less than other detection works, such as fruit disease, crop disease detection and other agricultural domains.

To fill this gap, the main objective of the current work is 1) building a CNN-computational method for classifying different health states in fish, 2) assessment of the model performance with the systematic use of numerous metrics and graphical representations of the classification outcomes, and 3) discuss the model which is trained to maintain low loss and high accuracy on the validation set.

Materials and Methods

Experimental setup

The model is constructed in an Anaconda environment on a Jupiter notebook, and training is performed on a computer with 16 GB RAM and Python v3.11 on the TPU-v3:8 environment. The Tensor Processing Unit (TPU), a hardware accelerator made by Google, is mainly intended for machine learning applications. The open-source machine learning library TensorFlow facilitates TPU usage. Keras is a high-level neural network API that can be used with TensorFlow as its backend. Therefore, for optimal performance when executing the model, these three components (TensorFlow, Keras, 8-core TPU) should be used to speed up the computations. The working principle of sequential CNNs is quite simple. It handles many kinds of data related to fish health and is used in aquaculture systems for disease diagnosis. In the first step, information is collected that includes genetic sequences, images of fish, and metrics related to water quality. Preprocessed images are intended to improve their quality and standardise them. Many convolutional layers and max-pooling layers are used. Flatten and fully connected segments also constitute a CNN model. These components are constructed for sequential data processing. Convolutional layers in the model detect patterns in the data. Pooling layers downscale dimensionality. Fully linked layers depict disease presence. The model learns to correlate input patterns with illness states by training on labelled data, and it adjusts its parameters to reduce prediction errors. The model's performance is evaluated throughout the validation and testing stages to make sure it can generalise to new data. The model is used in aquaculture systems for real-time disease monitoring once it has been verified. It continually examines incoming data streams to notify operators of any irregularities in fish health or possible disease outbreaks. Aquaculture systems may benefit from automated disease identification by using sequential CNNs. This can lead to better management practices and prompt interventions to protect the sustainability and health of fish populations.

Dataset collection

In this work, the open source database[20] is used to develop a fish disease detection model based on Convolutional Neural Networks (CNN). The dataset consists of seven classes: bacterial (aeromoniasis, bacterial gill disease, bacterial red disease), fungal (saprolegniasis), parasitic (parasitic disease), viral (white spot disease), and a healthy class, with 250 images in each category (Fig. 1a–d). The data was sourced 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, with expert assistance for accurate labelling. The dataset was divided into training (80 %), validation (10 %), and testing (10 %) subsets to ensure a robust foundation for developing and evaluating the CNN model. This division was implemented using the train_test_split function from the sklearn.model_selection library.

Image data preprocessing

The set of images is initially labelled with the relevant class. A thorough scan was performed using a hash-based duplicate detection method to ensure the dataset does not contain duplicate images. This approach computes unique hash values for each image and compares them to identify and remove any redundant samples. After that, to reduce the training time, the images are compressed and converted into 256×256 pixel tensor data. The images are scaled and resized to obtain the uniform input dimensionality required by Convolutional Neural Networks (CNNs) to train an optimised model. This process contributes to maintaining computational efficiency during the training phase. The process of adding new images to employed dataset through a variety of methods, such as rotation, flipping, noise addition, shear, shifts, etc., is known as image augmentation. There are two advantages of this process. Firstly, image augmentation allows the expansion of a constrained dataset by adding more images without having to create new ones manually. Secondly, image augmentation eases the process of developing an

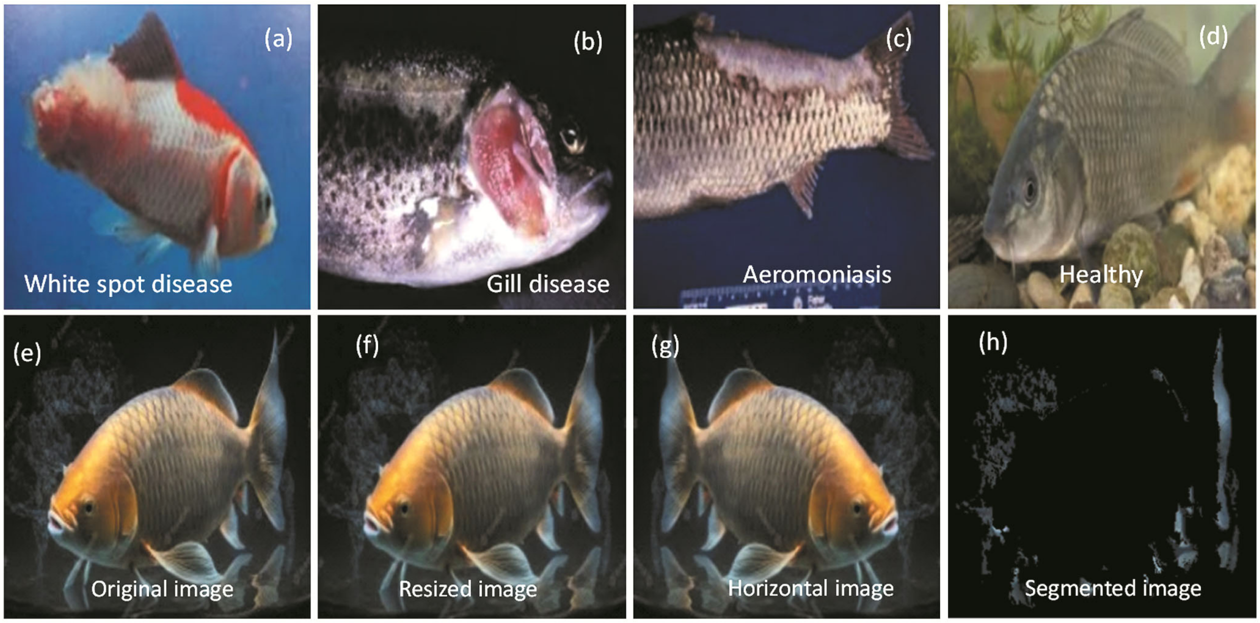

Fig. 1 — (a–d) Healthy and diseased fish images; and (e-h) Output of resized, flipping and segmented image

improved model by resolving the overfitting problem in deep learning.

Flipping is the process of manipulating an image by flipping the rows (horizontal flipping) or columns (vertical flipping) within its channels (Fig. 1e – h). Let us consider a picture with three dimensions (n × m) channels, written as S_{ijk}, where k stands for the three-color channels (red, green, and blue). Here is a summary of the mathematical expressions for the flipping operations

$$\textit{Vertical flipping} \quad S_{ijk} = S_{i(m+1-j)k} \qquad \text{... (1)}$$

$$\textit{Horizontal flipping} \quad S_{ijk} = S_{(n+1-i)jk} \qquad \text{... (2)}$$

In the data augmentation pipeline, horizontal and vertical flipping, as well as rotation, were applied. The rotation range used was between -0.2 and 0.2 radians, approximately -11.5 to 11.5 degrees. This was implemented using the Random Rotation layer in TensorFlow.

Modelling using CNN computations

Multiclass classification

Multiclass classification is the process of classifying an object into more than two categories. Six classes of fish diseases and one class for healthy fish that requires classification are included in this study. The general flow chart for modelling fish conditions is shown in Figure 2. In the flow chart, the convolution layer receives an input of 256×256 pixels and uses convolution to extract features. The size of the feature map is subsequently decreased by the pooling process. The reduced feature map is then converted via a dense layer into a vector that represents the final output classes.

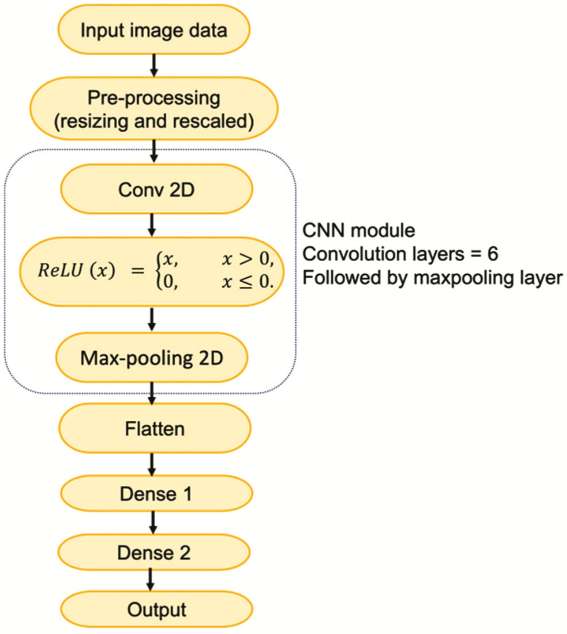

Fig. 2 — Flow chart of proposed model for classification

Convolution layer

To extract features from the image and determine the characteristics and interactions between the pixels in this layer, small squares of input data are utilised. This procedure is performed by the convolution of the input image matrix with a filter matrix.

$$[f(t) * g(t)] = \int_{-\infty}^{\infty} f(\tau) g(t-\tau) d\tau \qquad \text{... (3)}$$

Activation function

The model must be non-linear to process real-world data, which frequently consists of non-negative linear values. The non-linearity can be included through the activation function. The common activation functions used in CNN are expressed as:

$$ReLU(x) = \begin{cases} x, x > 0, \\ 0, x \leq 0. \end{cases} \qquad \text{... (4)}$$

$$ReLU(x) = \frac{e^x}{sum(e^x)} \qquad \text{... (5)}$$

$$ReLU(x) = \frac{e^x - e^{-x}}{e^x + e^{-x}} \qquad \text{... (6)}$$

In this work, equation (4) is used to introduce non-linearity in the model.

Pooling layer

The use of pooling layers reduces the number of parameters when working with large images. Here, the feature map matrix is subjected to max pooling with a stride value of 2.

Fully connected layer

The three-dimensional image is flattened into one dimension using a flattening layer to determine the probability value. Two fully connected dense layers with an optional activation function are then used for classification.

Accuracy measurements

The accuracy of a model is based on differentiating between healthy and diseased cases. The mathematical expression is as follows:

$$Accuracy\ pertange = \frac{TN+TP}{TN+TP+FP+FN} \times 100 \qquad \text{... (7)}$$

Precision is a performance metric in classification that measures the accuracy of the positive predictions given by the model.

$$Precision\ percentage(P\%) = \frac{TP}{FP+TP} \times 100 \quad \ldots (8)$$

The rate at which the model responds to input data frames is known as sensitivity (True Positive Rate or Recall). It can be expressed as follows:

$$Recall\ percentage(R\%) = \frac{TP}{FN+TP} \times 100 \quad \ldots (9)$$

Transfer learning

The problem of inadequate training data is addressed by transfer learning, a critical machine learning technique. It eliminates the need that training and testing data must be closely related by transferring knowledge from a source domain to a target domain. The process of gathering and analysing data is time-consuming and laborious overall and inadequate data is a frequent problem in many different contexts. The process by which a model learns through transfer learning is shown in Figure 3.

Algorithm of the presented CNN model

The proposed CNN model architecture is presented in Figure 4. The first layer, called sequential, retains the input data at (32, 256, 256, 3) in its original shape, where 32 represents the batch size, 256 × 256 are the image height and width in pixels, and 3 denotes the RGB color channels. After that, feature extraction and pattern recognition are handled by the first convolutional layer, called Conv2D, which has an output shape of (32, 254, 254, 64), where 64 is the number of feature maps (filters) and 254 × 254 are the reduced spatial dimensions after convolution. This layer contains 1,792 parameters. The spatial dimensions are subsequently reduced by half by the MaxPooling2D layer, producing an output shape of (32, 127, 127, 64), where 127 × 127 are the pooled height and width and 64 is feature maps. With slight modifications, this sequence of convolutional and max-pooling layers is repeated, capturing ever more complex features. As the model develops, more complex patterns are extracted from the input by deeper convolutional layers like Conv2D_3 and Conv2D_5, whose respective output shapes are (32, 28, 28, 256), where 32 represents the batch size, each feature map has a spatial resolution of 28 × 28, and there are 256 channels (feature maps); and (32, 4, 4, 512), where the batch still contains 32 images, but the spatial resolution has been further reduced to 4 × 4, while the depth has increased to 512 channels. Max-pooling layers MaxPooling2D_3 and MaxPooling2D_5 keep reducing the spatial dimensions. The last flatten layer prepares the data for the next fully connected layers by reshaping it into a

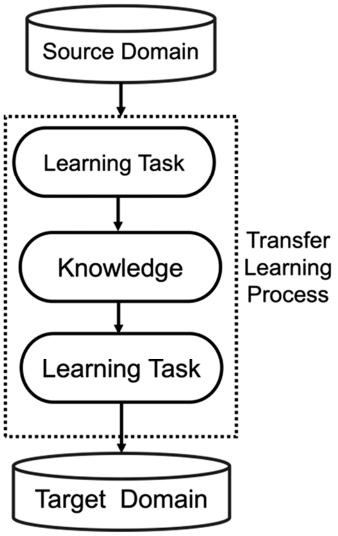

Fig. 3 — Transfer learning steps

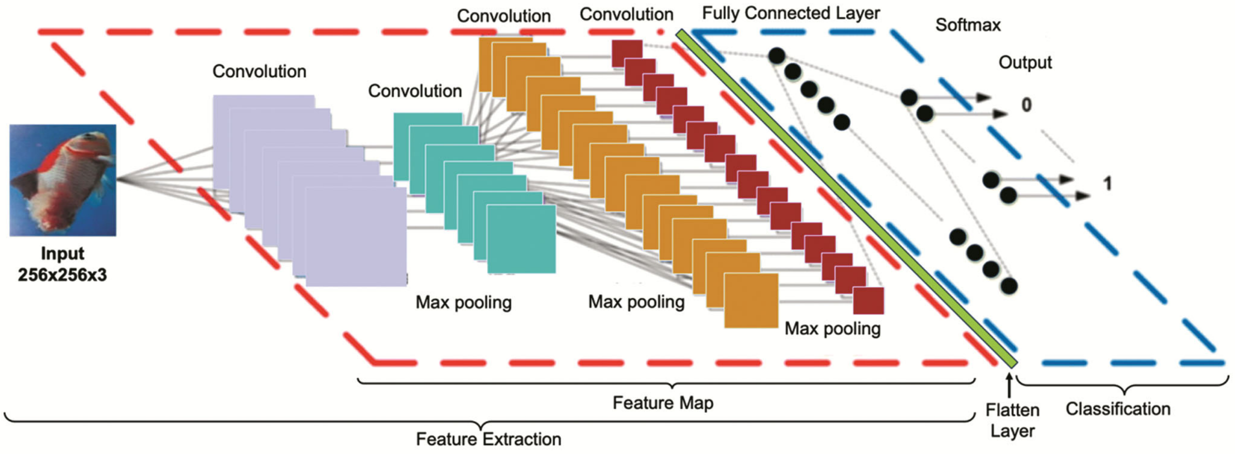

Fig. 4 — Model for feature extraction and classification of healthy and diseased fishes

one-dimensional array with an output shape of (32, 2048) (32 = images, 2048 = total features per image). The classifier consists of the dense layers Dense and Dense_1, whose output shapes are (32, 64) (32 = images, 64 = neurons) and (32, 7) (32 = images, 7 = output classes), respectively. To reduce the dimensionality, the dense layer connects every neuron in its layer to every neuron in the previous layer. Finally, the output layer Dense_1, with seven output neurons representing the seven classes of fish diseases, generates a classification result. The total number of trainable parameters in the model is 2,125,191. With the help of this architecture, the model can effectively classify images of fish diseases using the features it has learned after training.

Results and Discussion

Python programming is used in the identification and categorisation of diseases in fish. Testing is carried out using a dataset that includes seven different categories of images. The suggested system makes use of a CNN model to extract image features from the data for precise analysis. The accuracy and loss function for training and validation datasets over epochs are plotted in Figure 5. A positive relationship is observed between the number of iterations and prediction accuracy. After 150 epochs, the training loss reaches 0.2593, reflecting the algorithm's learning efficiency. The model achieves a training accuracy of 91.97 %, highlighting its strong predictive performance on the training dataset. When evaluated on an independent dataset not used during training, the model exhibits a validation loss of 0.2364 and a validation accuracy of 93.75 %. These results underscore the model's ability to generalise effectively to unseen data. The low validation loss and high validation accuracy indicate that the model successfully applies learned patterns from the training dataset to new data.

The actual and predicted labels of the classes obtained after testing the CNN algorithm, along with the confidence scores, are presented in Figure 6. For bacterial gill disease, the model correctly identifies the condition with a confidence score of 99.65 %. This shows its reliability in detecting the disease. Similarly, the model achieves a perfect score of 100.00 % for Aeromoniasis, demonstrating its precise detection capability. In the case of viral white tail disease, the model achieves a high confidence level of 97.69 %, proving its ability to recognise viral infections. For healthy fish, the model classifies them with a near-perfect confidence score of 99.94 %. This confirms its effectiveness in distinguishing between

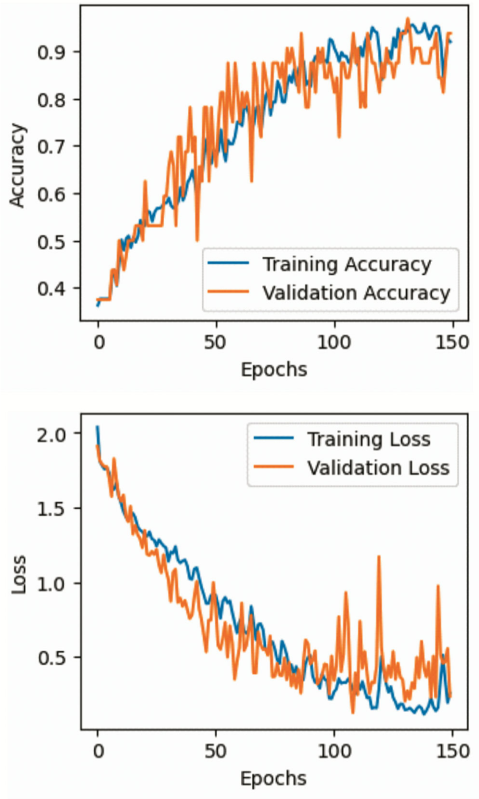

Fig. 5 — Training and validation accuracy and loss over 150 epochs

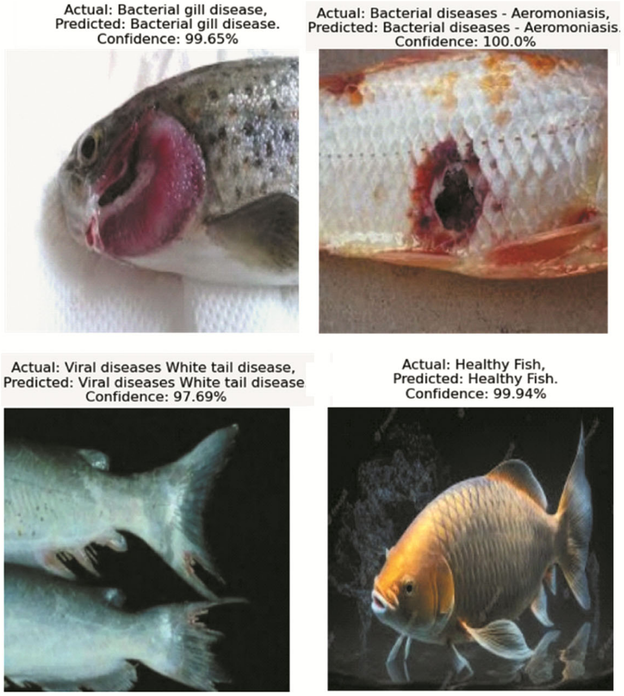

Fig. 6 — Confidence score for actual and predicted diseased classes

healthy and diseased specimens. The model consistently performs well, with confidence scores ranging from 97.69 to 100 %, reflecting its accuracy and reliability.

A thorough analysis of the confusion matrix makes it possible to evaluate the algorithm's performance and makes it easier to make improvements and modifications that will increase the accuracy in forecasting particular fish diseases (Table 1). Values of the matrix indicate the count of events falling into a specific class. Regarding the Bacterial Gill Disease, nine cases were correctly predicted (True Positives), and no cases were incorrectly predicted as other diseases (False Positives or False Negatives). Corr ect predictions are represented by the matrix's diagonal elements, and incorrect classifications are shown by the off-diagonal regions. The strengths and weaknesses of the model can be understood by examining the comparison basis across various diseases. With 24 accurate predictions and one incorrect classification, the model showed good accuracy in identifying healthy fish. In contrast, one false positive for fungal saprolegniasis disease suggests that some healthy fish may have been mistakenly diagnosed with the disease. Comparably, there have been two cases of Viral White Spot Disease misclassification, suggesting that there is still space for improvement in terms of differentiating this disease from others.

The evaluation matrices with the overall accuracy of the model are summarised in Table 2. The model achieves a high accuracy of 90.62 %. It performs particularly well in bacterial gill disease, with remarkable scores for Precision, Recall, and F1-Score. Similarly, healthy fish shows an F1-Score of 0.9412, with a good balance between Precision (0.9231) and Recall (0.9600). However, parasitic disease has the weakest performance, with an F1-Score of 0.6667. This is mainly due to the small number of instances, indicating the need for more data to improve accuracy. Other classes, such as bacterial red disease, bacterial disease – aeromoniasis, and fungal disease – saprolegniasis, perform well, with F1-Scores between 0.8571 and 1.0000, though some show slight variations between Precision and Recall. The macro average provides balanced results with Precision at 0.8793, Recall at 0.8707, and F1-Score at 0.8724. The weighted average, which considers class size, is slightly higher, showing stronger performance on larger classes like healthy fish. Overall, the model performs well, but improvements are needed, especially in handling smaller classes like parasitic diseases.

The performance of the classification model for various fish diseases is evaluated through the ROC curves and associated AUC values (Figure 7). The AUC scores of 1.0000 indicate that all four diseases: Bacterial Gill, Bacterial Aeromoniasis, Bacterial Red

Table 1 — Confusion matrix including true and false predictions

Actual \ predicted	**Red spot disease**	**Aeromoniasis**	**Gill disease**	**Saprolegniasis**	**Healthy fish**	**Parasitic disease**	**White spot disease**
Red spot disease	5	0	0	0	1	0	0
Aeromoniasis	0	5	0	0	0	0	0
Gill disease	0	0	9	0	0	0	0
Saprolegniasis	0	1	0	6	0	0	0
Healthy fish	0	0	0	1	24	0	0
Parasitic disease	0	0	0	0	0	2	1
White spot disease	0	0	0	0	1	1	7

Table 2 — Classification matrices of prediction of diseased and healthy fishes

Category	**Precision**	**Recall**	**F1-Score**	**Support**
Bacterial red disease	1.0000	0.8333	0.9091	6
Bacterial disease – Aeromoniasis	0.8333	1.0000	0.9091	5
Bacterial gill disease	1.0000	1.0000	1.0000	9
Fungal diseases Saprolegniasis	0.8571	0.8571	0.8571	7
Healthy fish	0.9231	0.9600	0.9412	25
Parasitic disease	0.6667	0.6667	0.6667	3
Viral disease - White spot disease	0.8750	0.7778	0.8235	9
Accuracy			0.9062	64
macro avg	0.8793	0.8707	0.8724	64
weighted avg	0.9081	0.9062	0.9053	64

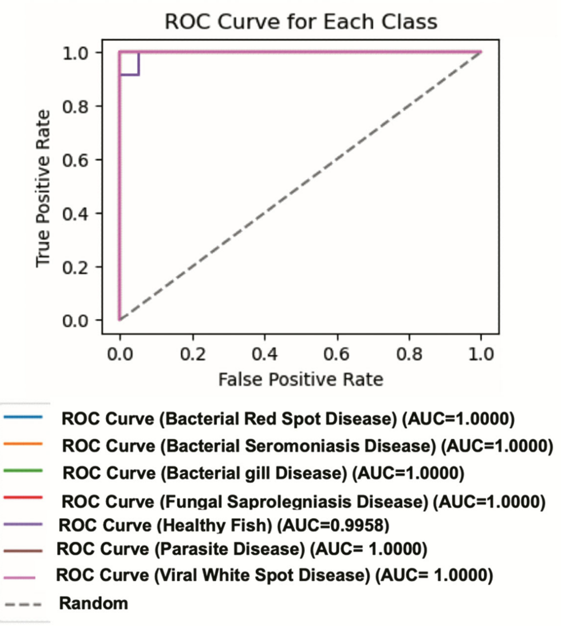

Fig. 7 — ROC and AUC curves for different classes of datasets

Spot, and Fungal Saprolegniasis display perfect differentiation between positive and negative events. These findings demonstrate the model's remarkable capacity to correctly identify these diseases. Healthy fish has an AUC of 0.9958, which is not perfect but still demonstrates good predictive power in differentiating between healthy and diseased samples. The model's ability to distinguish between viral white spot disease and parasitic disease is demonstrated by its AUC of 1. The subtle differentiation observed in healthy fish emphasises the model's exceptional accuracy in identifying health from disease, and its consistently high AUC scores across a range of diseases point to overall model performance.

The performance of the proposed sequential CNN model was compared with existing approaches in the field of fish disease detection (Figure 8). Dash *et al.*[21] employed a customised CNN integrated with ResNet-50 for classifying Indian Major Carp (IMC) diseases and achieved a testing accuracy of 87.46 %[(ref. 21)]. Mia *et al.*[22] utilised a Random Forest (RF) algorithm for fish disease recognition and reported an accuracy of 88.87 %, indicating its potential in practical applications[22]. Ahmed *et al.*[3] implemented Support Vector Machines (SVM) for salmon disease detection, achieving 91.42 % accuracy with augmented data[3]. However, they required extensive pre-processing techniques like adaptive histogram equalisation and k-means segmentation. Hasan *et al.*[18] reported the highest accuracy of 94.44 % using a CNN for detecting white spot and red spot diseases[18]. However, their dataset was limited to only 90 images and two disease categories.

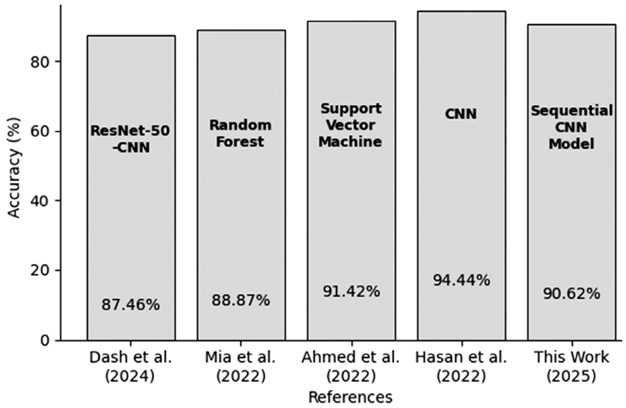

Fig. 8 — Comparison of accuracy obtained in proposed work with existing literature

In contrast, the proposed sequential CNN model achieved an accuracy of 90.62 % while handling a larger dataset with seven distinct disease categories, including bacterial and viral diseases. The proposed sequential CNN model balances high accuracy with the capacity to handle diverse disease categories, making it more suitable for real-world applications. The potential for further enhancements, such as integrating real-time datasets and multiple deep learning architectures, could elevate the model’s ability.

Conclusion

This work presents a convolutional neural network (CNN)-based machine learning method that classifies different health states in the fish. The proposed approach incorporates an advanced classifier algorithm that is intended to learn from an actual dataset. The dataset is systematically divided into classes of healthy and diseased fish. The results include numerous metrics and graphical representations of the classification outcomes. Promising results were found in the assessment of fish disease detection performance using a confusion matrix. The predicted efficacy is observed to be high. The overall performance of the proposed model is adequate.

Future work

In the future, different deep learning architectures will be included in the research to increase the accuracy and precision of fish disease detection. Working towards a real-time disease monitoring system, capturing images and analysing datasets with a minimum time gap will yield rewarding results in aquaculture health. Expanding the system's applicability to a larger range of fish datasets and aquaculture industry sectors remains the primary goal. With a focus on salmon fish due to their high demand, the goal is to improve the current dataset to ensure wider applicability and efficacy of the system.

Acknowledgements

This work was supported by the Ongoing Research Funding program (ORF-2025-395), King Saud University, Riyadh, Saudi Arabia.

Conflicts of Interest

The author declares that he has no conflict of interest.

Ethical Statement

This study did not involve any experiments on humans or animals. Ethical approval is not applicable in this study.

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