# An Enhanced Aquaculture Health Monitoring System For Fish Veterinarians For Identifying And Differentiating Different Types Of Freshwater Fish Diseases

**[1]V. Sivamurugan, [2]G. Lavanya**

[1,2]Department of Information Technology, Sri Sivasubramaniya Nadar College of Engineering, Chennai
Email: sivamuruganv@ssn.edu.in[1], lavanyag2420078@ssn.edu.in[2]

## ABSTRACT

In Aquatic Habitats, the fish population's viability is pivotal for preserving ecosystem stability and enhancing aquaculture productivity. Early and precise identification of fish diseases is of utmost importance for strategic management and risk reduction approaches. This investigation explores a robust approach for fish health assessment using transfer learning and pre-trained neural network architectures. The proposed methodology uses encoded representations derived from ten Fine-Tunable Pre-Trained Models, namely VGG-16, VGG19, ResNet50, MobileNet-V2, and Inception-V3, for designing a trained model for classification. Through rigorous experimental analysis using an extensive dataset, we have highlighted the importance of our suggested model designed using VGG16 in precisely recognizing seven different types of fish diseases namely Disease-free, fungal infection, parasitic infestation, and aquatic viral infections. The trained model designed using VGG16 outperformed other models in overall classification accuracy (0.97857), Positive Predictive Value (0.97901), True Positive Rate (0.97857), and Kappa (0.975) respectively. Our revelations expose the emerging strengths of transfer learning and customizing the layers for strengthening fish disease surveillance and classification, unlocking new opportunities for emerging research directions in aquatic health monitoring and aquaculture.

**Keywords**: Aeromoniasis, Bacterial Gill Disease, Bacterial Red Disease, Fungal diseases Saprolegniasis, Parasitic diseases, Pre-trained Convolutional Neural Network, and Viral diseases White tail disease

## Introduction

Aquaculture fulfills a pivotal role Worldwide in contributing food items rich in protein and fulfilling significantly for ensuring stable food supply and economic growth as reported by **Daoliang Li et al.[1]**. This change in seafood intake is reflected across both high-income and low-to-middle-income countries. Therefore, it's critical to strongly promote economic stability and biotic balance sustainability of the aquaculture sector based on the findings identified by A**. J. Dyck et al.[2]**. Over the course of recent years,Fish and aquaculture products are central to global food security and distribution, and enhancing economic prosperity across emerging countries as identified by **A. G. J. Tacon et al.**[3]. The vital need for the animal-based protein resources is underscored by the growing humanity globally. Recent research findings have revealed 25,000 different types of finfish species, with approximately 15,000 more species remaining undiscovered as mentioned by **S. N. Pauzi et al.[4]**. The international organization focused on ending hunger (FAO) has Furnished Recent Data as mentioned by [5]World Fisheries and Aquaculture. Aquaculture entails the organized cultivation, management, and cultivation and harvesting of diverse aquatic organisms living in aquatic habitats such as fish, aquatic vegetation, crustacean species, shellfish and additional species, incorporating activities such as breeding and cultivation as stated by **M. S. Ahmed et al.[6]**. **J. A. Hartigan et al.[7]** explained aquaculture as the planned cultivation of aquatic organisms to support food security and economic development. The aquaculture industry is primarily composed of two main branches: mariculture and fish farming. **B. Campbell et al.[8]** defined mariculture as the involvement of domestication of oceanic biological specimens for various derivatives such as medical compounds, food supplements, and similar items. As mentioned by **SUBIR BISWAS et al.[36]**, Marine species may be cultivated in their native marine habitats or in controlled facilities established on land or within aquatic environments, including rivers, lakes, and coastal waters. Throughout the world's coastlines, a broad spectrum of aquatic organisms, including mollusks, shrimp, marine fish, and other valuable species, are cultivated for commercial production. **M. S. Ahmed et al.[6]** described aquaculture as the systematic farming of fish in human-managed freshwater systems such as ponds, lakes, rivers, canals, and reservoirs for commercial purposes. Recent years have witnessed considerable growth in the aquaculture sector as a response to the escalating demand for fish products. The rapid growth of aquaculture and the increased density of fish culture systems have heightened concerns regarding fish health and disease management as mentioned by **Z. Zhu et al.[9]**. The late identification of disease outbreaks may lead to reduced growth performance and compromised fish welfare as outlined by **M. Bao et al.[10]**. In response to these challenges, the development of modern real-time diagnostic systems is crucial for enhancing fish productivity, detecting diseases at an early stage, and maintaining optimal fish health against bacterial, fungal, parasitic, and viral pathogens as narrated by **Mishra SS et al.**[11] which can adversely affect the health, growth, and productivity of farmed fish in aquaculture systems. Fish skin disease diagnosis utilizes both human expertise and AI-based image analysis techniques to achieve rapid and accurate disease identification as mentioned by **G. Yu et al.**[13] and **L. Sveen et al.**[14]. We have considered 7 different types of fish diseases including Healthy Fish for detection and classification. They are

**Aeromoniasis**

Aeromonas species are opportunistic bacteria that infect stressed or injured fish. Ulcers on skin or mouth, Red sores or hemorrhages, Popeye (exophthalmia) or dropsy (swollen body, raised scales), Fin rot and tail rot, and Lethargy, refusal to eat are the symptoms for Aeromoniasis disease.

**Bacterial Red Disease**

It is primarily caused by Aeromonas hydrophila or other Aeromonas species. Reddish patches on the skin, fins, and base of the tail, Hemorrhages (bleeding) under the skin and around fins, Ulcers or open wounds, Swollen abdomen (sometimes dropsy), Lethargy, loss of appetite, and Redness around anus are the different symptoms for this bacterial red disease.

**Bacterial Gill Disease (BGD)**

It is usually caused by Flavobacterium branchiophilum and other opportunistic bacteria, especially in overcrowded or poorly oxygenated tanks. Inflamed, swollen gill filaments, discoloration of gills (pale or brown), Gasping at the surface or near aerators, clamped fins, reduced activity, and Mucus buildup on gills are the different symptoms for this Bacterial Gill Disease.

**Fungal diseases Saprolegniasis**

Saprolegniasis is a widespread mycotic infection in freshwater species and fish eggs, caused by fungi of the genus Saprolegnia (a type of water mold). It usually affects fish that are already weakened by stress, injury, poor water conditions, or other infections. White, gray, or greenish fluffy patches on the skin, fins, gills, eyes, or eggs, Necrotic or dead tissue under fungal growth, Lesions or ulcers under fungal mats, Erosion of fins and scales, Discoloration (reddish or pale areas), Lethargy and reduced swimming activity, and Loss of appetite are the symptoms for this Fungal diseases Saprolegniasis.

**Parasitic diseases**

Parasitic diseases occur when parasites invade and harm their host organisms and survive by draining nutrients from the host. In aquatic environments, parasitic diseases are common in fish and amphibians, especially in farmed or stressed animals. Excess mucus secretion (especially on gills and skin), Rubbing or flashing (fish scratch against objects), Visible parasites on skin, fins, or gills, Loss of appetite Weight loss or poor growth, Lethargy or abnormal swimming, Ulcers or lesions (due to secondary infections), Gill damage or rapid gill movement (respiratory distress), and Pale gills or skin discoloration are the general symptoms for this disease.

**Viral diseases White tail disease**

White Tail Disease is a prawn-affecting condition triggered by a virus that affects freshwater prawns, particularly the giant freshwater prawn. It is caused primarily by Macrobrachium rosenbergii nodavirus (MrNV), often in combination with an associated virus called extra small virus (XSV). These viruses cause severe damage to the prawn's muscle tissue, especially in the tail region, leading to high mortality. White, opaque discoloration in the tail muscles (hence the name "white tail"), Muscle whitening usually starts in the tail (abdomen) and can extend forward, Lethargy or sluggish movement, Reduced feeding or complete loss of appetite, Weak or erratic swimming behavior, Surface floating before death, and High mortality, especially in post-larvae and juveniles are the external symptoms for this white tail disease.

**Healthy Fish**

A healthy fish is one that is physiologically, behaviorally, and physically normal, free from diseases, parasites, and stress, and capable of optimal growth, reproduction, and immune response. No emaciation or bloating are the general appearance of healthy fish.

**The key research findings and outcomes are presented as follows:**

- An extensive comparative analysis was undertaken to assess the effectiveness of nine of the most efficient and best-performing pre-trained deep convolutional neural network architectures identified in this study, namely on VGG-16 by **D. Muduli et al.**[16] and **S. Tammina et al.**[17], MobileNetV2 by **P. N. Srinivasu et al.**[18], InceptionV3 by **A. Demir et al.**[19], and ResNet-50 by **S. Mascarenhas et al.**[20]. Training design factors such as how quickly the model learns, how much data is processed at once, how many cycles are run, and which optimizer is applied have been thoroughly investigated to determine their influence on the overall outcomes. Finally, the most effective model with maximum validation accuracy has been selected, facilitating further research toward the development of accurate and efficient fish disease detection systems.

- To improve dataset quality and reduce the effects of data imbalance, various augmentation operations were performed to achieve equitable and balanced representation of instances from seven different categories.
- The proposed method leverages multiple pre-trained deep learning approaches for representation learning and feature extraction and utilizes the derived features and labels for training a classification model. The findings highlight the effectiveness of these approaches in achieving superior performance benchmarks.

## Literature Survey

Fish diseases have received extensive and sustained research attention from the scientific community due to their impact on aquaculture productivity and aquatic health management. **Malik et al.** [21] have discussed a disease called Epizootic Ulcerative Syndrome, a fungal infection associated with the pathogen Aphanomyces invadans, which causes severe ulcerative conditions in fish. The disease is clinically observed as red ulcerative spots, often leading to incorrect identification due to their similarity to other lesions. **Ahmed et al.**[6] have explained how the systematic process adopted for the identification and detection of salmon fish diseases in aquaculture environments through the detection of infected fish caused by various pathogens. For removing disruptions and improving the clarity of the images, they have implemented advanced image preprocessing techniques followed by robust segmentation methodologies for improved image analysis. **V. Sivamurugan et al.**[40] have separated the distinct features to classify the lumpy skin diseases by utilizing a kernelized Support Vector Machine (SVM) learning algorithm to improve nonlinear feature classification performance. The Support Vector Machine (SVM) model exhibited outstanding classification performance, achieving accuracy rates of 91.42% and 94.12%, thereby demonstrating its effectiveness for the given task. **H. Chakravorty et al.**[22] and **De Raad, K et al.**[23] have used the Principal Component Analysis (PCA)-based feature extraction framework for robust, accurate, and efficient identification and classification of fish diseases. K-means clustering is effectively employed to segment diseased regions in fish images using color features. HSV images and morphological operations are utilized to enhance the accuracy of diseased area detection and quantification. **Mathur et al.**[24] have utilized a pre-trained ResNet-50 model to transfer learned features. which leads to a notable increase in classification accuracy even when data is scarce. The proposed method demonstrated excellent validation performance, achieving accuracies of 84.92% on a smaller dataset and 98.44% on a larger dataset, highlighting its scalability and effectiveness. **Pauzi et al.**[4] have employed a comprehensive set of advanced image-processing techniques and classification methodologies, including hybrid machine learning and deep learning frameworks, statistical approaches, and rule-based expert systems to enhance classification performance and decision accuracy. By incorporating these strategies, they yielded top accuracy performance in Alexnet. **A. A. Nayan et al.**[25] have implemented machine learning-based algorithms to facilitate accurate and early-stage identification of fish diseases. In their experimental evaluation, a real-world dataset was employed, leading to high and reliable classification accuracy. A computational learning-based approach was employed to achieve high and reliable classification accuracy. In the data-driven framework, the Gradient Boosting technique was implemented, resulting in a high classification accuracy of 92%, demonstrating its effectiveness. **Rachman et al.**[26] have used a fish dataset comprising specimens affected by Epizootic Ulcerative Syndrome (EUS), a severe ulcerative disease in aquatic species. In their contribution, the integration of MobileNet and U-Net achieved the highest performance, resulting in a classification accuracy of 98.75%, demonstrating strong effectiveness. **Waleed et al.**[27] have proposed a fish farm automation framework for the accurate identification and monitoring of fish diseases in aquaculture systems. They have worked with CNN and specifically they have used AlexNet, ResNet-18, ResNet-50, and ResNet-101 methods by leveraging the RGB color space to achieve superior and optimal performance outcomes. **Mamun et al.**[28] have strategically employed predictive modeling and deep knowledge acquisition methods; they used CNN, VGG-16, VGG-19, and ResNet-50 models. After comprehensive evaluation of all implemented approaches, the VGG-16 and VGG-19 ensemble framework demonstrated superior performance, achieving a remarkable classification accuracy of 99%, thereby outperforming all other methods. In their work, a comprehensive and well-structured dataset was curated by systematically integrating data from multiple publicly accessible repositories, including Kaggle, to facilitate robust experimental analysis. **Hasan et al.**[29] have compiled approximately 90 images across three categories, namely healthy (30), red spot (30), and white spot (30). They have employed a single CNN model, which achieved 94.44% accuracy performance. **Sekhar et al.**[30] have investigated transfer learning methodologies employing the MobileNetV2 architecture to enhance feature representation and classification performance. Pre-trained on the ImageNet dataset, the model effectively extracted hierarchical and discriminative feature representations from fish images to enhance classification performance. This model demonstrated exceptional performance, establishing its robustness, reliability, and effectiveness for accurate fish species classification. **Chhabra et al.**[31] have employed combinatorial deep learning methodologies for robust and automated fish categorization, as presented in the ICETIT Symposium. They employed a combined deep learning framework, leveraging a stacked ensemble architecture based on VGG16 , trained beforehand to derive features and achieved a remarkable performance of 93.8% classification accuracy. **D. Krivoguz et. al.**[32] have implemented a deep neural network-based strategy for real-time epizootic fish disease monitoring, rigorously evaluated through two experimental setups employing distinct data augmentation techniques. **J. C. Chen**

**et al.**[33] have leveraged deep learning methodologies for creating a trained model for classification.. The model achieved 86.7% accuracy for infected fish and 86.9% for healthy fish on the source dataset. **Aditya Gupta Goodwin et al.**[34] have used CNN for robust and reliable identification of wounds and parasitic lice infestations in Atlantic salmon fish for effective health monitoring. The algorithm proposed by them located lice and infected areas in a real-world, live salmon aquaculture farming environment for continuous monitoring and analysis. Their proposed framework utilized a CNN architecture with approximately 15 convolutional layers and 5 fully connected layers to enable accurate and robust identification of fish lice and wounds in fish images. **Fitrianah et al.**[35] have systematically analyzed the performance of MobileNetV2 and VGG-16 architectures under hyperparameter tuning to assess their effectiveness and classification capability. To that end, continuous monitoring of threatened and endangered fish species was carried out, making it easier to map and define areas restricted from fishing activities. They systematically optimized key hyperparameters, including batch size, number of epochs, learning rate, and optimizer, to enhance model training performance on fish image datasets. Among all evaluated models, VGG-16 achieved the highest classification accuracy, demonstrating superior performance and robustness. **Saubir Biswas et al.**[36] have fused features from VGG-16, MobileNet-V2, and Inception-V3 for training a SVM classifier for improving the performance during classifying the test images. All the above studies illustrated how AI technologies could reshape aquaculture and contribute to global food stability by employing machine learning techniques to classify fresh water fish diseases. **V Sivamurugan et al.**[38] have used image captioning techniques for classification of different severity levels of Diabetic Retinopathy.

## Materials And methods

### Data Collection

The dataset having flourished ecologically important freshwater fish and data representing six distinct fish illnesses was extracted from Kaggle[15]. a collaborative portal offering ML datasets, competitions, and community insights. This dataset repository features a dataset of 2,444 images organized into seven groups: red bacterial disease, Aeromonas infection, gill disease, fungal infection (Saprolegniasis), healthy fish, parasitic disease, and viral disease (white tail). The data division strategy includes 90% for model training and 10% for evaluation. We have adopted nearly 1747 images belonging to seven classes for training, 350 images for validating the trained model created using 10 different pre-trained CNN models and 350 images for testing the trained model. This type of allocation of images for training, validation and testing addresses overfitting challenges while enabling strong evaluation metrics for smaller datasets was emphasized by **Sivakumar et al.**[12].

### Proposed Analytical Framework

The deep learning-based approach adopted for fish disease classification in the proposed model is presented in Figure 3. The model is designed to analyze the input image and predict the disease type along with its category. The following section provides a systematic and detailed specification of each step involved in the proposed methodology.

### Data Preprocessing

To use the downloaded compiled set of data from Kaggle Website for learning the 10 different selections of CNN models with pre-learned weights, Diverse preprocessing steps were carried out to enhance the performance of the ten distinct pre-trained convolutional neural networks. All images were scaled to 224 ×224 for feeding to VGG16, VGG19, ResNet50, DenseNet121, DenseNet169, DenseNet201, and MobileNetV2 and 299*299 pixels, for feeding to InceptionV3, Xception and InceptionResNetV2. This resizing operation will standardize input resolutions and reduce computational overhead, which provides guidance for the model to interpret each individual image optimally. The number of batches used for training and validation are computed by using both the full count of training images and the image count per batch.

### Feature extraction performed by a pre-trained CNN to assist in training models

An instance of Keras' Image Data Generator Class is created and used to preprocess image data before feeding it into pre-trained CNN models. The image generator class available in Keras facilitated the initialization of the training and validation data generators. To ensure uniform contribution to the loss, the training generator rescaled the input images. The validation generator ensured evaluation was based solely on original data by applying only rescaling. The generators were set up to adjust the image size uniformly to a resolution of 224 or 299 pixels per side, while scaling the pixel levels were mapped onto a range from 0 to 1. The image pixel intensities were normalized to a range of 0 to 1 by multiplying them by 1/255, aiding in faster convergence while training the model. **N. Hasan et al.**[29]. Then we used the function 'datagen.flow_from_directory' to load and preprocess images from a directory structure into batches suitable for training or validation with a Keras model.

### Training the model on embeddings produced by pre-trained convolutional neural networks

We have created a stream of precomputed feature/label batches from disk (via HDF5) into our training routine without loading everything into memory at once. We have used the function ‘features_from_file’ to read features and labels from train.h5 and val.h5(HDF5) files that contain pre-extracted features from the pre-trained models such as VGG16, VGG19 etc. This function returns the total number of batches (i.e., steps per epoch) available in that .h5 file. It also returns a Python generator that yields (x, y) pairs (i.e., features and labels) one batch at a time, for training. We have then defined, implemented and trained a learning model for classification using the functional API. This training model is defined with one input layer that expects a tensor of shape 7×7×512 or 7×7×1024 or, 7×7×2048 based on VGG16/ResNet. A Conv2D operation with 64 filters of size 1x1 is used after the layer applying convolution filters. Post-convolution, batch normalization and ReLU activation are performed. This has reduced or transformed the feature dimensions. Then dropout regularization is applied randomly setting 50% of values to zero during training. This will prevent overfitting during training. Then the flatten layer unrolls the 3D tensor (feature map) into a 1D vector for input to a Dense (fully connected) layer. Final classification layer. The classification layer outputs a probability distribution across 7 classes using the softmax activation function. The created training model with input layer having dimensions aligned with the feature vector and output layer with softmax activation function with 7 neurons is now ready for compilation and training.

**Compiling the Training Model ready for training**

The optimization procedure is undertaken using the Adam algorithm, which enhances convergence speed and overall model performance to compile the training model due to its efficiency and adaptability to the learning rate. In multi-class classification tasks like this, Sparse categorical loss function is typically used as the loss criterion. The training is further fine-tuned by introducing additional callbacks. Early stopping was adopted to track fluctuations in validation loss and avoid redundant training. Callbacks are defined in Keras, which are utilities that allow us to monitor the training process and take actions automatically at certain stages (e.g., after each epoch). One of the purposes of callback is to save the best trained model to disk during training whenever the validation accuracy improves. The second purpose of the callback function is to reduce the learning rate dynamically when the validation accuracy stops improving and hence to help the model to converge better. Finally, the training model is trained by using a data generator for 50 epochs as mentioned by **V. Sivamurugan et al.**[39]. A dynamic checkpoint saves the best model, which is then used for classification. The different steps used in creating the trained model in the proposed methodology and finally used for classification using the trained model is visualized in Figure1.

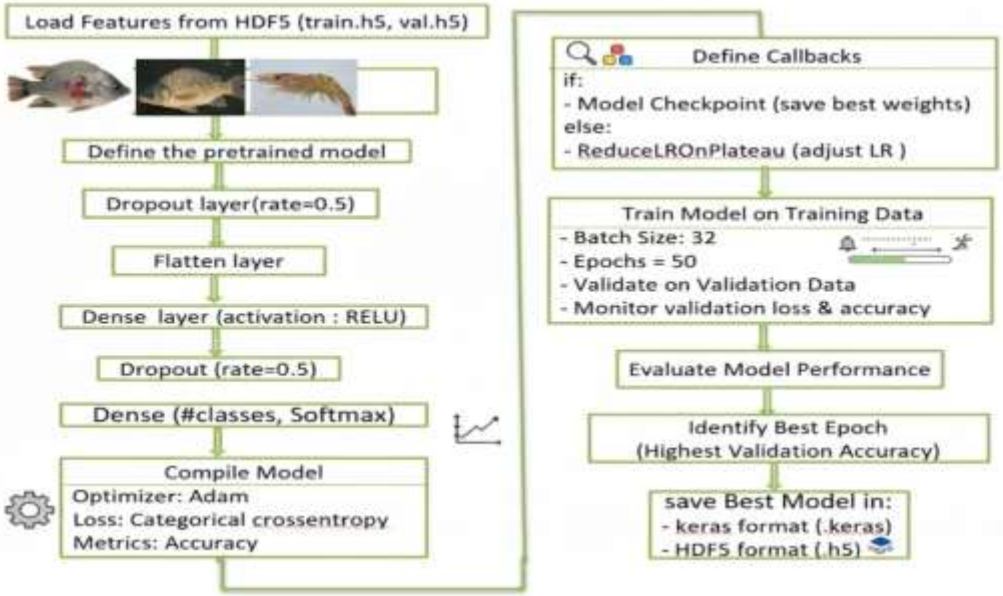

**Figure 1** visualizes the proposed framework to create the trained model.

Table 2.1 displays the performance metrics obtained during training using five distinct pre-trained CNN models.

**Table 1** showing accuracy and loss obtained during the creation of trained model

| CNN variants for feature extraction | CNN variants used for trained model creation | Training Accuracy | Training Loss | Validation Accuracy | Validation Loss |
|---|---|---|---|---|---|
| VGG16 | VGG16 | 0.9719 | 0.1104 | 0.9688 | 0.0847 |
| VGG19 | VGG19 | 0.9668 | 0.1360 | 0.9500 | 0.1309 |
| ResNet50 | ResNet50 | 0.9707 | 0.1286 | 0.9500 | 0/1955 |

| | | | | | |
|---|---|---|---|---|---|
| DenseNet201 | DenseNet201 | 0.8565 | 0.4635 | 0.8687 | 0.4461 |
| MobileNetV2 | MobileNetV2 | 0.8693 | 0.3781 | 0.8625 | 0.3429 |

### Classification of Fish Disease using the Learned Model

Initially the learned model is set to the inference (test) mode, not training mode. CNN models pre-trained on ImageNet after excluding the top layer are loaded for extracting the representations captured from the images. The trained model already saved is loaded for classification. A Python list called classes that contains the class labels (i.e., category names) for a fish disease classification task is defined. Each string in the list represents any one of the disease categories or health conditions of a fish. This list is used in classification tasks to map numerical predictions (e.g., 0, 1, 2, …) back to human-readable labels. This list is also used to interpret the output of a trained model. The input image for testing is transformed into a NumPy array with pixel data standardized to values from 0 to 1. The preprocessed image is passed through the base model (e.g., VGG16 without the top layer) to output a feature map. This feature map or extracted features acts as an input to our custom classification model designed using trained models for classification. The predict () function returns the softmax probabilities for each fish disease class. .

## Results And Discussion

### Results of classification using trained models

Figure 2 shows classification results for the trained models created from the pre-trained CNN models namely VGG16, VGG19 and ResNet50 after customizing the layers along with confidence intervals.

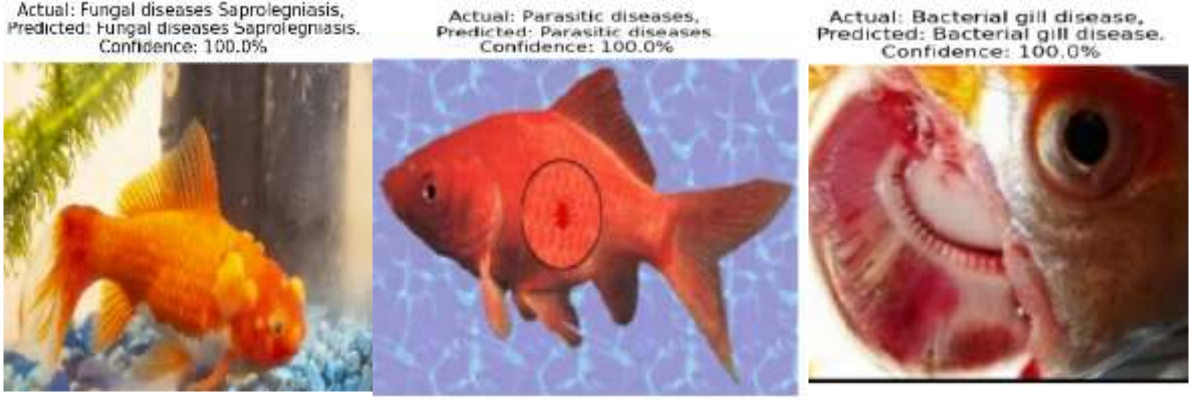

**Figure 2** shows the prediction made by VGG16 , VGG19 and ResNet50 based classifiers for Parasitic and Bactorial Gill Diseases along with 100% confidence

### Confusion Matrix For Different from Distinct CNN Variants Based Classifier

A confusion matrix visually represents how well a classification model predicts labels compared to the actual labels. It helps to visualize how well the model is performing, especially in multi-class classification. The confusion matrix is organized with true classes in the rows and predicted classes in the columns. Properly classified labels fall on the diagonal, and wrong predictions are found off-diagonal. The Figures from 3 to 7 shows the confusion matrix obtained from different trained models used for freshwater fish diseases classification.

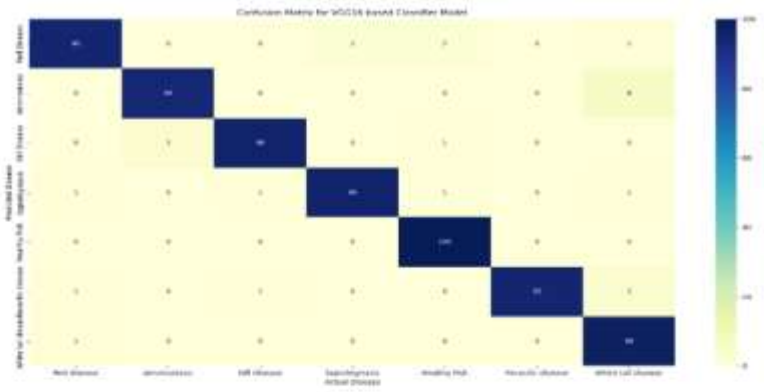

**Figure 3** Confusion table for VGG16 based Classifier

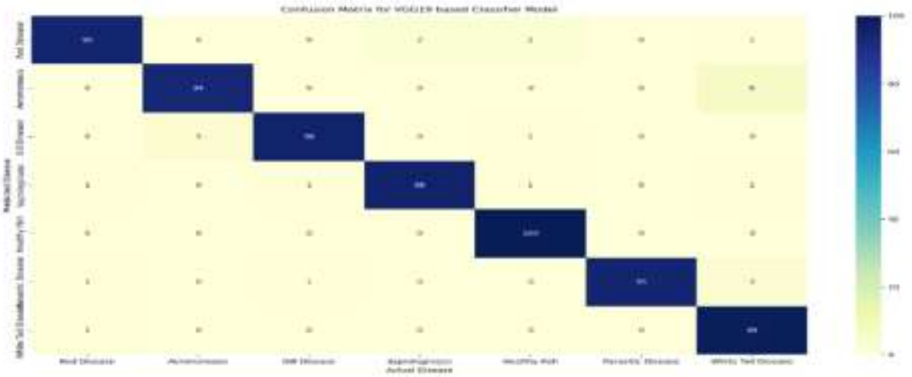

**Figure 4** Confusion chart for VGG19 based classifier

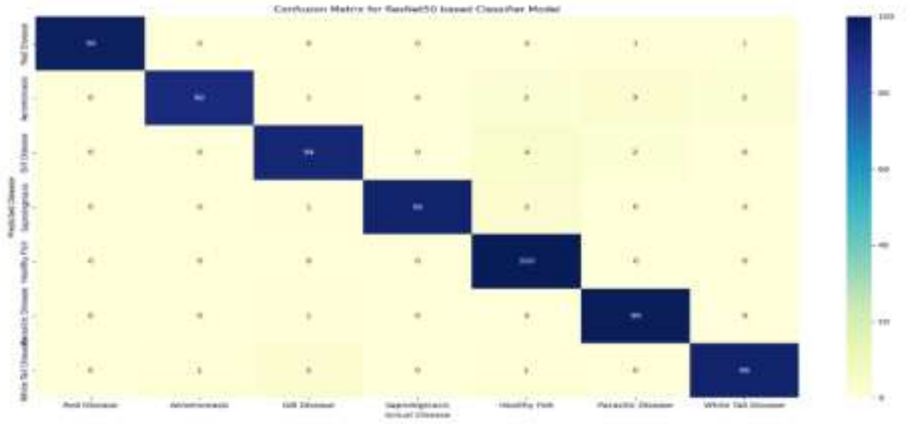

**Figure 5** Prediction matrix for ResNet50 based classifier

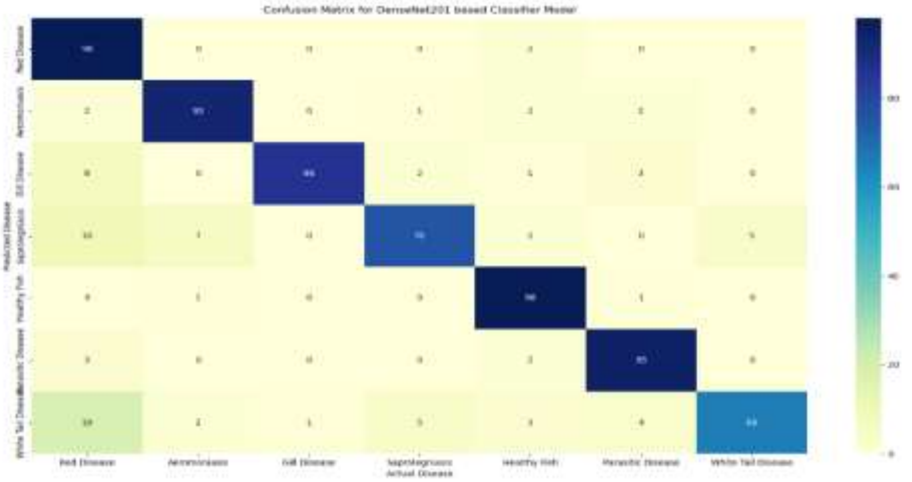

**Figure 6** Diagnostic matrix for DenseNet201 based classifier

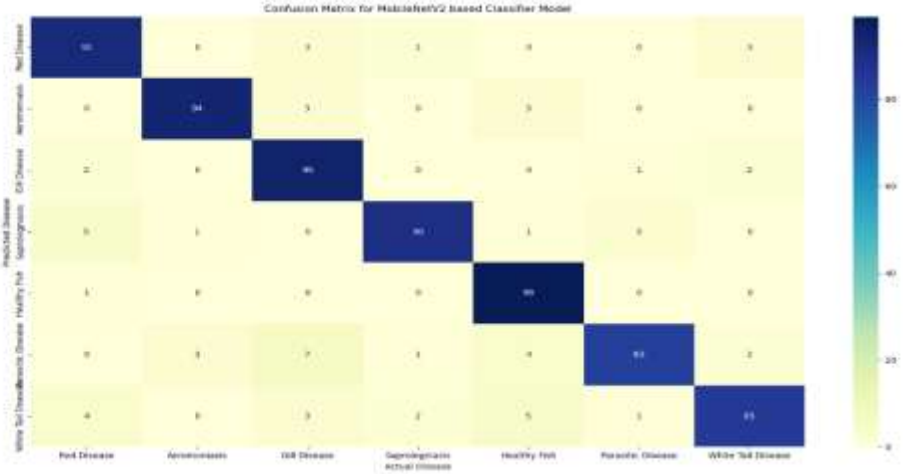

**Figure 7** Evaluation matrix for MobileNetV2 based classifier

### Overall statistical summary for the classification of fish diseases

Several relevant performance metrics were used for analysis and comparative study. Only the best-trained models, as determined by various metrics, are included in this analysis. They provide insights into how well the classifier performs under test conditions. This study will help in choosing the best classifier that can aid fish veterinarians in evaluating and identifying diseases.

**Table 2** Overall performance statistics analysis

| CNN Models | Kappa | Overall accuracy | PVR_Macro | PVR_Micro | TPR_Macro | TPR_Micro |
|---|---|---|---|---|---|---|
| **VGG16** | 0.975 | 0.97857 | 0.97901 | 0.92244 | 0.97857 | 0.97857 |
| **VGG19** | 0.95833 | 0.96429 | 0.9656 | 0.96429 | 0.96429 | 0.96429 |
| **ResNet50** | 0.95673 | 0.96291 | 0.96441 | 0.96291 | 0.96293 | 0.96291 |
| **DenseNet201** | 0.85333 | 0.87429 | 0.88878 | 0.87429 | 0.87429 | 0.87429 |
| **MobileNetV2** | 0.89667 | 0.91143 | 0.91401 | 0.91045 | 0.91143 | 0.91143 |

### Performance Analysis Using Kappa

**V. Sivamurugan et al.**[37] have used the kappa statistics to evaluate the strength of image classifiers. Kappa relies on observed accuracy and expected accuracy for its computation. Essentially, the kappa statistic evaluates how well the labels predicted by a trained CNN-based model align with expert-labeled ground truth, accounting for expected accuracy. The trained model used for image classification which has used VGG16 for feature extraction and for creating a trained model has a maximum kappa value equal to 0.975 when compared with all the other models as shown in Table 4.1. The strength of agreement is excellent if the kappa value is greater than 0.85.

### Performance review through overall accuracy

The net classification accuracy reflects how many images from all severity levels were correctly classified out of the total images. The accuracy across all classes is equal to 0.97857 as shown in Table 4.1 for the designed model incorporating VGG16 for both feature extraction and for creating a customized trained model. This is also evidence for suggesting this model to the Fish Veterinarians for assisting their diagnosis in diagnosing various categories of fish diseases. Figure 4.2 exhibits the comparative analysis of overall accuracy metrics for classifiers built on five Pre-initialized convolutional neural networks.

### Evaluation of performance using PVR_MACRO

Macro-averaging treats each class equally by computing metrics separately for each disease and averaging the outcomes. For datasets with class imbalance It is observed that fish disease classification systems with VGG16 for designing both feature extraction and image classification attained the highest PVR_Macro value of 0.97901 as shown in Table 4.1. This metric also strengthens the recommendation of this model concerning the Fish Veterinarians to explore the various types of fish diseases. Figure 4.3 shows the comparative analysis of PVR_MACRO metrics for classifiers built on five pre-trained CNN models.

**Performance investigation using PVR_MICRO**

A micro-average calculates the metric based on total contributions from all the classes together. Micro-averaging is the preferred approach for multi-class classification when uneven class frequencies exist. Findings indicate that classification systems with VGG16 for attribute extraction and image classification reported a maximum PVR_Macro of 0.92244 as shown in Table 4.1. Therefore, this metric supports recommending the model to fish veterinarians for diagnosing various fish diseases.

**Performance investigation employing TPR_MACRO and TPR_MICRO**

The ability to detect positive instances correctly quantifies the correctly identified positives relative to all actual positives, including misclassified ones. The achieved True Positive Rate is 0.97857 as shown in Table 4.1 for the classification model designed with VGG16. This is also an acknowledgement for recommending this image classification model to the Fish Veterinarians to assess the different categories of fish diseases.

**Class-wise performance statistics for freshwater fish diseases**

Classifiers showing the smallest validation loss can be benchmarked against reciprocally to determine the top-performing image classification system. Each of the seven classes is evaluated through six different measures and compared for each of the individual classes. The analysis involves Accuracy, F1 Score, F2 Score, Precision, Sensitivity and Specificity value. We observed that a model built with VGG16 architecture accurately predicted symptoms in all seven classes. Tables 3 to 9 present class-specific performance information for each disease.

**Table 3** Illustration of evaluation metrics for Aeromoniasis

| CNN Model Used in creating Trained Model | Accuracy | F1 Score | F2 Score | Precision | Specificity | Sensitivity |
|---|---|---|---|---|---|---|
| **VGG16** | 0.99571 | 0.98492 | 0.98196 | 0.9899 | 0.99833 | 0.98 |
| **VGG19** | 0.98714 | 0.95431 | 0.94567 | 0.96907 | 0.995 | 0.94 |
| **ResNet50** | 0.98716 | 0.95337 | 0.93306 | 0.98925 | 0.99834 | 0.92 |
| **DenseNet201** | 0.97571 | 0.91626 | 0.92445 | 0.90291 | 0.98333 | 0.93 |
| **MobileNetV2** | 0.98571 | 0.94949 | 0.94378 | 0.95918 | 0.99333 | 0.94 |

**Table 4** Outlining the performance data for Gill Disease Detection

| CNN Model Used in creating Trained Model | Accuracy | F1 Score | F2 Score | Precision | Specificity | Sensitivity |
|---|---|---|---|---|---|---|
| **VGG16** | 0.99143 | 0.97059 | 0.98214 | 0.95192 | 0.99167 | 0.99 |
| **VGG19** | 0.99143 | 0.9697 | 0.96386 | 0.97959 | 0.99667 | 0.96 |
| **ResNet50** | 0.98288 | 0.94 | 0.94 | 0.94 | 0.99002 | 0.94 |
| **DenseNet201** | 0.97857 | 0.91979 | 0.88296 | 0.98851 | 0.99833 | 0.86 |
| **MobileNetV2** | 0.97 | 0.90047 | 0.90047 | 0.85586 | 0.97333 | 0.95 |

**Table 5** highlights the individual performance statistics of of Healthy Fish

| CNN Model Used in creating Trained Model | Accuracy | F1 Score | F2 Score | Precision | Specificity | Sensitivity |
|---|---|---|---|---|---|---|
| **VGG16** | 0.99571 | 0.98522 | 0.99404 | 0.97087 | 0.995 | 1.0 |
| **VGG19** | 0.99429 | 0.98039 | 0.99206 | 0.96154 | 0.99333 | 1.0 |
| **ResNet50** | 0.98573 | 0.95238 | 0.98039 | 0.90909 | 0.98336 | 1.0 |
| **DenseNet201** | 0.98 | 0.93333 | 0.96078 | 0.89091 | 0.98 | 0.98 |
| **MobileNetV2** | 0.98 | 0.93396 | 0.9668 | 0.88393 | 0.97833 | 0.99 |

**Table 6** contains the metrics evaluation for Parasitic Disease

| CNN Model Used in creating Trained Model | Accuracy | F1 Score | F2 Score | Precision | Specificity | Sensitivity |
|---|---|---|---|---|---|---|
| **VGG16** | 0.99571 | 0.98492 | 0.98196 | 0.9899 | 0.99833 | 0.98 |
| **VGG19** | 0.99286 | 0.97436 | 0.9596 | 1.0 | 1.0 | 0.95 |
| **ResNet50** | 0.99001 | 0.96585 | 0.9802 | 0.94286 | 0.99002 | 0.99 |
| **DenseNet201** | 0.97857 | 0.92683 | 0.94059 | 0.90476 | 0.98333 | 0.95 |
| **MobileNetV2** | 0.96857 | 0.88298 | 0.85041 | 0.94318 | 0.99167 | 0.83 |

**Table 7** presents the performance statistics for Viral Red Disease

| CNN Model Used in creating Trained Model | Accuracy | F1 Score | F2 Score | Precision | Specificity | Sensitivity |
|---|---|---|---|---|---|---|
| **VGG16** | 0.99 | 0.96373 | 0.9432 | 1.0 | 1.0 | 0.93 |
| **VGG19** | 0.98857 | 0.9596 | 0.95382 | 0.96939 | 0.995 | 0.95 |
| **ResNet50** | 0.99715 | 0.9899 | 0.98394 | 1.0 | 1.0 | 0.98 |
| **DenseNet201** | 0.93714 | 0.81667 | 0.90741 | 0.7 | 0.93 | 0.98 |
| **MobileNetV2** | 0.97143 | 0.90196 | 0.9127 | 0.88462 | 0.98 | 0.92 |

**Table 8** provides the statistical analysis for Saprolegniasis Classification

| CNN Model Used in creating Trained Model | Accuracy | F1 Score | F2 Score | Precision | Specificity | Sensitivity |
|---|---|---|---|---|---|---|
| **VGG16** | 0.99286 | 0.97512 | 0.97804 | 0.9703 | 0.995 | 0.98 |
| **VGG19** | 0.99143 | 0.9697 | 0.96386 | 0.97959 | 0.99667 | 0.96 |
| **ResNet50** | 0.99429 | 0.97959 | 0.96774 | 1.0 | 1.0 | 0.96 |
| **DenseNet201** | 0.95429 | 0.82609 | 0.78512 | 0.90476 | 0.98667 | 0.76 |
| **MobileNetV2** | 0.97857 | 0.92308 | 0.90909 | 0.94737 | 0.99167 | 0.9 |

**Table 9** presents the performance statistics for White Tail Disease

| CNN Model Used in creating Trained Model | Accuracy | F1 Score | F2 Score | Precision | Specificity | Sensitivity |
|---|---|---|---|---|---|---|
| **VGG16** | 0.99571 | 0.98507 | 0.98802 | 0.9802 | 0.99667 | 0.99 |
| **VGG19** | 0.98286 | 0.94286 | 0.97059 | 0.9 | 0.98167 | 0.99 |
| **ResNet50** | 0.98859 | 0.96 | 0.95427 | 0.9697 | 0.995 | 0.96 |
| **DenseNet201** | 0.94429 | 0.77193 | 0.70064 | 0.92958 | 0.99167 | 0.66 |
| **MobileNetV2** | 0.96857 | 0.88542 | 0.86382 | 0.92391 | 0.98833 | 0.85 |

### Performance Analysis Using Individual Accuracy

A model utilizing VGG16 for feature 0.99571 extraction achieved an individual accuracy of 0.99571, 0.99143, 0.99571, 0.99571, 0.99, 0.99286 and 0.99571 for Aeromoniasis, Gill Disease, Healthy Fish, Parasitic Disease, Viral Red Disease, Saprolegniasis, and White Tail Disease respectively as shown in Tables from 3 to 8. For achieving accurate class predictions, Individual Accuracy is vital when the model is trained with balanced class data.

### Analyzing classification accuracy using the F1 score

The F1 Score is derived by harmonically averaging precision and recall. The F1 Score is designed to account for errors from both incorrectly identified positives and missed actual positives. In scenarios with skewed image scattering across classes in training, F1 Score outperforms accuracy in usefulness. A model utilizing VGG16 for feature extraction achieved an F1 Score of 0.98492, 0.97059, 0.98522, 0.98492, 0.96373, 0.97512 and 0.98507 for Aeromoniasis, Gill Disease, Healthy Fish, Parasitic Disease, Viral Red Disease, Saprolegniasis, and White Tail Disease respectively as shown in Tables from 3 to 8 For achieving accurate class predictions, F1 Score is vital when the model is trained with imbalanced class data.

### Performance metrics reviewed using the F2 Score

F2 Score combines precision and recall using a weighted average approach. The F2 Score simultaneously addresses false positives and false negatives. F2 Score provides a better evaluation than accuracy when classes are unequally represented in the training data. The classifier model designed with VGG16 has an F2Score of 0.98196, 0.98214, 0.99404, 0.98196, 0.9432, 0.97804 and 0.988802 for Aeromoniasis, Gill Disease, Healthy Fish, Parasitic Disease, Viral Red Disease, Saprolegniasis, and White Tail Disease respectively as shown in Tables from 3 to 8.

### Assessment of model effectiveness through precision

This measure is known as the positive predictive value (PPV). A precision score of 1.0 means all positive predictions are correct, whereas 0.0 means none are correct. The classifier model designed with VGG16 has precision of 0.9899, 0.95192, 0.97087, 0.9899, 1.0, 0.9703 and 0.9802 for Aeromoniasis, Gill Disease, Healthy Fish, Parasitic Disease, Viral Red Disease, Saprolegniasis, and White Tail Disease respectively as shown in Tables from 3 to 8.

**Performance assessment carried out using sensitivity**

Sensitivity is calculated as true positives over the total number of actual positive cases. It goes by the names true positive rate (TPR) and recall. High sensitivity suggests that few actual positive cases are missed by the model. When sensitivity equals 1.0, the model detects all actual positives, while 0.0 reflects total failure. The classifier model designed with VGG16 has sensitivity of 0.98, 0.99, 1.0, 0.98, 0.93, 0.98, and 0.99 for Aeromoniasis, Gill Disease, Healthy Fish, Parasitic Disease, Viral Red Disease, Saprolegniasis, and White Tail Disease respectively as shown in Tables from 3 to 8.

**Performance Analysis Using Specificity**

Specificity reflects how many actual negative cases are correctly detected by the model. The true negative rate (TNR) is another term used for this metric. This metric shows how effectively the model distinguishes non-diseased cases. A perfect specificity of 1.0 shows the model correctly classifies all actual negatives, while 0.0 shows it fails entirely. The classifier model designed with VGG16 has specificity of 0.99833, 0.99167, 0.995, 0.99833, 1.0, 0.995, and 0.99667 for Aeromoniasis, Gill Disease, Healthy Fish, Parasitic Disease, Viral Red Disease, Saprolegniasis, and White Tail Disease respectively as shown in Tables from 3 to 8.

## Conclusion

Early detection of fish skin infections helps aquaculture farmers control disease transmission and reduce fish mortality. In this direction, we have created a unique trained model for classification by using each of the different pre-trained CNN models by transferring learning the pre-trained CNN models after adding new layers. Then the optimum trained models were used for classification on test datasets having 50 images for each disease. Then the performance of the best models are compared with each other to identify the best model. The best model created using the VGG16 model can be recommended to the Fish Veterinarians to assist them for Identifying and Differentiating Freshwater Fish Diseases. In future the features extracted from two or three models are fused and then the fused features are used to train the model to create a trained model for classification. Explainable AI techniques can also be used to identify the region in the image for which the model has given more focus during classification to notify the reason for prediction to a specific disease.

## References

[1] D. Li, X. Li, Q. Wang, and Y. Hao, ''Advanced techniques for the intelligent diagnosis of fish diseases: A review,'' Animals, 2022, **12**(21), 2938, 1-26. https://doi.org/10.3390/ani12212938.

[2] A. J. Dyck and U. R. Sumaila, ''Economic impact of ocean fish populations in the global fishery,'' J. Bioeconomics, **20**10, **12**(3), 227–243. https://doi.org/10.1007/s10818-010-9088-3.

[3] A. G. J. Tacon and M. Metian, ''Fish matters: Importance of aquatic foods in human nutrition and global food supply,'' Reviews in Fisheries Science, 2013, **21**(1), 22–38. https://doi.org/10.1080/10641262.2012.753405.

[4] S. N. Pauzi, M. G. Hassan, N. Yusoff, N. H. Harun, A. H. A. Bakar, and B. C. Kua, ''A review on image processing for fish disease detection,'' Journal of Physics, Conference Series, 2021, 1997(1), Art. no. 012042. http://dx.doi.org/10.1088/1742-6596/1997/1/012042.

[5] The state of World Fisheries and Aquaculture, Sustainability in Action, Food and Agriculture Organization, Rome, Italy, 2020, 1–244. https://doi.org/10.4060/ca9229en.

[6] M. S. Ahmed, T. T. Aurpa, and M. A. K. Azad, ''Fish disease detection using image based machine learning technique in aquaculture,'' 2021,1-15, arXiv:2105.03934. https://doi.org/10.48550/arXiv.2105.03934.

[7] J. A. Hartigan and M. A. Wong, ''Algorithm AS 136: A K-means clustering algorithm,'' J. Roy. Stat. Soc. Ser. C Appl. Statist., 1979, **28**(1), 100-108. https://doi.org/10.2307/2346830.

[8] B. Campbell and D. Pauly, ''Mariculture: A global analysis of production trends since 1950,'' Mar. Policy, 2013, **39**(C), 94–100. https://doi.org/10.2307/2346830.

[9] Z. Zhu, C. Duan, C. Dong, S. Weng, and J. He, ''Epidemiological situation and phylogenetic relationship of Vibrio Harveyi in marine-cultured fishes in China and Southeast Asia,'' Aquaculture, 2020, 529-541, 735652. https://doi.org/10.1016/j.aquaculture.2020.735652.

[10] M. Bao, G. J. Pierce, N. J. C. Strachan, S. Pascual, M. González-Muñoz, and A. Levsen, ''Human health, legislative and socioeconomic issues caused by the fish-borne zoonotic parasite anisakis: Challenges in risk assessment,'' Trends IN Food Science and Technology, 2019, **86**, 298–310.
https:// doi.org/10.1016/j.tifs.2019.02.013.

[11] Mishra SS, Rakesh D, Dhiman M, Choudhary P, Debbarma J, Sahoo SN, Barua A, Giri BS, Ramesh R, Ananda K, Mishra CK and Swain P ''Present status of fish disease management in freshwater aquaculture in India: State-of-the-art-review,'' Aquaculture Fisheries, 2017, **1**(1), 1–9.. http://doi.org/10.24966/AAF-5523/100003.

[12]. Sivakumar, M.; Parthasarathy, S.; Padmapriya, T. Trade-off between training and testing ratio in machine learning for medical image processing. PeerJ Computer Science, 2024, 10, 1-7. e2245. [CrossRef] [PubMed]. https://doi.org/10.7717/peerj-cs.2245.

[13] G. Yu, J. Zhang, A. Chen, and R. Wan, ‘‘Detection and identification of fish skin health status referring to four common diseases based on improved YOLOv4 model,’’ Fishes, 2023, **8**(4), 1-14. https://doi.org/10.3390/fishes8040186.

[14] L. Sveen, G. Timmerhaus, L.-H. Johansen, and E. Ytteborg, ‘‘Deep neural network analysis—A paradigm shift for histological examination of health and welfare of farmed fish,’’ Aquaculture, 2021, **532**, Art. no. 736024. https://doi.org/10.1016/j.aquaculture.2020.736024.

[15]. 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-aquaculturein-south-asia/data (accessed from 26 January 2025).

[16]. D. Muduli, R. Dash, and B. Majhi, ‘‘Enhancement of deep learning in image classification performance using VGG16 with swish activation function for breast cancer detection,’’ in Proc. Int. Conf. Comput. Vis. Image Process. Singapore: Springer, 2021, 191–199. http://dx.doi.org/10.1007/978-981-16-1086-8_17

[17] S. Tammina, ‘‘Transfer learning using VGG-16 with deep convolutional neural network for classifying images,’’ International Journal of Scientific and Research Publications (IJSRP), 2019, **9**(10), 143–150. http://dx.doi.org/10.29322/IJSRP.9.10.2019.p9420.

[18]. P. N. Srinivasu, J. G. Sivasai, M. F. Ijaz, A. K. Bhoi, W. Kim, and J. J. Kang, ‘‘Classification of skin disease using deep learning neural networks with MobileNet V2 and LSTM,’’ Sensors, 2021, **21**(8), 2852, 1-27. https://doi.org/10.3390/s21082852.

[19]. A. Demir, F. Yilmaz, and O. Kose, ‘‘Early detection of skin cancer using deep learning architectures: Resnet-101 and Inception-v3,’’ in Proc. Medical Technologies National Conference(TIPTEKNO), 2019, 1–4. http://dx.doi.org/10.1109/TIPTEKNO47231.2019.8972045.

[20]. S. Mascarenhas and M. Agarwal, ‘‘A comparison between VGG16, VGG19 and ResNet50 architecture frameworks for image classification,’’ in Proc. Int. Conf. Disruptive Technol. Multi-Disciplinary Res. Appl. (CENTCON), 2021, **1**, 1-17. .http://dx.doi.org/10.21203/rs.3.rs-2863523/v1.

[21] S. Malik, T. Kumar, and A. K. Sahoo, ‘‘Image processing techniques for identification of fish disease,’’ in Proc. IEEE 2nd Int. Conf. Signal Image Process. (ICSIP), 2017, 55–59. http://dx.doi.org/10.1109/SIPROCESS.2017.8124505.

[22] H. Chakravorty, R. Paul, and P. Das, ‘‘Image processing technique to detect fish disease,’’ International Journal of Computer Science Security, 2015, **9**(2), 121–131. https://www.cscjournals.org/manuscript/Journals/IJCSS/Volume9/Issue2/IJCSS-1013.pdf

[23]. 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. Proceedings of the 2021 IEEE 18th International Symposium on Biomedical Imaging (ISBI), Nice, France, 13–16 April 2021; IEEE: Piscataway, NJ, USA, 2021, 655–658. [CrossRef]. https://doi.org/10.1109/ISBI48211.2021.9433952.

[24] M. Mathur and N. Goel, ‘‘FishResNet: Automatic fish classification approach in underwater scenario,’’ Social Networking and Computer Science, 2021, 2(4), 273, 1-12. https://link.springer.com/article/10.1007/s42979-021-00614-8

[25] A. A. Nayan, A. N. Mozumder, J. Saha, K. R. Mahmud, and A. K. Al Azad, ‘‘Early detection of fish diseases by analyzing water quality’’ Trends in Sciences, 2020, 18(21), 351, 1–11. https://doi.org/10.48550/arXiv.2102.09390.

[26] F. Rachman, M. Akbar, and E. Putera, ‘‘Fish disease detection of epizootic ulcerative syndrome using deep learning image processing technique,’’ in Proc. International Conference on Fisheries and Aquaculture, 2023, 23–34. https://doi.org/10.17501/23861282.2023.8102.

[27] A. Waleed, H. Medhat, M. Esmail, K. Osama, R. Samy, and T. M. Ghanim, ‘‘Automatic recognition of fish diseases in fish farms,’’ in Proc. 14th Int. Conf. Comput. Eng. Syst. (ICCES), 2019, 201–206. http://dx.doi.org/10.1109/ICCES48960.2019.9068141.

[28] M. R. I. Mamun, U. S. Rahman, T. Akter, and M. A. Azim, ‘‘Fish disease detection using deep learning and machine learning,’’ International Journal of Computer Applications, 2023, **185**(36), 1–9. http://dx.doi.org/10.5120/ijca2023923079.

[29] N. Hasan, S. Ibrahim, and A. A. Azlan, ‘‘Fish disease detection using convolutional neural network (CNN),’’ International Journal of Nonlinear Analysis and Applications, 2022, **13**(1), 1977–1984. http://dx.doi.org/10.22075/ijnaa.2022.5839.

[30] B. C. Sekhar, K. Rangaswamy, P. Anjaiah, K. Naveen, and K. Sumalatha, ‘‘Fish species detection and recognition using mobilenet V2 architecture: A transfer learning approach,’’ Rivista Italiana di Filosofia Analitica Junior, 2023, **14**(1), 173–185. https://rifanalitica.it/index.php/journal/article/view/58/52.

[31] H. S. Chhabra, A. K. Srivastava, and R. Nijhawan, ‘‘A hybrid deep learning approach for automatic fish classification,’’ in Proc. ICETIT Emerg. Trends Inf. Technol. Cham, Switzerland: Springer, 2020, 427–436. http://dx.doi.org/10.1007/978-3-030-30577-2_37.

[32] D. Krivoguz, ‘‘Deep learning approach of using inception deep neural network for real-time epizootic monitoring of fish diseases’’, 1-9. Tech. Rep. http://dx.doi.org/10.13140/RG.2.2.12502.93761.

[33] J. C. Chen, T.-L. Chen, H.-L. Wang, and P.-C. Chang, ‘‘Underwater abnormal classification system based on deep learning: A case study on aquaculture fish farms in Taiwan,’’ Aquacultural Engineering, 2022, **99**, Art. no. 102290. 102290. http://dx.doi.org/10.1016/j.aquaeng.2022.102290.

[34]. A. Gupta, E. Bringsdal, K. M. Knausgård, and M. Goodwin, ‘‘Accurate wound and lice detection in Atlantic salmon fish using a convolutional neural network,’’ Fishes, 2022, **7**(6), 345, 1-10. https://doi.org/10.3390/fishes7060345.

[35] D. Fitrianah, K. M. Suryaningrum, N. T. M. Sagala, V. Ayumi, and S. M. Lim, ‘‘Fine-tuned MobileNetV2 and VGG16 algorithm for fish image classification,’’ in Proc. Int. Conf. Informat., Multimedia, Cyber Inf. Syst. (ICIMCIS), 2022, 384–389. http://dx.doi.org/10.1109/ICIMCIS56303.2022.10017901.

[36] SUBIR BISWAS, DEBENDRA MUDULI, (Member, IEEE), MD ARIFUL ISLAM , ANURADHA SHANTANU KANADE, ABU TAHA ZAMANI, SHANTANU PANDURANG KANADE, (Member, IEEE), AND NIKHAT PARVEEN, ‘‘Empirical Evaluation of Deep Learning Techniques for Fish Disease Detection in Aquaculture Systems: A Transfer Learning and Fusion-Based Approach,’’ IEEE Access, 2024, 12. 176136–176154. https://ieeexplore.ieee.org/stamp/stamp.jsp?arnumber=10759657.

[37] Sivamurugan Vellakani, and Indumathi Pushbam, ‘‘An enhanced OCT image captioning system to assist ophthalmologists in detecting and classifying eye diseases,’’ Journal of X-Ray Science and Technology, 2020, vol. 28, pp. 975-988. https://doi.org/10.3233/xst-200697.

[38] V. SIVAMURUGAN, K.R. UTHAYAN, V. THANIKACHALAM, ‘‘ENHANCED RETINAL IMAGE CAPTIONING SYSTEM FOR IDENTIFYING AND DIFFERENTIATING SEVERITY LEVELS OF DIABETIC RETINOPATHY,’’ GENETIKA, 2023, Vol. 55 No3, pp. 983-996. https://doi.org/10.2298/GENSR2303983S.

[39] V. Sivamurugan, P. Indumathi, V. Thanikachalam and R. Rajakumar, ‘‘Clinical Decision Support System for Ophthalmologists for Eye Disease Classification,’’ IETE JOURNAL OF RESEARCH, 2023, Vol. 68, pp. 8717-8734. http://dx.doi.org/10.1080/03772063.2022.2101552.

[40] V. Sivamurugan, K.R. Uthayan, and V. Thanikachalam, ‘‘Cow Disease (LSD) Classification System for predicting different Severity levels,’’ International Journal of Early Childhood Special Education (INT-JECSE), 2022, Vol. 14, no. 8, pp. 2860-2873. ttps://www.int-jecse.net/media/article_pdfs/LSD_JOURNAL_PAPER_1_ANTxwk5.pdf