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Enhancing Disease Detection in the Aquaculture Sector Using Convolutional Neural Networks Analysis

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Abstract: The expansion of aquaculture necessitates innovative disease detection methods to ensure sustainable production. Fish diseases caused by bacteria, viruses, fungi, and parasites result in significant economic losses and threaten food security. Traditional detection methods are labor-intensive and time-consuming, emphasizing the need for automated approaches. This study investigates the application of convolutional neural networks (CNNs) for classifying freshwater fish diseases. Such CNNs offer an efficient and automated solution for fish disease detection, reducing the burden on aquatic health experts and enabling timely interventions to mitigate economic losses. A dataset of 2444 images was used across seven classes—bacterial red disease, bacterial Aeromoniasis disease, bacterial gill disease, fungal disease, parasitic diseases, white tail disease, and healthy fish. The CNNs model incorporates convolutional layers for feature extraction, max-pooling for down-sampling, dense layers for classification, and dropout for regularization. Categorical cross-entropy loss and the Adam optimizer were used over 50 epochs, with continuous training and validation performance monitoring. The results indicated that the model achieved an accuracy of 99.71% and a test loss of 0.0119. This study highlights the transformative potential of artificial intelligence in aquaculture for enhancing food security.

Keywords: aquaculture; convolutional neural networks (CNN); disease detection; freshwater fish; image classification; deep learning

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1. Introduction

The global aquaculture sector has achieved remarkable growth, setting a new record in 2022 with a production of 130.9 million tons valued at USD 313 billion [1]. This includes 94.4 million tons of aquatic animals and 36.5 million tons of algae [1]. Asia remains the global leader, contributing an impressive 91.4% of total production, with China, Indonesia, and India among the top ten producers responsible for nearly 90% of the global output [1]. For the first time, the aquaculture production of animal species (51%) surpassed capture fisheries, driven by inland aquaculture, which accounted for 62.6% of total farmed aquatic animals [1]. A significant 7.6% growth from 2020, predominantly in Asia (87.9%), was fueled by finfish aquaculture (58.1%), followed by crustaceans (24.6%) and mollusks (15.6%) [1,2]. This expansion highlights the sector's critical role in global food security and economic development [1,3,4].

The Food and Agricultural Organization's (FAO) global aquaculture production statistics dataset for 1950–2022, released in March 2024, highlights the remarkable diversity of farmed aquatic species worldwide, reporting a total of 731 statistical units, or "species items", up from 652 in 2022 [1]. These include 564 species identified at the species level,

7 inter-specific finfish hybrids, 99 genus-level species groups, and 61 higher-level taxonomic groups [1]. Among the 564 recognized farmed species, finfish dominate with 368 species spanning over 200 genera, followed by 88 species of mollusks, 62 species of crustaceans, 32 species of algae, and a smaller representation of non-finfish species [1].

Despite the remarkable diversity in farmed aquatic species, global aquaculture production is concentrated around a limited number of economically valuable "staple" species. These include popular finfish like carps, catfishes, and salmonids, as well as widely cultivated crustaceans like penaeid shrimps and mollusks such as oysters and clams [1]. This focused cultivation reflects the industry's emphasis on high-demand species, balancing economic returns with the need to sustain aquatic biodiversity.

However, as aquaculture intensifies and becomes increasingly commercialized, the risks associated with major disease outbreaks grow in parallel. The sector faces significant challenges from pathogens, including viruses, bacteria, fungi, and parasites, which collectively pose a substantial threat to aquatic species. Diseases not only constrain production capacity but also impact global economic and social development [5,6]. Intensified aquaculture environments—characterized by high stocking densities and suboptimal water quality exacerbate the spread of infectious diseases, underscoring the urgent need for effective disease management strategies [7,8].

The economic repercussions of disease outbreaks in aquaculture are staggering. The World Bank [9] estimates that global industry incurs annual losses of approximately USD 6 billion due to diseases. In major aquaculture-producing nations like China, India, and Vietnam, diseases account for up to 30% of production losses, while some studies suggest that disease-related losses can reach 50% in certain cases [10–15]. The rapid transmission of pathogens often leads to widespread infections, resulting in high mortality rates and subsequent environmental degradation through water pollution. For instance, the catfish industry in eastern Mississippi in the USA reported direct economic losses of USD 16.9 million during the 2016 production season due to disease outbreaks [16], with some farms ceasing operations entirely due to parasitic infections [17]. Similarly, bacterial infections have led to significant losses, including USD 4 million in Nile tilapia production [18].

While these challenges illustrate the urgent need for effective solutions, current disease detection methods are often time-consuming and imprecise. This highlights the need for advanced diagnostic systems to provide rapid, accurate, and scalable solutions. This study bridges this gap by proposing a robust convolutional neural networks (CNN)-based model tailored to classify freshwater fish diseases with high precision. It aims to mitigate these economic and ecological losses while addressing key global aquaculture challenges.

The profound economic and ecological ramifications of fish diseases underscore the pressing need for effective diagnostic and management approaches. Traditional methods, such as postmortem biopsies and clinical tests, are time-consuming and often lack precision [19]. Furthermore, limited access to advanced diagnostic methods in remote aquaculture regions delays timely intervention, exacerbating the scale of disease outbreaks [20,21]. To address these challenges, this study focuses on developing a robust convolutional neural network (CNN) model to detect and classify freshwater fish diseases with high precision, enabling timely interventions and reducing economic losses [22,23]. CNNs, a subset of advanced deep learning technologies, have emerged as transformative tools in aquaculture by facilitating early disease detection, reducing fish mortality, and mitigating the financial impacts of outbreaks. These advancements offer a path toward more sustainable and resilient aquaculture practices amidst growing global demand. To enhance practicality and scalability, this study recommends adopting lightweight CNN architectures, such as MobileNet, for real-time applications, incorporating data augmenta-

tion techniques to improve robustness, and developing user-friendly mobile applications for field-based disease detection.

CNNs excel in image classification tasks, including disease detection in aquaculture [16,24]. Their ability to accurately identify fish diseases provides a crucial window for timely intervention, helping to minimize both economic losses and environmental consequences [24]. Comparative studies have further demonstrated the efficacy of CNNs relative to traditional diagnostic methods. For instance, Kartika and Herumurti [25] achieved a remarkable 97% accuracy using classical image processing techniques with K-means clustering on Koi carp, while Yu et al. [26] reached an impressive 98.65% accuracy employing a MobileNet v3-87GELU-YOLOv4 model. For instance, Pei et al. [27] highlighted the utility of very large Kernel Convolutional Networks (RepLKNet) for agricultural disease recognition, emphasizing their relevance for aquaculture diagnostics. Hasan [20] attained an accuracy of 94.44% by using CNNs to detect fish diseases. Despite these advancements, many prior studies utilized small or imbalanced datasets, limiting their generalizability to real-world applications [20,28,29]. Addressing this gap, the current study employs a robust dataset encompassing seven disease categories, providing comprehensive insights into the model's performance in practical scenarios.

The adoption of CNNs in fish disease diagnostics has garnered significant attention due to its potential to revolutionize aquaculture methods. Prior research on CNN analysis demonstrates that CNNs can effectively detect and classify diseases using image datasets, achieving higher accuracy than conventional techniques [20,21]. By leveraging advanced CNN architectures, this study showcases the potential for improved precision and efficiency in early disease detection, contributing to sustainable aquaculture practices. Moreover, it aims to advance the field by developing and evaluating a novel CNN-based technique specifically for freshwater fish disease classification. Such innovations represent a critical step toward addressing global food security challenges by enhancing the sustainability and efficiency of aquaculture systems. The integration of artificial intelligence and deep learning technologies signals a promising future for disease management and the broader aquaculture industry [30]. The integration of artificial intelligence, particularly CNNs, into aquaculture disease management holds immense potential to not only reduce losses but also empower small-scale farmers with accessible diagnostic tools, thereby fostering inclusivity and resilience in the industry [26,31,32].

2. Materials and Methods

2.1. Data Collection

A variable dataset of images depicting healthy freshwater fish and different fish diseases was collected via Kaggle [28], an online community and competition platform for data scientists and machine learning practitioners. This repository, entitled "Freshwater Fish Disease Aquaculture in South Asia", contains 2444 images categorized into seven groups: bacterial red disease, bacterial Aeromoniasis disease, bacterial gill disease, fungal Saprolegniasis disease, healthy fish, parasitic disease, and viral disease/white tail disease. We employed approximately a 70/30 split in our current deep learning modeling study as it represents a standard practice in machine learning, providing sufficient data for training while reserving a significant portion for validation to assess model generalizability. This ratio effectively mitigates overfitting and ensures robust performance evaluation, especially with datasets of this size, as highlighted by Sivakumar et al. [33]. Out of those total images:

- The training set comprises 1747 images (71.48% of total images used). Here, every class contains around 250 images, except for the "viral disease/white tail disease" class, which has 247 images.

- The validation set comprises 697 images (28.52% of total images used). The validation set consists of approximately 100 images per class, verifying that it aligns with the training dataset's consistency. The model was developed using Keras, a high-level API built on TensorFlow, due to its simplicity and user-friendly design, which facilitates rapid prototyping and development of deep learning models. While Keras is widely adopted, alternatives like PyTorch 2.3.0 offer additional flexibility and lower-level control, making them better suited for certain advanced research and production environments [22,23]. Future studies could explore PyTorch to improve compatibility with broader frameworks and optimize performance for resource-constrained setups.

Equitable data allocation across all classes is essential to ensure that the model learns from each category in a balanced manner, minimizing potential bias toward any specific disease category. However, we anticipate that the slight reduction in three images will not significantly impact the results or introduce noticeable bias.

These images exhibit a wide range of characteristics, depicting different phases and forms of diseases in various environmental circumstances. The presence of diverse data is crucial for effectively training the CNN model to identify and reliably categorize diseases in real-world situations. The dataset is essential for constructing a resilient model that can effectively adapt to various conditions and disease stages, offering a comprehensive tool for managing aquaculture diseases.

2.1.1. Data Preprocessing

To prepare the dataset for training the convolutional neural network (CNN), several preprocessing steps were implemented to ensure effective learning. All images were resized to 150 × 150 pixels, standardizing input sizes and reducing computational complexity, which allows for the model to process each image efficiently. Pixel values were normalized by rescaling them from 0 to 1 using a scaling factor of 1/255, facilitating faster convergence during training [29].

From preprocessing to developing the model, we used Python 3.9.13, sci-kit-learn, and the TensorFlow library [23]. The Python code was compiled on a MacBook Pro with Apple M1 Pro Chip, 16 GB memory, and Sequoia macOS. The IDE used for this project was Jupiter Notebook 6.4.12. The CNN model was trained solely on the original dataset without additional artificial variations. Additionally, no transfer learning was applied, as the CNN model was built and trained entirely from scratch, specifically for fish disease detection. The model was compiled using the Adam optimizer, which adapts the learning rate during training to ensure efficient and stable convergence. These preprocessing steps standardized the dataset, allowing for the model to learn directly from the original data, tailored specifically for fish disease detection without added complexities.

2.1.2. Data Generation

As illustrated in Figure 1, the training and validation data generators were initialized using the Keras Image Data Generator class, which preprocesses images. The training data generator applied rescaling to make the images contribute more evenly to the total lost when training a model. The validation data generator took the rescaled data and only used them to ensure that we evaluated the untouched data. Both generators were set to scale the images to 150 × 150 pixels and normalize pixel values between 0 and 1.

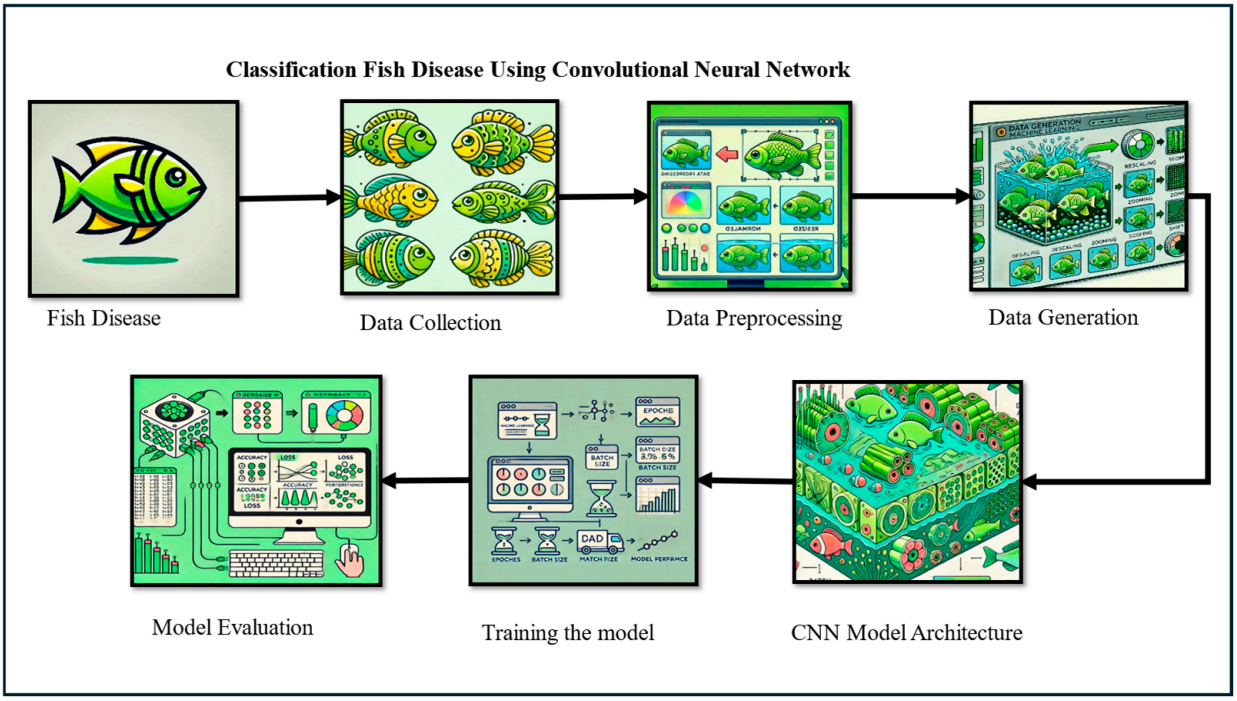


Figure 1. Flowchart of fish disease classification experiment using CNN. Image generated using OpenAI's DALL·E model. Available online: https://docs.google.com/presentation/d/1gPuxNkAZjZ3OicKzyTP7rKycFVp4hmis/edit?usp=sharing&ouid=109059284489742000095&rtpof=true&sd=true (accessed and downloaded on 20 September 2024). Image available upon request.

2.2. Model Evaluation

The CNN model architecture classifying freshwater fish diseases contains a substantial section of spatial feature extraction and absorption from the input images. We utilize 3 Conv2D layers that use filters of sizes 128, 64, and then 32 to obtain patterns at different granularity levels. After each convolutional layer, ReLU (Rectified Linear Unit) activation is applied to introduce non-linearity and batch normalization to improve the robustness of deep neural networks and accelerate the training process, max-pooling, which permutes spatial complexities, as shown in Figure 2. To prevent overfitting, the network has dropout layers at every stage, deactivating neurons randomly during training, meaning that they will not be affected by the optimization process. The flattened output from the feature extraction layers continues to a dense layer with 256 units and ReLU activation, allowing for an integrated presentation of all the extracted features before classification. The last output layer uses a SoftMax activation function to produce the probabilities across the seven disease classes. It intuitively makes predictions based on what it thinks is most likely for each image. Here, we have introduced a balance of complexity and efficiency in designing our architecture to achieve robust learning (without overfitting) while ensuring improved disease identification.

2.2.1. Model Compilation

The CNN model was compiled using the Adam optimizer, which could be very efficient and adapt to the learning rate. Categorical cross-entropy is a standard loss function used for multi-class classification tasks. Additional callbacks were introduced to optimize training: Reduce LROn (Learning Rate On) Plateau was a callback that decreased the learning rate when it detected that validation loss had plateaued. Early stopping ensured that training would cease if there were no improvements in validation loss for a specified number of epochs.

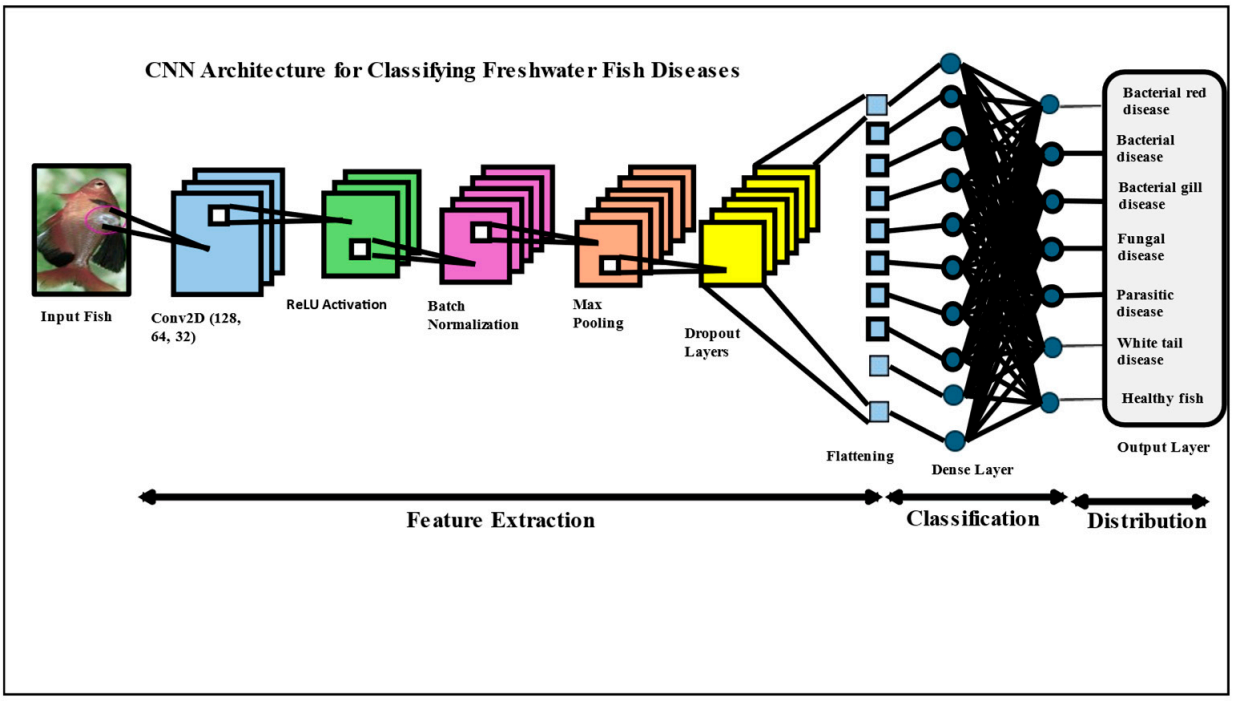


Figure 2. CNN architecture for classifying freshwater fish diseases (source: created by the current authors).

2.2.2. Training the Model

The CNN model was compiled using the Adam optimizer and the categorical cross-entropy loss function, which were well suited for multi-class classification tasks. The Adam optimizer was chosen for its efficiency in handling sparse gradients on noisy problems, making it ideal for this application (Figure 3). The training is run for 50 epochs with a batch size of 32, meaning that the model is trained on all images in parts of mini batches (containing only such an amount each time). This also enables better generalization and memory utilization.

To improve the training, a Reduced LROn Plateau callback reduced the learning rate by multiplying it after several epochs with no improvement in validation loss. This adaptation allows the model to converge better without getting stuck in the local minimum. Furthermore, the early stopping callback was used to stop training if validation loss did not improve for a certain number of epochs, and both use l1 kernel regularization, so it will reduce overfitting and do an excellent job of saving computational resources. The training and validation accuracies, the percentages of images that were classified correctly by the network, were also monitored along with its losses during training to see how well it generalizes. For the training history, all users made progress on accuracy, and loss decreased over time, with some early signs of overfitting controlled by this set of callbacks.

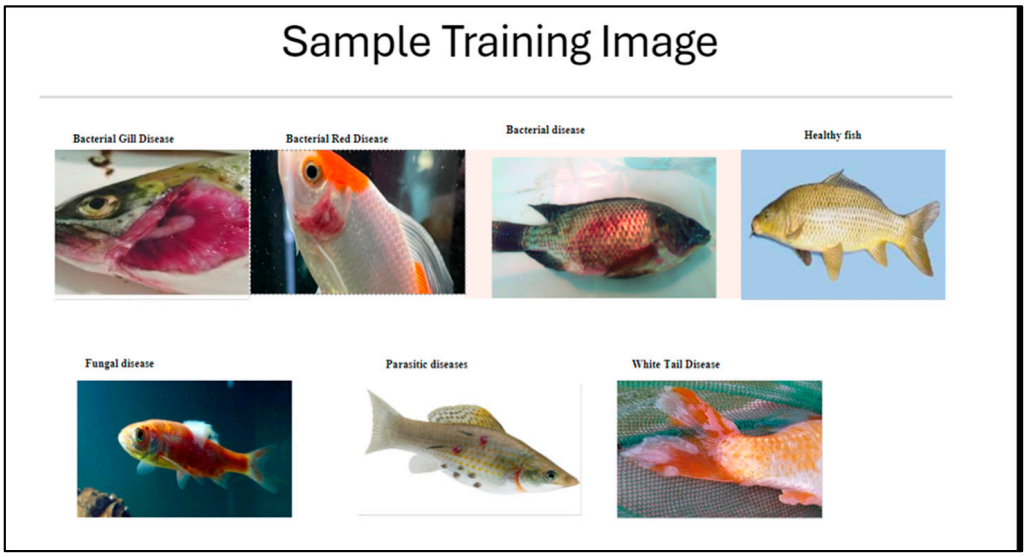


Figure 3. Sample training images for fish disease detection model (source: current dataset).

2.3. Evaluation Criteria

Classifying fish diseases using the CNN model was evaluated on a training dataset containing 1747 images in seven classes (Figure 4). Next, precision, recall, and F1-scores were calculated for each class to evaluate the model's performance further for most classes; precision (a measure used to determine optimistic predictions) and recall (assesses whether the model captures all instances) were high. According to the F1-score (balanced between precision and recall), the model performance indicated strong robustness and generalization ability when applied to fish disease classification.

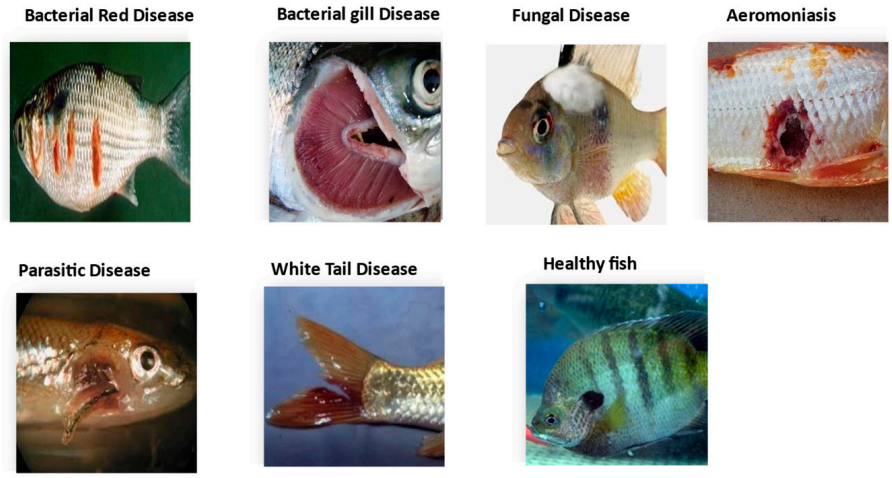


Figure 4. Test dataset predictions for fish disease detection CNN model (source: current dataset).

A confusion matrix was generated alongside quantitative metrics, providing a graphical representation of the model's performance across all disease categories. This visualization highlights areas of highest accuracy and performance, as well as instances of misclassification. Analyzing these confusion matrices and corresponding heatmaps offers valuable insights into the sources of misclassification, enabling a deeper understanding of the model's weaknesses. Such findings are crucial for refining the model, ensuring its effective transfer to real-world applications in fish disease management.

3. Results and Discussion

The outcomes of the CNN model in diagnosing freshwater fish diseases reflect this application-based device's great capacity and versatility. A test accuracy of 99.71% means that the model can effectively categorize all the seven disease classes concealed in a test dataset containing 697 images (Figure 5). This is demonstrated by the low-test loss of 0.0119, indicating that this model will help classify new unseen data with minimal error. While the recall for certain classes leads one to believe that there may be some false negatives, this exercise appears to classify actual instances of fish diseases well. It has high precision on all ground truth labels. Numerous validation metrics provide supporting evidence that the model is working acceptably; all together, these line plots are shown in Figure 6. The values demonstrate the reliable behavior of this deep learning approach, which can be suitable for real-case scenarios such as aquaculture management or disease tracking when the immediate and precise diagnosis of diseases is essential.

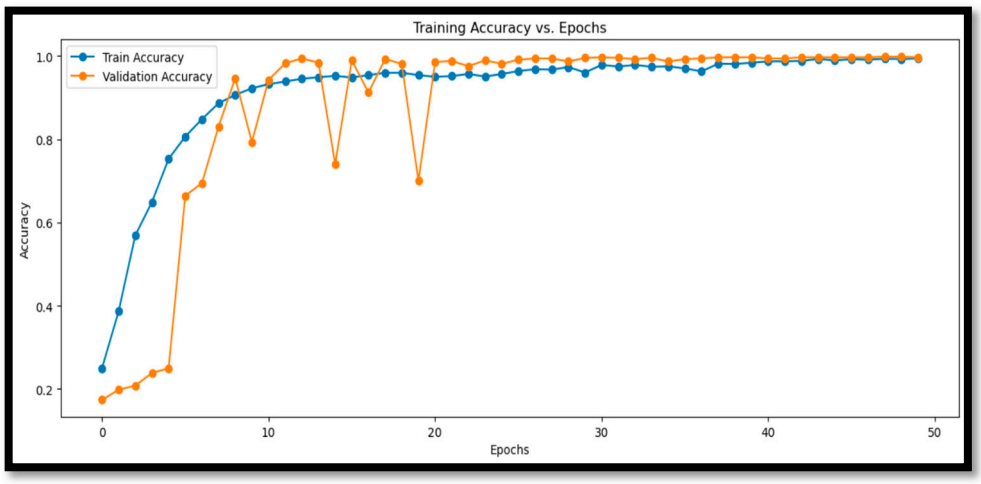


Figure 5. Accuracy of CNN model expressed through line plotting (source: current data analysis).

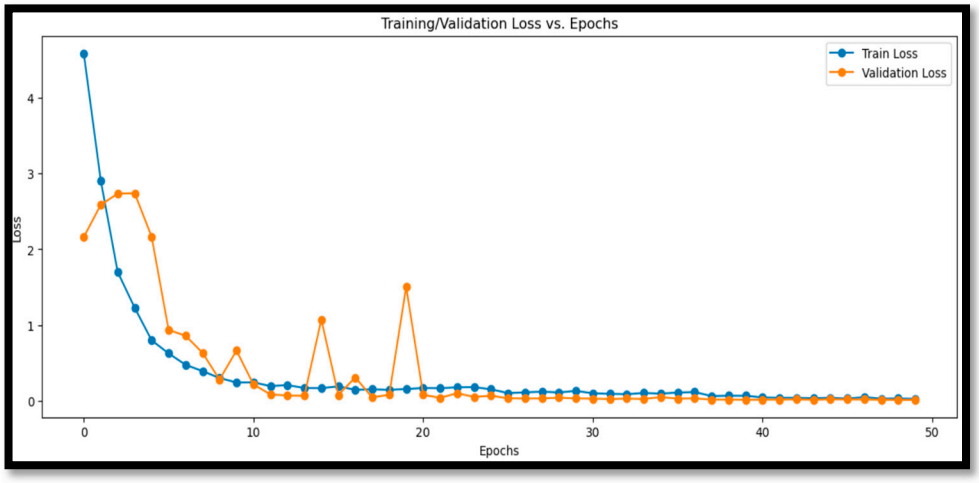


Figure 6. Loss of CNN model expressed through line plotting (source: current data analysis).

Nevertheless, while the final performance of the model was excellent overall, some error analyses revealed valuable areas for improvement. False negatives were mainly observed between visually similar disease classes, i.e., primarily bacterial gill disease and bacterial red disease (Table 1). These subtle similarities contribute to occasional misclassifications, which can be addressed by improving the dataset and refining the model's architecture. Specifically, introducing more diverse and representative images for challenging classes such as Aeromoniasis and fungal diseases could significantly enhance

the model's ability to distinguish between similar conditions. Additionally, employing advanced techniques like attention mechanisms and more sophisticated feature extraction processes could help the model focus on critical features unique to each disease class. The confusion matrix analysis exposed the minimal number of misclassifications that took place and demonstrated how generally robust and trustworthy the model was, as shown in Figure 7. Overall, the effectiveness of the CNN model against multiple challenges, coupled with ongoing refinements, likely improves its resilience, accuracy, and utility for deployment in aquaculture or analogous fields. Additionally, the model correctly detects different fish diseases, explaining the high value of all classification metrics (precision, recall, and F1-score) across every class, as shown in Figure 8.

Table 1. The CNN architecture used in modeling (source: current data analysis).

Layer (Type)	Output Shape	Parameters (Param #)
Conv2d_3 (Conv2D)	(None, 146, 146, 128)	9728
Activation_3 (Activation)	(None, 146, 146, 128)	0
Max_pooling2d_3 (maxpooling2d)	(None, 73, 73, 128)	0
Batch_normalization_3 (batch-normalization)	(None, 73, 73, 128)	512
Conv2d_4 (Conv2D)	(None, 71, 71, 64)	73,792
Activation_4 (Activation)	(None, 71, 71, 64)	0
Max_pooling2d_4 (maxpooling2d)	(None, 35, 35, 64)	0
Batch_normalization_4 (batch-normalization)	(None, 35, 35, 64)	256
Conv2d_5 (Conv2D)	(None, 33, 33, 32)	18,464
Activation_5 (Activation)	(None, 33, 33, 32)	0
Max_pooling2d_5 (maxpooling2d)	(None, 16, 16, 32)	0
Batch_normalization_5 (batch-normalization)	(None, 16, 16, 32)	128
Flatten_1 (Flatten)	(None, 8192)	0
Dense_2 (Dense)	(None, 256)	2,097,408
Dropout_1 (Dropout)	(None, 256)	0
Dense_3 (Dense)	(None, 7)	1799

Total parameters: 2,202,087 (8.40 MB); **Trainable parameters:** 2,201,639 (8.40 MB); **Non-trainable parameters:** 448 (1.75 KB); **Param # (Parameters Count)** refers to the number of trainable weights (parameters) in each layer.

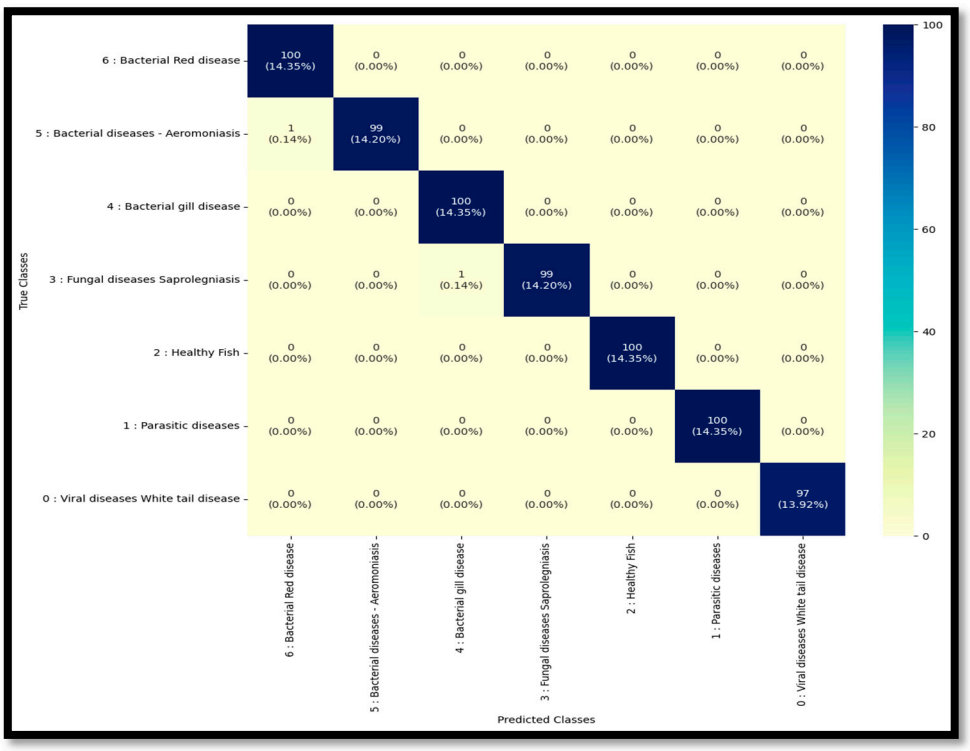


Figure 7. Confusion matrix for CNN model (source: current data analysis).

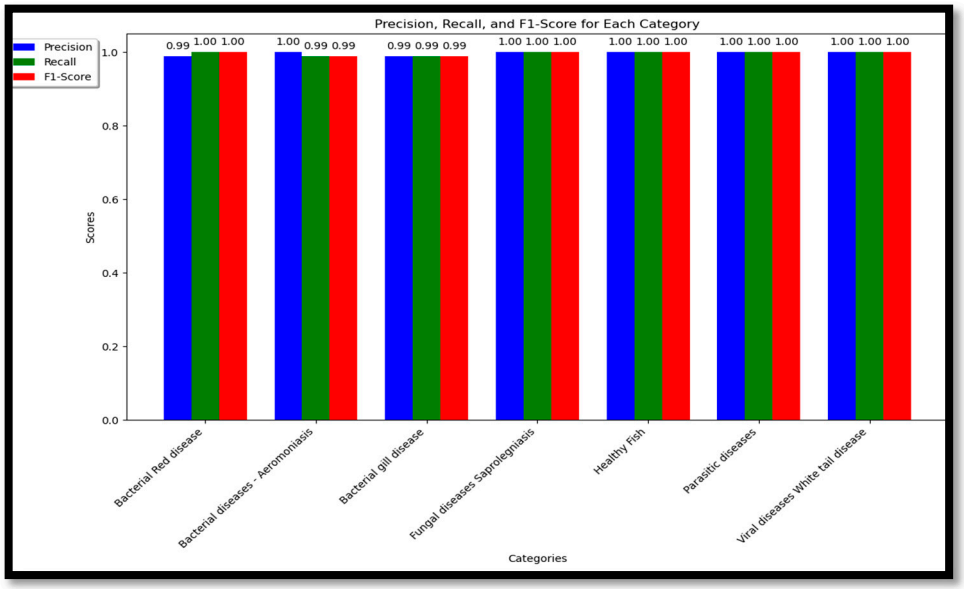


Figure 8. Performance comparison of all classes (source: current data analysis).

The CNN model was trained and inferred at a reasonable time complexity based on the task difficulty. The training is executed over 50 epochs, and each epoch lasts around 29–30 s. Using techniques like batch normalization and dropout layers has made the training part of this model more efficient by making learning stable, such that it is not prone to overfitting, which also helped improve both the accuracy and efficiency of the performance. While quite a bit more computationally expensive, using convolution layers with different filter sizes gave our model an advantage in capturing spatial features without losing finer detailed scales due to processing all scales simultaneously using parallelism exploited during training on modern GPUs. The model balances performance and computational efficiency, making it practical for use in aquaculture.

Previous studies have highlighted the effectiveness of convolutional neural networks (CNNs) in advancing aquaculture practices, particularly in fish detection and disease classification. For instance, Rekha et al. [21] reported that their CNN analysis achieved an accuracy of 90% in fish detection and 92% in classification. Similarly, Hasan et al. [20] demonstrated that applying CNNs for detecting fish diseases across diverse testing datasets yielded an impressive accuracy of 94.44%. Their findings also indicated that CNNs are highly effective in identifying and classifying various disease types among infected fish. In this study, 90 images were tested, including healthy fish and two disease categories—white spot and red spot—to further explore CNN's potential in enhancing disease detection accuracy and classification [20].

Comparative studies have demonstrated various levels of efficacy in disease diagnosis when employing different methodologies. For instance, Tseng and Lin [34] attained an accuracy of 88.87% by using CNNs in conjunction with K-means clustering to detect fish diseases. Similarly, Ahmed et al. [23] utilized CNNs and achieved an accuracy rate of 87.46%. Mia et al. [32] examined various machine learning algorithms, such as Logistic Regression, Back Propagation Network (BPN), Counter Propagation Network (CPN), Gradient Boosting, Support Vector Machine (SVM), Random Forest, K-means clustering, K-Star, and K-Nearest Neighbors (KNNs). They achieved random forest to be best performed among all with an average accuracy of 88.87%. Chakravorty et al. [35] utilized Principal Component Analysis (PCA) with K-means clustering, achieving a superior accuracy rate of 90%. Malik et al. [36] implemented the fish detection network (FD_Net) model, which attained an average precision score of 95.30% on the testing dataset. Kartika and

Herumurti [25] achieved the most remarkable recorded accuracy of 97% by employing classical image processing techniques and K-means clustering on koi carp. In a recent study, Yu et al. [26] Successfully applied a MobileNet v3-GELU-YOLOv4 model, achieving 98.65% accuracy using a dataset of 500 images from Penghu and Yellow Sea submersible cages, expanded to 4550 images via augmentation. The dataset was divided into 8:1:1 for training, validation, and testing focused on detecting four fish diseases: hemorrhagic septicemia, saprolegniasis, benedeniasis, and scuticociliatosis.

While our study demonstrated strong performance with a custom-built CNN achieving an accuracy of 99.71%, we acknowledge the need for broader comparisons with state-of-the-art techniques and exploration of alternative methods. Preliminary experiments with ResNet50 transfer learning yielded a lower validation accuracy of 70.83%, highlighting the effectiveness of our tailored CNN architecture. Future research will focus on comparing our model with advanced architectures, such as EfficientNet, MobileNet, or attention-based networks, and integrating hybrid approaches like clustering techniques to enhance feature extraction and robustness.

3.1. Model Time Complexity

The CNN model is computationally heavy due to its convolutional, max-pooling, and dense layers. The time complexity of applying a single convolutional layer is given as follows:

$$\textit{Model time complexity} = O\left(K \times M \times N \times C\right) \quad (1)$$

where, K is the kernel size, M and N are the dimensions of the feature map, and C denotes the number of input channels. Convolutional layers are the most computationally intensive components of CNNs, with complexity growing with the number of filters and input dimensions, as highlighted by Lee and Chen [37]. Simplifying the model architecture can maintain performance while reducing complexity, especially in resource-constrained environments, as demonstrated by Oyedare et al. [38]. The complexity grows disproportionately with the number of filters and layers, making training computationally expensive, especially for large datasets. However, max-pooling layers reduce the spatial dimensions of feature maps, thereby lightening the computational load to some extent. Nevertheless, the time cost remains significant for high-dimensional inputs. Dense layers further contribute to increased complexities, depending on the number of neurons and connections.

Despite these computational demands, the model is well optimized for modern GPU parallel processing, enabling efficient training and inference. Techniques such as batch normalization and dropout stabilize and accelerate the training process, making the model suitable for large-scale applications.

In practice, each training epoch was completed in approximately 30 s, with the full training process (50 epochs) taking around 1500 s (25 min). The evaluation phase consisted of 22 steps, each lasting about 3 s, totaling an additional 66 s. Thus, the entire process, including training and evaluation, required approximately 1566 s, or roughly half an hour.

While CNN modeling is highly effective in identifying fish diseases, these models are likely to face challenges related to computational complexity and training duration. For instance, Hasan et al. [20] reported that their CNN model required approximately 25 min to train over 50 epochs, with an additional 66 s for evaluation, totaling around 26 min for the entire process. Similarly, Ramachandran et al. [39] observe comparable training times in their Dense Inception CNN model for shrimp disease detection. In contrast, Wang et al. [40] introduced the DFYOLO network, an enhanced YOLOv5 architecture, which achieved a high detection accuracy of 99.38% mAP50, maintained a fast inference speed of 93.21 FPS, and occupied less memory (13.6 MB), without providing specific details on training time. These findings suggest that while traditional CNN models are computation-

ally intensive, optimized architectures like DFYOLO can offer improved performance and efficiency, making them more suitable for large-scale applications in resource-constrained environments.

3.2. Confusion Matrix Analysis

The classification model demonstrates exceptional performance in predicting and classifying various fish diseases, as highlighted by the confusion matrix analysis and classification report, as shown in Figure 7. This model achieves high precision, recall, and F1-scores for every disease category tested, highlighting the ability of our method to detect diseases in freshwater fish aquaculture. The model is incredibly efficient in labeling diseases like bacterial gill disease and fungal diseases (Saprolegniasis), as it had very few false positives and a false negative rate. For example, the final model was extremely good at classifying 'bacterial red disease' with a precision of 0.99, recall of 0.98, and F1-score of 0, as shown in Table 1. The model's performance is slightly changed for viral diseases (white tail disease), but overall, its accuracy does not vary. The confusion matrix (Figure 7) further highlights the model's excellent performance while revealing minor errors. For instance, out of 100 samples for Aeromoniasis, one image was misclassified as another class, resulting in a single false negative. Similarly, one misclassification was observed for fungal diseases (Saprolegniasis), aligning with the recall score of 0.99 for this class. Despite these small errors, the confusion matrix confirms the model's reliability and demonstrates its ability to distinguish between visually similar diseases.

Previous studies have demonstrated the effectiveness of convolutional neural networks (CNNs) in achieving high precision and recall rates for accurately detecting and classifying various fish diseases. For example, Haddad and Mohammed [41] reported that their CNN model achieved a precision of 0.99 and a recall of 0.98 in identifying bacterial red disease. Similarly, Thakur et al. [42] highlighted the model's efficiency in classifying diseases, such as bacterial gill disease and Saprolegniasis, with minimal false positives and negatives. These findings are consistent with the current study, where the confusion matrix analysis reveals exceptional performance in predicting and classifying various fish diseases. The model achieves high precision, recall, and F1-scores across all the tested disease categories, indicating its robustness in detecting diseases within freshwater fish aquaculture. Notably, the model excels in labeling diseases like bacterial gill disease and Saprolegniasis, exhibiting very low false positive and false negative rates. However, the confusion matrix also highlights challenges in distinguishing between visually similar severe bacterial diseases, leading to occasional misclassifications. Despite these challenges, the overall high performance metrics underscore the model's effectiveness in disease detection for freshwater fish aquaculture.

3.3. Performance Metrics

The performance metrics were used to assess our CNN model for detecting different types of fish diseases from images. Accuracy gives an overall score of how many we got right. Precision provides a measure of accuracy for the positive class predictions. Remembering or sensitivity reflects the model's response to recognizing all true positive classes and F1-score brands, such as precision and recall, that generate better for imbalanced datasets. The support indicates the number of actual occurrences of each class, which can reveal weaknesses in the classifier. Using these metrics, we can derive whether the model is competent or needs to improve at predicting to evaluate its performance holistically.

The following formulas were used to compute the performance metrics:

$$\bullet \text{ Accuracy} = \frac{\text{TP} + \text{TN}}{\text{TP} + \text{TN} + \text{FP} + \text{FN}} \quad (2)$$

$$\bullet \text{ Precision} = \frac{TP}{TP + FP} \quad (3)$$

$$\bullet \text{ Recall} = \frac{TP}{TP + FN} \quad (4)$$

$$\bullet \text{ F1-Score} = 2 \times \frac{P \times R}{P + R} \quad (5)$$

Note: "TP" stands for True Positive, "TN" stands for True Negative, "FP" stands for False Positive, and "FN" stands for False Negative; P = Precision; R = Recall.

3.3.1. Enhanced Quantitative Analysis of Accuracy and Errors

The CNN model achieved an impressive test accuracy of 99.71% and a low-test loss of 0.0119, reflecting its robustness in classifying seven freshwater fish disease categories. While these metrics highlight the model's overall efficacy, a detailed analysis of its quantitative performance provides deeper insights into its strengths and limitations. Class-wise performance metrics, including precision, recall, and F1-score, were computed to assess the model's accuracy in identifying diseases. Table 2 presents a summary of these metrics:

Table 2. The performance metrics across classes (source: current data analysis).

Disease Class	Precision	Recall	F1-Score	Support
Bacterial Red Disease	99.71	1.00	1.00	100
Bacterial Diseases (Aeromoniasis)	1.00	0.99	0.99	100
Bacterial Gill Disease	0.99	1.00	1.00	100
Fungal Diseases (Saprolegniasis)	1.00	0.99	0.99	100
Healthy Fish	1.00	1.00	1.00	100
Parasitic Diseases	1.00	1.00	1.00	100
Viral Diseases (White Tail Disease)	1.00	1.00	1.00	97

The model demonstrates excellent performance across all disease categories, with precision, recall, and F1-scores nearing 1.00 for most classes. A slightly lower recall of 0.99 for Aeromoniasis and fungal diseases indicates a minimal presence of false negatives. Overall, the balanced scores reflect the model's robustness and ability to generalize effectively to diverse samples.

This study utilized the key performance metrics of accuracy, precision, recall, and F1-Ssore to assess the effectiveness of the convolutional neural network (CNN) model in detecting fish diseases. Accuracy represents the proportion of total correct predictions, providing an overall measure of the model's performance. Precision indicates the accuracy of positive predictions, reflecting the proportion of correctly identified positive instances among all instances predicted as positive. Recall, or sensitivity, measures the model's ability to identify true positive cases, indicating how well the model captures actual positive instances. The F1-score, as the harmonic mean of precision and recall, offers a balanced metric, especially valuable in scenarios with imbalanced datasets. These metrics, alongside the confusion matrix, which details the counts of true positives, true negatives, false positives, and false negatives, provide comprehensive insights into the model's strengths and areas for improvement in classifying fish diseases. This approach aligns with methodologies in similar studies, such as those by Haddad et al. [41] and Ssekitto et al. [43], which emphasize the importance of these metrics in evaluating CNN models for fish disease detection [20,44].

3.3.2. Error Analysis

In the error analysis, the model exhibited a high level of accuracy, with a test accuracy of approximately 99.71%. However, despite this strong performance, some misclassifica-

tions were still observed. The confusion matrix and classification report reveal that these errors are distributed across various classes, though they are minimal. For instance, a few false negatives were identified in Aeromoniasis and fungal diseases, likely due to overlapping visual features with other disease categories. Additionally, subtle visual similarities between diseases such as bacterial red disease and bacterial gill disease contributed to occasional misclassifications. This indicates that the model occasionally confuses visually similar disease manifestations, particularly among bacterial diseases (Figure 9). This could be attributed to the subtle differences in visual patterns between certain conditions, which are challenging even for advanced models to distinguish. Error analysis provides insights for identifying common errors and their causes, as discussed in other domains like language learning [45]. The error images show that the true labels and predicted labels are often close in nature, suggesting that while the model is highly effective, further refinements, such as increased data augmentation or more complex architectures, might help reduce these errors even further. Despite these minor errors, the overall high precision, recall, and F1-scores across classes underscore the model's robustness and suitability for practical use in aquaculture. These findings indicate that while the model is reliable for practical use, ongoing adjustments could help achieve near-perfect accuracy.

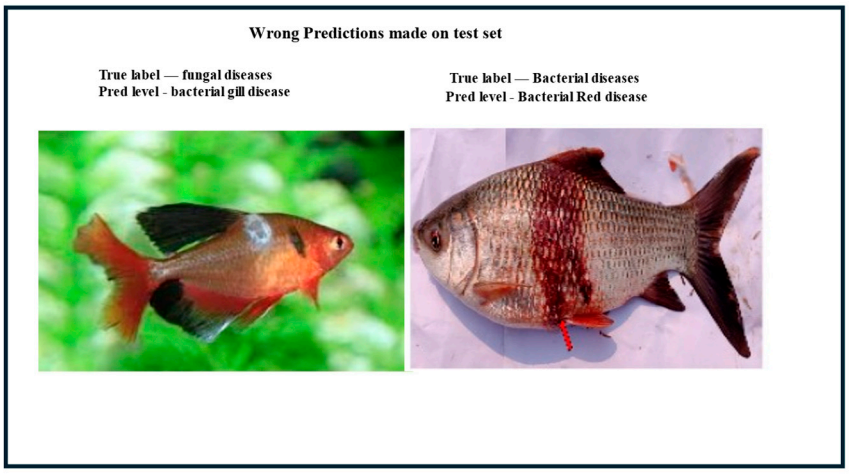


Figure 9. Error analysis of wrong prediction in fish disease detection/CNN model (source: current data analysis).

Previous studies have demonstrated both the promise and limitations of using deep learning models for marine species' identification and fish disease detection, often emphasizing the importance of addressing misclassification challenges. For instance, Nanthini et al. [46] achieved a test accuracy of 99.71% for marine species' classification using CNNs but noted misclassifications among visually similar species attributed to subtle morphological differences. Similarly, Muhammad et al. [47] reported a mean average precision (mAP) of 0.237 in detecting fish diseases with DCNNs, with confusion occurring due to visually similar disease manifestations. Furthermore, Thakur et al. [42] identified similar issues in aquatic disease detection, where a lack of high-resolution imagery led to misclassifications, particularly for early-stage disease symptoms. Collectively, these studies underscore the need for refined techniques, such as increased data augmentation, improved data diversity, and novel architectures like attention-based CNNs, to overcome the challenges posed by subtle visual differences and class imbalances [48].

3.4. CNN Model Architecture and Performance

The CNN model architecture was used with convolutional layers for feature extraction, a max-pooling layer for down-sampling, and the dense layer fully connected, and dropout

layers were successfully classified accordingly, achieving good accuracy. Although this study had limitations, such as a small number of datasets and class imbalance, the results demonstrated that CNNs could automatically detect fish disease. The robustness and reliability of the model are demonstrated by its high accuracy and detailed evaluation metrics. CNNs are designed to automatically extract hierarchical features from images, making them highly effective for classification tasks. This is achieved through convolutional layers that capture spatial hierarchies and dense layers that perform classification based on extracted features, as demonstrated by Lokesh et al. [49].

Additionally, CNNs have been shown to achieve high accuracy in various image classification tasks. For instance, a study comparing different CNN architectures reported that MobileNet V2 achieved an accuracy of 92.80% in object recognition tasks, highlighting the capability of CNN models for classification challenges [50]. These findings underline the effectiveness of CNNs in delivering reliable results even when applied to complex datasets, as shown in Figure 8.

Previous studies have consistently demonstrated the effectiveness of convolutional neural networks (CNNs) in addressing the challenges of fish disease detection within aquaculture, highlighting their versatility and adaptability across various datasets and architectures. Ahmed and Jeba et al. [23] emphasized the utility of the Salmon Scan dataset, with its 1208 images of healthy and infected salmon, in training robust CNN models capable of extracting hierarchical features, thereby enhancing classification accuracy. Similarly, Dash et al. [51] demonstrated the efficacy of a customized ResNet-50 model in classifying Indian Major Carp (IMC) diseases with high reliability, despite dataset limitations such as size and class imbalance. Azhar et al. [52] further illustrated the robustness of GoogleNet, achieving 90% accuracy in detecting Protozoan white spot disease through convolutional and dense layers that excel in feature extraction and classification. Additionally, Islam et al. [53] highlighted the superiority of CNN models like VGG16 and VGG19, which achieved 99.64% accuracy, outperforming traditional machine learning approaches in fish disease detection. These studies collectively underscore the potential of CNN architectures in automating complex classification tasks, with their effectiveness being driven by hierarchical feature extraction capabilities. However, they also highlight recurring challenges, such as limited dataset diversity and class imbalance, emphasizing the need for more extensive datasets and advanced architectures to enhance performance further.

3.5. Error Visualization Insights

The error visualization gave us much more information regarding the model's mistakes. We would display misclassified images and their actual and predicted labels to help us identify patterns responsible for incorrect classification. Previous work has shown the effectiveness of such techniques in refining model performance [54]. This study gives an excellent example of the capability of CNNs in classifying freshwater fish diseases and represents considerable development within aquaculture disease detection. The CNN model built in this research obtained an impressive overall accuracy of 99.71% and a test loss of 0.0119, demonstrating its potential for classifying (healthy fish vs. those affected with different diseases such as bacterial infection, viral infection, parasitic infection, and fungal infection).

Previous studies have demonstrated the utility of error visualization techniques in refining CNN performance by identifying patterns leading to misclassifications For example Muhammad et al. [47] emphasized the role of displaying misclassified images with their actual and predicted labels to uncover recurring errors, aiding in improving model training and fine-tuning. Such techniques have proven themselves to be vital in enhancing CNN robustness for classifying freshwater fish diseases, achieving accuracies as high as

99.67% when utilizing advanced architectures like gradients from the CNN itself to create adversarial examples. Similarly, Ramachandran et al. [39] demonstrated the application of an improved Dense Inception CNN (DICNN) for detecting White Spot Syndrome Virus (WSSV) in shrimp, achieving a high accuracy of 97.22%, though their study did not focus on error visualization. Akram et al. [44] further extended CNN applications to aquaculture infrastructure, detecting net defects with semantic segmentation methods to ensure healthy growth environments. This body of work underscores the versatility of CNNs in aquaculture, not only for disease detection but also for ensuring broader system integrity. The current study builds on these advancements, achieving an accuracy of 99.71% with a test loss of 0.0119 for classifying healthy and diseased fish, demonstrating the capability of CNNs in addressing complex classification tasks and reinforcing the value of error visualization for ongoing model improvement.

4. Conclusions

This study demonstrates the potential of convolutional neural networks (CNNs) in enhancing disease detection in freshwater aquaculture. Achieving 99.71% accuracy with a test loss of 0.0119, the model effectively identifies diseases caused by bacteria, fungi, parasites, and viruses. By introducing a reliable and automated diagnostic tool, this research addresses critical challenges in aquaculture disease management, contributing to sustainability and reducing economic losses. Future work should address limitations such as small dataset size and class imbalance, which affect generalizability. Expanding the dataset with diverse and representative images, especially rare disease cases, is essential. Additionally, exploring resource-efficient architectures like MobileNet or implementing optimization techniques like pruning can make the solution accessible for aquaculturists in resource-limited settings.

The following steps include leveraging advanced architectures like ResNet or attention mechanisms to enhance feature extraction and classification accuracy. Integrating transfer learning with pre-trained models can reduce training costs and hardware requirements. Developing intuitive interfaces and mobile applications would increase practical usability, especially for small-scale farmers. Key research questions to explore are as follows: (1) How can real-time disease detection systems be designed for affordability and scalability? (2) What methods can improve performance for diseases with overlapping visual features? (3) How can hybrid models combine CNNs and traditional machine-learning approaches to optimize classification accuracy? This study underscores the vital role played by artificial intelligence in sustainable aquaculture and global food security, advocating for continued innovation and broader adoption.

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References

1. FAO (Food and Agricultural Organization). The State of World Fisheries and Aquaculture 2024: Blue Transformation in Action; UN: The United Nations: United States of America. 2024. Available online: https://coilink.org/20.500.12592/2rbp5z6 (accessed on 30 November 2024).
2. Nie, P.; Hallerman, E. Advancing the sustainability of aquaculture. *Rev. Aquac.* **2021**, *13*, 781. [CrossRef]
3. Boyd, C.; D'Abramo, L.; Glencross, B.; Huyben, D.; Juarez, L.; Lockwood, G.; McNevin, A.; Tacon, A.; Teletchea, F.; Tomasso, J., Jr.; et al. Achieving sustainable aquaculture: Historical and current perspectives and future needs and challenges. *J. World Aquac. Soc.* **2020**, *51*, 578–633. [CrossRef]
4. Mohanty, B.; Mahanty, A.; Ganguly, S.; Mitra, T.; Karunakaran, D.; Anandan, R. Nutritional composition of food fishes and their importance in providing food and nutritional security. *Food Chem.* **2019**, *293*, 561–570. [CrossRef]
5. Bayissa, T.; Geerardyn, M.; Gobena, S.; Vanhauteghem, D.; Du Laing, G.; Wakijra Kabeta, M.; Janssens, G. Impact of species and their edible parts on the macronutrient and mineral composition of fish from the same aquatic environment, the Gilgel Gibe Reservoir, Ethiopia. *J. Anim. Physiol. Anim. Nutr.* **2022**, *106*, 220–228. [CrossRef] [PubMed]
6. Bondad-Reantaso, M.; Subasinghe, R.; Arthur, J.; Ogawa, K.; Chinabut, S.; Adlard, R.; Tan, Z.; Shariff, M. Disease and Health Management in Asian Aquaculture. *Vet. Parasitol.* **2005**, *132*, 249–272. [CrossRef] [PubMed]
7. Bosma, R.; Verdegem, M. Sustainable aquaculture in ponds: Principles, practices and limits. *Livest. Sci.* **2011**, *139*, 58–68. [CrossRef]
8. Snieszko, S. Recent advances in scientific knowledge and developments pertaining to diseases of fishes. *Adv. Vet. Sci. Comp. Med.* **1973**, *17*, 291–314.
9. World Bank. Reducing Disease Risks in Aquaculture. In *World Bank Report 88257-GLB*; World Bank: Washington, DC, USA, 2014.
10. Asche, F.; Eggert, H.; Oglend, A.; Roheim, C.; Smith, M. Aquaculture: Externalities and policy options. *Rev. Environ. Econ. Policy* **2022**, *16*, 282–305. [CrossRef]
11. Behringer, D.C.; Silliman, B.R.; Lafferty, K.D. Disease in fisheries and aquaculture. In *Marine Disease Ecology*; Behringer, D.C., Silliman, B.R., Lafferty, K.D., Eds.; Oxford University Press: Oxford, UK, 2020. [CrossRef]
12. Lafferty, K.; Harvell, C.; Conrad, J.; Friedman, C.; Kent, M.; Kuris, A.; Powell, E.; Rondeau, D.; Saksida, S. Infectious Diseases Affect Marine Fisheries and Aquaculture Economics. *Annu. Rev. Mar. Sci.* **2015**, *7*, 471–496. [CrossRef]
13. Karunasagar, I.; Karunasagar, I.; Otta, S. Disease Problems Affecting Fish in Tropical Environments. *J. Appl. Aquac.* **2003**, *13*, 231–249. [CrossRef]
14. Mohd-Aris, A.; Muhamad-Sofie, M.; Zamri-Saad, M.; Daud, H.; Ina-Salwany, M. Live vaccines against bacterial fish diseases: A review. *Vet. World* **2019**, *12*, 1806. [CrossRef]
15. Subramani, P.; Michael, R. Prophylactic and Prevention Methods Against Diseases in Aquaculture. In *Fish Diseases: Prevention and Control Strategies*; Jeney, G., Ed.; Elsevier Inc: Amsterdam, The Netherlands, 2017; Chapter 4; pp. 81–117. [CrossRef]
16. Peterman, M.; Posadas, B. Direct Economic Impact of Fish Diseases on the East Mississippi Catfish Industry. *N. Am. J. Aquac.* **2019**, *81*, 222–229. [CrossRef]
17. Overstreet, R.; Curran, S. Defeating Diplostomoid Dangers in USA Catfish Aquaculture. *Folia Parasitol.* **2004**, *51*, 153–165. [CrossRef] [PubMed]
18. Maldonado-Miranda, J.; Castillo-Pérez, L.; Ponce-Hernández, A.; Carranza-Álvarez, C. Summary of Economic Losses Due to Bacterial Pathogens in Aquaculture Industry. In *Bacterial Fish Diseases*; Elsevier: Amsterdam, The Netherlands, 2022; pp. 399–417.
19. Singh, A.; Gupta, H.; Srivastava, A.; Srivastava, A.; Joshi, R.; Dutta, M. A novel pilot study on imaging-based identification of fish exposed to heavy metal (Hg) contamination. *J. Food Process Preserv.* **2021**, *45*, e15571. [CrossRef]
20. Hasan, N.; Ibrahim, S.; Azlan, A. Fish Diseases Detection Using Convolutional Neural Network (CNN). *Int. J. Nonlinear Anal. Appl.* **2022**, *13*, 1977–1984. [CrossRef]
21. Rekha, B.; Srinivasan, G.; Reddy, S.; Kakwani, D.; Bhattad, N. Fish detection and classification using convolutional neural networks. In *Computational Vision and Bio-Inspired Computing: ICCVBIC 2019*; Springer: Berlin/Heidelberg, Germany, 2020; pp. 1221–1231.
22. Abadi, M.; Barham, P.; Chen, J.; Chen, Z.; Davis, A.; Dean, J.; Devin, M.; Ghemawat, S.; Irving, G.; Isard, M.; et al. TensorFlow: A System for Large-Scale Machine Learning. In Proceedings of the 12th USENIX Symposium on Operating Systems Design and Implementation (OSDI), Savannah, GA, USA, 2–4 November 2016; USENIX Association: Berkeley, CA, USA, 2016; pp. 265–283. Available online: https://www.usenix.org/conference/osdi16/technical-sessions/presentation/abadi (accessed on 20 January 2025).
23. Ahmed, M.S.; Jeba, S.M. SalmonScan: A Novel Image Dataset for Machine Learning and Deep Learning Analysis in Fish Disease Detection in Aquaculture. *Data Brief* **2024**, *54*, 110388. [CrossRef]
24. Chakravorty, H.; Paul, R.; Das, P. Image processing technique to detect fish disease. *Int. J. Comput. Sci. Secur. (IJCSS)* **2015**, *9*, 121–131.
25. Kartika, T.; Herumurti, D. Detection of Koi Carp Diseases Using Traditional Image Processing Techniques and K-Means Clustering. *Int. J. Imaging Sci. Technol.* **2016**, *26*, 78–86.

26. Yu, X.; Li, Q.; Wang, Z.; Zhang, Y. Fish disease detection using Mobile Net v3-GELU-YOLOv4 model. *IEEE Trans. Image Process.* **2023**, *32*, 789–798.
27. Pei, G.; Wu, W.; Zhou, B.; Liu, Z.; Li, P.; Qian, X.; Yang, H. Research on Agricultural Disease Recognition Methods Based on Very Large Kernel Convolutional Network-RepLKNet. *Preprints* **2024**, 1–12. [CrossRef]
28. Kaggle. Dataset of Freshwater Fish Diseases and Healthy Specimens. 2024. Publicly Available Under the Kaggle License Permitting Academic Use. Available online: https://www.kaggle.com/datasets/subirbiswas19/freshwater-fish-disease-aquaculture-in-south-asia/data (accessed on 26 January 2024).
29. De Raad, K.; van Garderen, K.A.; Smits, M.; van der Voort, S.R.; Incekara, F.; Oei, E.; Hirvasniemi, J.; Klein, S.; Starmans, M.P. The Effect of Preprocessing on Convolutional Neural Networks for Medical Image Segmentation. In Proceedings of the 2021 IEEE 18th International Symposium on Biomedical Imaging (ISBI), Nice, France, 13–16 April 2021; IEEE: Piscataway, NJ, USA, 2021; pp. 655–658. [CrossRef]
30. Ghosh, R.; Cingreddy, A.R.; Melapu, V.; Joginipelli, S.; Kar, S. Application of artificial intelligence and machine learning techniques in classifying extent of dementia across alzheimer's image data. *Int. J. Quant. Struct. Prop. Relatsh. (IJQSPR)* **2021**, *6*, 29–46. [CrossRef]
31. Ahmed, M.S.; Aurpa, T.T.; Azad, M.A.K. Fish Disease Detection Using Image-Based Machine Learning Technique in Aquaculture. *J. King Saud Univ.—Comput. Inf. Sci.* **2022**, *34*, 5170–5182. [CrossRef]
32. Mia, M.; Rahman, M.; Hasan, M.; Islam, M. Comparative Analysis of Multiple Machine Learning Algorithms for Fish Disease Detection. *Mach. Learn. Aquacult.* **2022**, *14*, 450–465.
33. Sivakumar, M.; Parthasarathy, S.; Padmapriya, T. Trade-off between training and testing ratio in machine learning for medical image processing. *PeerJ Comput. Sci.* **2024**, *10*, e2245. [CrossRef] [PubMed]
34. Tseng, C.; Lin, Y. Fish Disease Detection Using CNNs Combined with K-Means Clustering. *Comput. Biol. Bioinform.* **2023**, *18*, 144–152.
35. Chakravorty, S.; Das, S.; Chakrabarti, A. Fish Disease Detection Using Principal Component Analysis and K-Means Clustering. *J. Aquat. Sci.* **2015**, *12*, 234–241.
36. Malik, H.; Naeem, A.; Hassan, S.; Ali, F.; Naqvi, R.A.; Yon, D.K. Multi-classification deep neural networks for identification of fish species using camera captured images. *PLoS ONE* **2023**, *18*, e0284992. [CrossRef]
37. Lee, R.; Chen, I.Y. The time complexity analysis of neural network model configurations. In Proceedings of the 2020 International Conference on Mathematics and Computers in Science and Engineering (MACISE), Madrid, Spain, 14–16 January 2020; pp. 178–183.
38. Oyedare, T.; Shah, V.K.; Jakubisin, D.J.; Reed, J.H. Keep it simple: CNN model complexity studies for interference classification tasks. In Proceedings of the IEEE INFOCOM 2023—IEEE Conference on Computer Communications Workshops (INFOCOM WKSHPS), New York, NY, USA, 17–20 May 2023; IEEE: Piscataway, NJ, USA, 2023; pp. 1–6.
39. Ramachandran, L.; Mohan, V.; SenthilKumar, S.; Sankara Ganesh, J. Early Detection and Identification of White Spot Syndrome in Shrimp Using an Improved Deep Convolutional Neural Network. *J. Intell. Fuzzy Syst.* **2023**, *45*, 6429–6440. [CrossRef]
40. Wang, Z.; Liu, H.; Zhang, G.; Yang, X.; Wen, L.; Zhao, W. Diseased Fish Detection in the Underwater Environment Using an Improved YOLOv5 Network for Intensive Aquaculture. *Fishes* **2023**, *8*, 169. [CrossRef]
41. Haddad, M.; Hassan, F.; Mohammed, H. A Convolutional Neural Network Approach for Precision Fish Disease Detection. *Evol. Stud. Imaginative Cult.* **2024**, *8*, 1018–1033. [CrossRef]
42. Thakur, K.; Shetty, M.; Singh, S.; Khanapuri, J. Enhancing Fish Disease Detection: A Comprehensive Review for Sustainable Aquaculture. In Proceedings of the 2023 IEEE International Conference on Advanced Science and Technology (ICAST), Pune, India, 15–17 March 2023; pp. 191–196. [CrossRef]
43. Ssekitto, I.; Oyoka, D.; Mwebembezi, G.; Mubuuke, J.K.; Lule, E.; Ggaliwango, M. Explainable Machine Vision Techniques for Fish Disease Detection with Deep Transfer Learning. In Proceedings of the International Conference on Electrical, Computer, and Systems Engineering (ICECSE), Kampala, Uganda, 15–17 March 2024; pp. 1218–1227. [CrossRef]
44. Akram, W.; Hassan, T.U.; Toubar, H.; Ahmed, M.D.F.; Mišković, N.; Seneviratne, L.; Hussain, I. Aquaculture Defects Recognition via Multi-Scale Semantic Segmentation. *Expert Syst. Appl.* **2023**, *237*, 121197. [CrossRef]
45. Phettongkam, H. Error Analysis and Its Implications in Communicative English Language Teaching. *Thammasat Rev.* **2013**, *16*, 96–108.
46. Nanthini, N.; Arul, S.; Kumaran, K.; Ashiq, A.; Aakash, V.S.; Bhuvaneshwaran, M.J. Convolutional neural networks (CNN) based marine species identification. In Proceedings of the 2022 International Conference on Advanced Computing and Robotic Systems. (ICACRS), Pudukkottai, India, 13–15 December 2022; pp. 602–607. [CrossRef]
47. Yasruddin, M.L.; Ismail, M.A.H.; Husin, Z.; Tan, W.K. Feasibility study of fish disease detection using computer vision and deep convolutional neural network (DCNN) algorithm. In Proceedings of the 2022 International Conference on Control, Power, and Artificial Intelligence. (CSPA), Guangzhou, China, 21–23 October 2022; pp. 272–276. [CrossRef]

48. Khabusi, S.P.; Huang, Y.P.; Lee, M.F. Attention-Based Mechanism for Fish Disease Classification in Aquaculture. In Proceedings of the 2023 International Conference on System Science and Engineering (ICSSE), Ho Chi Minh, Vietnam, 27–28 July 2023; IEEE: New York, NY, USA, 2023; pp. 95–100. [CrossRef]
49. Lokesh, Y.; Rithvik, M.; Madhavi, M.; Madhu, S.; Rajeshwar Rao, K. Image Classification Using CNN with CIFAR-10 Dataset. *Int. J. Res. Appl. Sci. Eng. Technol.* **2024**, *12*, 229–231. [CrossRef]
50. Surve, Y.; Pudari, K.; Bedade, S.; Masanam, B.D.; Bhalerao, K.; Mhatre, P. Comparative Analysis of Various CNN Architectures in Recognizing Objects in a Classification System. In Proceedings of the 2024 IEEE 9th International Conference for Convergence in Technology (I2CT), Pune, India, 5–7 April 2024; IEEE: Piscataway, NJ, USA; pp. 1–5. [CrossRef]
51. Dash, S.; Ojha, S.; Muduli, R.K.; Patra, S.P.; Barik, R.C. Fish Type and Disease Classification Using Deep Learning Model Based Customized CNN with ResNet-50 Technique. *J. Adv. Zool.* **2024**, *45*, 32. [CrossRef]
52. Azhar, A.S.B.M.; Harun, N.H.B.; Hassan, M.G.B.; Yusoff, N.B.; Pauzi, S.N.B.M.; Yusuf, N.N.; Kua, B.C. Early Screening Protozoan White Spot Fish Disease Using Convolutional Neural Network. *J. Adv. Res. Appl. Sci. Eng. Technol.* **2024**, *37*, 73–79. [CrossRef]
53. Islam, M.R.; Rahman, U.S.; Akter, T.; Azim, M.A. Fish Disease Detection Using Deep Learning and Machine Learning. *Int. J. Comput. Appl.* **2023**, *975*, 8887. [CrossRef]
54. Malik, S.; Kumar, T.; Sahoo, A.K. Image Processing Techniques for Identification of Fish Disease. In Proceedings of the 2017 IEEE 2nd International Conference on Signal and Image Processing (ICSIP), Singapore, 4–6 August 2017; IEEE: Piscataway, NJ, USA, 2017; pp. 55–59. [CrossRef]

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