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## RESEARCH ARTICLE

# Empirical Evaluation of Deep Learning Techniques for Fish Disease Detection in Aquaculture Systems: A Transfer Learning and Fusion-Based Approach

SUBIR BISWAS<sup>1</sup>, DEBENDRA MUDULI<sup>1</sup>, (Member, IEEE), MD ARIFUL ISLAM<sup>1</sup>,  
ANURADHA SHANTANU KANADE<sup>2</sup>, ABU TAHA ZAMANI<sup>3</sup>,  
SHANTANU PANDURANG KANADE<sup>4</sup>, (Member, IEEE), AND NIKHAT PARVEEN<sup>5</sup>

<sup>1</sup>Department of Computer Science and Engineering, C.V. Raman Global University, Bhubaneswar, Odisha 752054, India

<sup>2</sup>Department of Computer Science and Applications, Dr. Vishwanath Karad MIT World Peace University, Pune 411038, India

<sup>3</sup>Department of Computer Science, Northern Border University, Arar 73211, Saudi Arabia

<sup>4</sup>Symbiosis School for Online and Digital Learning, Symbiosis International Deemed University, Pune, Maharashtra 412115, India

<sup>5</sup>Department of Computer Science and Engineering, Koneru Lakshmaiah Education Foundation (Deemed to be University), Guntur, Andhra Pradesh 522302, India

Corresponding author: Debendra Muduli (muduli.debendra@gmail.com)

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**ABSTRACT** In aquatic environments, the health of fish populations is crucial for maintaining ecological balance and sustaining aquaculture industries. Timely and accurately detecting fish diseases is paramount for effective management and mitigation strategies. This paper presents a novel approach for fish disease detection leveraging transfer learning and ensemble techniques. Our method combines features extracted from three pre-trained deep learning models, namely VGG-16, MobileNet-V2, and Inception-V3, with a Support Vector Machine (SVM) for classification. Through empirical experimental evaluation on a comprehensive dataset, we demonstrate the effectiveness of our proposed model in accurately detecting various fish diseases. The results showcase significant improvements in sensitivity and specificity compared to existing approaches. Additionally, we analyze the impact of different transfer learning strategies and feature fusion techniques on the model's overall performance. Our findings underscore the potential of transfer learning and ensemble methods in enhancing fish disease detection systems, offering promising avenues for future research in aquatic health management and aquaculture.

**INDEX TERMS** Aquaculture, VGG-16, MobileNet-V2, SVM.

## I. INTRODUCTION

Aquaculture plays a vital role globally in providing a protein source and contributing significantly to food security and the economy [1]. This trend in fish consumption is evident across both industrialized and developing nations. Growing in popularity as a sustainable way to guarantee a steady supply of fish in response to the rising demand worldwide in the aquaculture sector. Therefore, it's vital to make sure

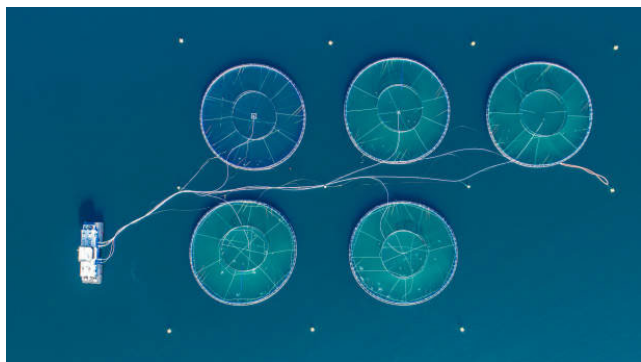
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that the economic and ecological viability of the aquaculture industry [2]. Over the last few years, aquatic products have been pivotal in the worldwide food distribution network, exerting a substantial influence on the economy and the societal advancement of emerging nations [3].

Fish's merits within the necessary supply of animal-based proteins are highlighted by the fact that the human population is growing worldwide. Recent scientific discoveries have identified 25,000 fish species, with another 15,000 potentially awaiting recognition [4]. The Food and Agriculture Organization (FAO) has produced the most recent data, which is based

on national reports and estimations for those nations that have not been informed. The State of World Aquaculture and Fisheries 2020 edition indicated 622 “the species items,” but the term (1950-020) under 652 units is officially considered a higher number [5].

Aquaculture refers to the practice of cultivating and harvesting various aquatic organisms, such as fish, aquatic plants, crustaceans, mollusks, and other species, involving processes like breeding and rearing that show in **Figure 1** [6]. Comprises managing the growth of freshwater and saltwater organisms in order to create food and goods [7]. Aquaculture is primarily categorized into two types there are: (1) Mariculture and another is (2) Fish farming, both have explained below.



**FIGURE 1.** Sample image of aquaculture system.

### A. MARICULTURE

Mariculture [8] involves the farming of oceanic organisms for various products such as pharmaceuticals, food additives, and more. Marine organisms are cultivated in either their natural marine habitat or in enclosed environments on land or at sea, including rib and lake. Along the coastlines of the world, mollusks, shrimps, oceanic fish, and an assortment of other minor species such as politburo idea, etc are part of the extensive range of organisms currently under cultivation. Marine organisms derive their composition from seawater nutrients, encompassing carbon, nitrogen, phosphorus, calcium, and carbonate. It encourages the growth of local society’s economy and supports the promotion of sustainable food production.

### B. FISH FARMING

Aquaculture [6] involves the farming of fish for commercial purposes in rivers, and canals, produced by humans in ponds, lakes, along other water reservoirs. In recent times, the aquaculture fish farming industry has become larger to cater to the growing need for fish products. Typically, certain common varieties of fish such as channel catfish, catla, carp, goldfish, and many more types of fish are farmed.

With the escalating utilization of aquaculture fish products and the consequent rise in the density and intensity of fish farming, the health of fish has become a big problem

of affairs for clients [9]. For that reason, if the fish disease is detected late it can become a hindrance to the growth of the fish [10]. In this scenario, it is imperative to develop modern or real-time techniques promptly to enhance fish growth, identify fish diseases, and maintain fish health, thereby enabling the early detection of fish diseases like Bacterial diseases-aeromoniasis, bacterial gill disease, bacterial red disease, fungal diseases, parasitic diseases, viral diseases white tail disease [11] which can affect farm fish. Fish disease detection is therefore a critical component of contemporary aquaculture, and on-time finding is essential to ensuring accurate and timely management of these illnesses. Monitoring and diagnosing fish skin diseases in aquaculture involves a combination of human observation, which depends on visual expertise, and artificial intelligence (AI) technology, which employs image analysis, deep learning, and machine learning [12] to enhance the precision and speed of disease identification [13], [14]. In the initial stages, machine learning methods like color segmentation and K-means clustering were used to diagnose illnesses in fish [15], [16].

Thus, nine CNN models that had already been trained were employed in this study. In many different image-processing applications, CNN models have shown to be quite successful. For fish disease classification, we employed seven pre-trained CNN models: VGG-16 [17], MobileNetV2 [18], MobileNetV3 [19], InceptionV3 [20], ResNet-50 [21], ResNet-34 [22], EfficientNetB7 [23], ConvNeXtXLarg [24]. The findings of the research are outlined as follows:

- A thorough comparison has been conducted on the effectiveness of the top seven pre-trained deep CNN models, including VGG-16 [17], MobileNetV2 [18], InceptionV3 [20], ResNet-50 [21], ResNet-34 [22], EfficientNetB7 [23], ConvNeXtXLarg [24]. Various hyperparameters such as learning rate, batch size, number of epochs, and optimization techniques have been analyzed for their impact. Ultimately, the most optimal model has been identified, providing researchers with a foundation for developing a more efficient CNN-based solution for early detection of fish disease infection.
- In order to address the limited and imbalanced nature of the data within publicly accessible datasets, we implemented multi-operation data augmentation techniques, ensuring equal representation of samples from seven different classes.
- Our novel approach leverages the collective power of three pre-trained models for deep learning feature extraction, seamlessly integrating them to enhance SVM classification. Our discoveries showcase the transformative capabilities of these methods, setting new standards for performance benchmarks.

The paper’s remaining material is summarized here. The section II mentioned in the related work. The section III prescribes the proposed methodology. The section IV displayed

the experimental results and evaluated them. The section V suggested work is narrated and concludes.

## II. RELATED WORK

Fish diseases have received a great deal of research attention to date. We looked at studies that were relevant to ours.

Malik et al. [25], the paper discusses a disease called Epizootic Ulcerative Syndrome: a fungal infection that causes this condition known as *Aphanomyces invadans*. The disease appears as red spots that resemble ulcers, often leading to misidentification. There are two sections of the research paper. The initial phase uses a variety of identification of edges algorithms to find relevant information and approaches to segmentation to improve the image. On the image of the afflicted fish, morphological procedures have been applied. The accuracy of the data was improved up to 86% by utilizing Principle Component Analysis. Ahmed et al. [6], the paper explains how the salmon fish disease in aquaculture was identified by detecting the infected fish through various pathogens. To reduce noise and enhance the images, the paper applied image pre-processing and segmentation techniques. The involved features were extracted and classified for the diseases using the SVM [26], [27] machine learning algorithm, using a kernel function. The SVM model was applied to the earliest portion of produced images, which performed remarkably well with an accuracy of 91.42% and 94.12%. Authors of [28] and [29], this paper uses the PCA method to identify fish diseases. The suggested method uses K-means clustering to divide the diseased region about the fish image utilizing coloring data. HSV images as well as anatomical operations are used to increase the accuracy of diseased area detection and measurement. The suggested method was evaluated using four fish with Epizootic Ulcerative Syndrome (EUS) as an example study. The experiment's outcomes demonstrated unambiguous proof of how successful it was in enhancing diseased identification with a higher degree of accuracy and accurately computing the area of disease. The outcomes of the simulation show an accuracy greater than 90 percent. Mathur and Goel [30]. To solve the problem they used Transfer learning with the ResNet-50 model which significantly boosts classification accuracy, even with limited data. Impressively, the suggested method obtains an accuracy rate for validation of 84.92% for a smaller dataset and 98.44% for a larger dataset. Pauzi et al. [4], they employ a variety of image-processing categorization approaches, such as hybrid methods like machine learning and deep learning, [31], [32], statistical methods, and rule-based expert systems. By using deep learning techniques they achieved the highest accuracy which is 99.0446% achieved by Alexnet. Al-Akhir Nayan, Early fish disease identification via machine learning-based algorithms quality of water analysis [33], In their experiment, they used a real dataset to get high accuracy. To get high accuracy they use a Machine Learning Algorithm. In the Machine Learning algorithm, they use the Gradient boosting technique and they have got 92% accuracy. Rachman et al. [34],

they use a fish dataset infected with EUS. In their paper, they use Deep learning techniques where approaches include MobileNet, ResNet, and Convolutional Network (FCN). They achieved the best outcome in the circumstances across MobileNet as well as Unet by utilizing each of the available approaches, resulting in an accuracy of 98.75%. Waleed et al. [35], presented Fish Farm Automation for the Identification of Diseases in Fish. The authors of this work use CNN (Convolutional Neural Network). In CNN models they use AlexNet, ResNet-18, ResNet-50, and ResNet-101 methods with RGB color space to get the best result. They got the highest accuracy on their ResNet-50 with RGB color space which is 98%. Mamun et al. [36] have been used deep learning and machine learning techniques they used CNN, VGG-16, VGG-19, and ResNet-50 models. After implementing all models they found the highest accuracy of 99% is accomplished by the VGG-16 and VGG-19 ensemble models. On this occasion, they created a dataset that they collected from multiple publicly accessible locations and Kaggle. Hasan et al. [37], gathered around 90 images across all under the three categories of healthy (30), red spot (30), and white spot (30). With an accuracy rating of 94.44%, they employed a single CNN model. Sekhar et al. [38], have been employed Transfer Learning Approach in Rivista Italiana di Filosofia Analitica Junior used the MobileNetV2 architecture, it underwent pre-training within the ImageNet collection, as well as extract hierarchical features from fish images. With a test set accuracy of 99.94%, the model demonstrated exceptional performance, making it reliable and effective in categorizing fish species. Chhabra et al. [39], have been Combinatorial deep learning Method for Automated Fish Categorization in the ICETIT Symposium used a combined deep learning technique, employing an ensemble stacked model for classifying and a pre-trained VGG16 model with feature extraction, with 93.8% classification accuracy, the model performed remarkably well. D. Krivoguz in the beginning of a deep neural network-based method for immediate time fish diseases epizootic monitoring conducted two experiments differing basically in data augmentation techniques [40]. In paper [16], [41], they have also used deep learning techniques. The model's accuracy in the original dataset was 86.7% for classifying infected fish and 86.9% for healthy fish. However, the detection accuracy increased dramatically when he employed several augmentation tools, hitting 96.9% for diseased fish and 96.7% for healthy fish. James C. Chen's paper An analysis of a Taiwanese aquaculture fish farm case study [42]. Engineering Society (AES) demonstrated the InceptionV3 a pre-trained model, employed to divide into the three different kinds of anomalous appearances in fishes grouped in the dataset, attained a phenomenal 98.94% average accuracy in the task's second phase. Rum and Nawawi [43], used an application for Fish Identification via Image Recognition International Journal of Advanced Applications and Computer Science, Vol. 12, No. 3, 2021 studied the saltwater fishes in Malaysia. The model achieved around 87% accuracy. Aditya Gupta

Goodwin in Reliable Identification of Wounds and Lice in Atlantic Salmon Fish with the Use of a CNN [44], proposed an ML algorithm based on images to identify lice and wounds in the live salmon fish farm environment. In this model, They suggested using a CNN with about 15 convolutional as well as 5 dense layers for the identification of fish lice along with wounds. Test accuracy of 96.7% for the suggested technique has been contrasted to 91.2% and 92.8% for the existing VGG-19 and VGG-16 models, subsequently. Fitriannah et al. [45], have purposed this study was to determine how well MobileNetV2 and VGG-16 performed when parameters were tuned. To that end, fish species that were deemed threatened or endangered were monitored, and it became easier to map areas that were off-limits to fishing by determining the values of batch size, epoch, learning rate, and optimizer for fish image datasets. The model with the greatest accuracy value was VGG-16. The accuracy of the test for VGG16 in the absence of fine-tuning is 98.07%. Monika Mathur The tough challenge of classifying underwater fish species using CNN was tackled by Sprinkler in SN Computer Science, using an automated way to fish classification in an underwater scenario [30]. To solve the problem they used Transfer learning with the ResNet-50 model which significantly boosted classification accuracy, even with limited data. Impressively, the suggested method obtained a validation accuracy of 84.92% for a lesser number of data as well as 98.44% for a larger dataset. Table 1 lists relevant works in summary form.

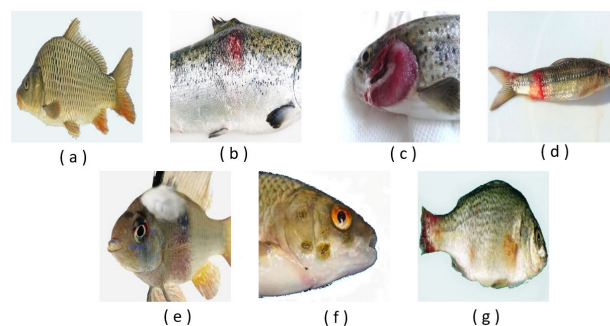
### III. MATERIALS AND METHOD

This section contains a thorough explanation of the approach used to identify fish disease as well as the dataset that was used to verify the model.

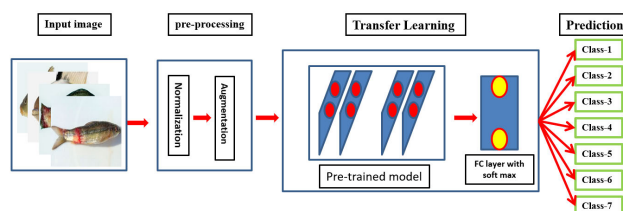
#### A. DATASET

In this study, we used a total of 3 datasets, they are dataset-1 [46] Fresh Water Fish Disease Data set The dataset is publicly available and consists of a total of seven classes. The dataset-2 [47], the total number of images is 305 with two classes. They are Fresh Fish contained a total of 163 image files, while Infected Fish contained 142 image files.

In this publicly available dataset, there are less number of images. So we created our own custom dataset-3 (Freshwater Fish Disease Aquaculture in South Asia). To create the dataset, the fish images have been collected from various sources to validate the suggested approach. For example, some images were obtained from a university agricultural department, while others came from an agricultural farm in ODISHA, INDIA, with the help of expert who can identify fish diseases. Some images are collected from agricultural website portal. The dataset comprises approximately 2,450 images categorized into seven classes: Aeromoniasis, Bacterial Gill Disease, Bacterial Red Disease, Saprolegniasis, Healthy Fish, Parasitic Diseases, and White Tail Disease. Each class contains 350 images, providing a balanced distribution for analysis. As detailed in Table 2, the dataset



**FIGURE 2.** Samples of input images from the dataset-3: (a) Healthy Fish, (b) Bacterial diseases-Aeromoniasis, (c) Bacterial gill disease, (d) Bacterial Red disease, (e) Fungal diseases, (f) Parasitic diseases, (g) Viral diseases White tail disease.



**FIGURE 3.** Overview of the proposed method using images, here Healthy Fish, Bacterial diseases-Aeromoniasis, Bacterial gill disease, Bacterial Red disease, Fungal diseases, Parasitic diseases, Viral diseases White tail disease.

consists of 350 images for each of the seven classes, ensuring a balanced distribution for analysis. Several image samples from the dataset-3 are displayed in Figure 2. To address the relatively small dataset size, data augmentation techniques were employed during training to increase the diversity and robustness of the model.

#### B. PROPOSED METHODOLOGY

The deep learning approach used in the suggested model for fish diagnosis of diseases is displayed as illustrated in Figure 3. The model will classify the input image and identify the disease type and category. The section that follows provides specifics about each step.

##### 1) PREPROCESSING

A description of the techniques used during the pre-processing stage is given in this section.

**Normalization** is an essential step that is usually used in CNN systems to guarantee numerical consistency. A CNN model has the potential to acquire normalization quicker and its inclination descending is more probable to be solid to achieve excellent accuracy [48]. The research has normalized the provided values for pixels in this instance.

**Augmentation** In the CNN models, more data means effective training and better performance [49]. In our dataset there is less number data to solve this problem we used the data augmentation technique. In our dataset, we encountered a shortage of data and to address this issue we employed

**TABLE 1.** Summary of related works on fish disease detection.

Reference	Classification	Feature Extraction	Accuracy (%)	Year
Ahmed et al. [6]	SVM	GLCM	93.75	2021
Malik et al. [25]	NN + K-NN	FAST+ HOG	86.00	2017
Waleed et al. [35]	AlexNet +ResNet50 +ResNet18 +ResNet101	CNN	99.04	2019
Chakravorty et al. [28]	PCA	HSV	90.00	2015
Mathur et al. [30]	FishResNet +AlexNet +VGG +MobileNet +GoogleNet +ResNet	ResNet-50	98.44	2021
Chen et al. [42]	InceptionV3	CNN	98.94	2022
Gupta et al. [44]	CNN	K-Means clustering	96.70	2022
Fitriannah et al. [45]	VGG16+ MobileNetV2	CNN	99.74	2022
Sekhar et al. [38]	MobileNetV2	CNN	99.94	2023
Krivoguz et al. [40]	InceptionV3	-	96.70	
Rum et al. [43]	VGG16+ AlexNet	CNN	95.00	2021
Li et al. [1]	SVM	Deep CNN	94.00	2022
Yu et al. [12]	YOLOv4+ MobileNetV1- YOLOv4 +MobileNetV2- YOLOv4 +MobileNetV3- YOLOv4 +MobileNetV3- GELU-YOLOv4	MobileNet	99.00	2023
Tamma et al. [17]	VGG16 +CNN	CNN	95.40	2019
Demir et al. [20]	ResNet101 +InceptionV3	HOG	87.42	2019
Rachman et al. [34]	FCN-32- MobileNet+ ResNet50-Unet + MobileNet-Unet	MobileNet	96.20	2023
Mamun et al. [36]	Ensemble model + ResNet-50	VGG	99.64	2023

**TABLE 2.** Details of “freshwater fish disease aquaculture in South Asia” dataset-3.

Class	Original dataset-3		
	Total images	Train	Test
Bacterial diseases	350	250	100
Bacterial gill disease	350	250	100
Bacterial Red disease	350	250	100
Fungal diseases	350	250	100
Parasitic diseases	350	250	100
Viral diseases White tail disease	350	250	100
Healthy Fish	350	250	100

the augmentation technique shown in Figure 4. The array of data augmentation methods discussed emphasizes the importance of augmentations in bolstering the resilience and performance of image recognition systems. By exploring the range of choices at their disposal researchers and practitioners can make informed decisions to enhance the precision and dependability of their image recognition models [50]. The images in the dataset were subjected to several augmentation

techniques to increase their variability and improve the performance of the machine learning model. The images in the dataset were subjected to several augmentation techniques to increase their variability and improve the performance of the machine learning model like flipped horizontally and shifted in width and height by a range of 0.2. The images were rotated clockwise by 20,40,60 degrees, scaled by a factor of 1.0/255. Implemented varying brightness levels. The fill mode used for the shifting operation was “nearest”. After augmentation dataset -3, we got a total of 10500 images, and increase 6 times bigger than the original dataset that shown in Table 3, and some results of data augmentation that shown in Figure 5. After augmentation, we split data into 60% for training, 20% testing, and 20% validation.

## 2) FISH DISEASE PREDICTION USING PRE-TRAINED CNN MODELS

Numerous applications for image processing have demonstrated the great efficacy of CNN models. Because there aren't enough examples available, it might be difficult to train

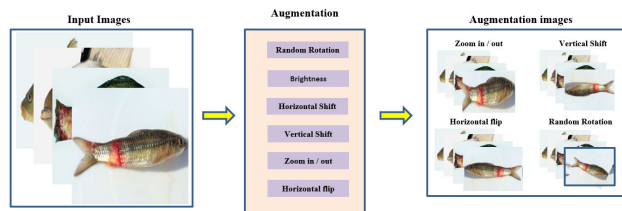


FIGURE 4. Illustration of different data augmentation techniques used in this study.

TABLE 3. Details of the augmented dataset-3 used in the experiment.

Class	Total image	Train	Validation
Bacterial diseases	1500	1050	450
Bacterial gill disease	1500	1050	450
Bacterial Red disease	1500	1050	450
Fungal diseases	1500	1050	450
Parasitic diseases	1500	1050	450
Viral diseases White tail disease	1500	1050	450
Healthy Fish	1500	1050	450

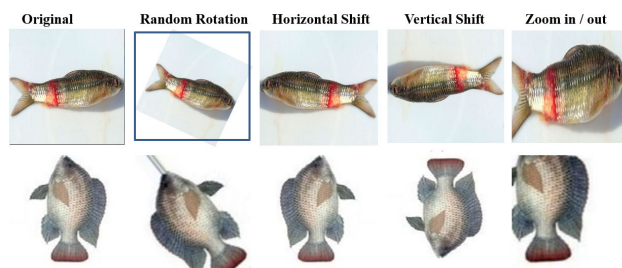


FIGURE 5. Sample results of augmented image from freshwater fish disease aquaculture in South Asia dataset.

these models from scratch for fish disease prediction. In these situations, transfer learning (TL)-trained models [51] could be a really good option. To tackle a comparable task with a smaller dataset, TL applies the information acquired from a deep learning model trained on a big dataset. As a result, deep learning algorithms that are trained from scratch do not require as large of a dataset and may learn faster.

Here, we employed nine CNN models that had already been trained.: VGG-16 [17], VGG-19 [36], MobileNetV2 [18], MobileNetV3 [19], InceptionV3 [20], ResNet-50 [21], ResNet-34 [22], EfficientNetB7 [23], ConvNeXtXLarge [24] to classify and detect fish disease in dataset-3 (Freshwater Fish Disease Aquaculture in South Asia). These models have proven notable efficacy across a broad spectrum of computer vision applications. It's important to note the fact that such models had been initially trained with extensive labeled datasets. A new Fully Connected (FC) layer having an outcome dimension that represented the several classes linked to fish disease detection had been integrated into the above models in place of the final layer being an aspect of the improving procedure. Even the last FC layer during these modified models underwent retraining, while the rest of the layers retained their pre-trained weights. The study

maintained consistent hyperparameter settings across these deep learning models to ensure a fair comparison. Table 4 provides an architectural outline of CNN models that have been trained, while their major components are shown in Figure 6. VGG-16 network [17], Thirteen convolutional layers including the three layers. This network's filters are limited to  $3 \times 3$  with a stride and padding of 1. More than a million images in one thousand categories were used to train the model.

- **Simplicity and Modularity:** VGG-16 uses very uniform architecture with  $3 \times 3$  convolution filters and a consistent structure of convolutional blocks followed by max pooling layers. This simplicity makes it easy to understand and modify.
- **Effective Feature Extraction:** Despite its relatively simple architecture, VGG-16 is highly effective at extracting features from images, making it a popular choice for transfer learning.
- **High-Resolution Image Classification:** VGG-16 is particularly good at tasks that involve high-resolution image classification because of its deep architecture which allows it to capture fine details.
- **Transfer Learning:** It's frequently used for transfer learning due to its robust feature extraction capabilities.

. VGG-19 [36], model resembles VGG16 but contains 19 weight layers, consisting of 3 fully connected layers and 16 convolutional layers. The primary distinction from VGG16 is the deeper architecture achieved by the incorporation of additional convolutional layers. ConvNeXtXLarge [24] carries out a higher level of effectiveness compared to EfficientNetB7 [23] consists of 10 residual blocks in its architecture. Each block has its own set of convolutional layers, helping the network learn hierarchical features from the input data. Inception V3 also scores well, which was developed by Google. It consists of 48 layers and includes modules like the Inceptionv3 [20] modules, which use different kernel sizes for convolutions to capture features at multiple scales.

- **High Accuracy:** This model is designed to achieve high accuracy on various computer vision tasks, benefiting from modern architectural advances.
- **Scalability:** It is highly scalable, allowing it to handle complex and large datasets effectively.
- **Large-Scale Image Classification:** Excels in large-scale image classification tasks where a high level of detail and accuracy is required.
- **Flexible and Generalizable:** Performs well across a wide range of computer vision problems, from image classification to segmentation.

. It's designed to be computationally efficient while providing strong performance in image classification and other computer vision tasks.

MobileNetV2 [18] is a neural network architecture designed by Google for mobile and edge devices. It is known for its excellent performance and has been implemented to be

lightweight and efficient. The architecture comprises inverted residual blocks linear obstructions as well as depth-wise differentiated convolutions to minimize computational costs while still maintaining good performance. With 53 layers, MobileNetV2 is recognized for its speed and accuracy in various computer vision tasks, especially on devices with limited resources.

- **Lightweight and Fast:** Designed to be highly efficient with low computational requirements, making it ideal for mobile and edge devices.
- **High Performance:** Despite its efficiency, it maintains good performance levels across various tasks.
- **Resource-Constrained Devices:** Performs exceptionally well on devices with limited computational power, such as smartphones and embedded systems.
- **Real-Time Applications:** Well-suited for real-time applications where both speed and accuracy are important.

MobileNetV3 [19], is more optimized than MobileNetV2 for mobile devices and edge computing than MobileNetV2, It incorporates the swish activation function.

ResNet-50 and ResNet-35 are both variations of the ResNet (Residual Networks) architecture, but they differ in terms of the number of layers. ResNet-50 has 50 layers, and it is a deeper architecture compared to ResNet-35. The “50” in ResNet-50 [21], indicates the total number of layers, including both convolutional and fully connected layers. On the other hand, ResNet-35 [22], would have 35 layers in total. The number after “ResNet” indicates the entire amount for network layers.

- **Efficient Architecture:** While not as deep as ResNet-50, ResNet-35 provides a good balance between complexity and computational efficiency.
- **Residual Learning:** Benefits from the residual connections that prevent the vanishing gradient problem, allowing it to maintain high performance without being excessively deep.
- **Moderate-Complexity Tasks:** Excels in tasks that require a balance between depth and computational efficiency, such as mid-complexity image classification and object detection.
- **General Use:** Provides solid performance across a range of computer vision tasks without requiring the extensive resources needed by deeper models.

EfficientNetB7 [52], consists of 66 layers organized into several MBConv blocks with up to 640 filters per layer. It employs depthwise separable convolutions to reduce computational complexity, and includes global average pooling followed by a dropout layer before a final dense layer with 1,280 neurons for output. The architecture is designed to balance depth, width, and resolution efficiently.

- **Efficiency:** EfficientNetB7 uses a compound scaling method that balances network depth, width, and resolution, making it both computationally efficient and powerful.

- **High Performance:** Achieves high accuracy with fewer parameters compared to other models of similar capacity.
- **Resource-Constrained Environments:** Ideal for applications where computational resources are limited but high performance is still required.
- **Image Classification and Transfer Learning:** Performs exceptionally well in image classification tasks and is commonly used for transfer learning due to its efficient architecture.

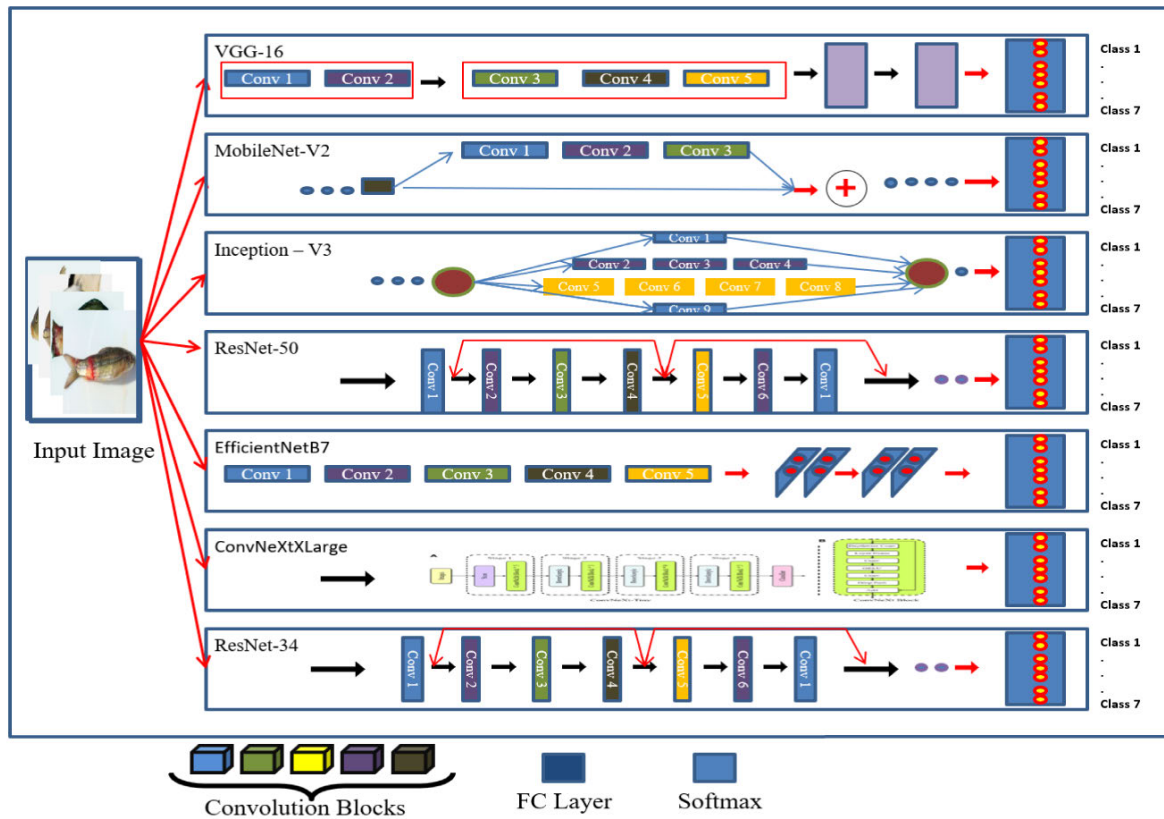
InceptionV3 [53], is a deep convolutional neural network architecture designed to achieve high performance while minimizing computational cost. It consists of 48 layers in total, including 5 convolutional layers and several Inception modules which capture multi-scale features using filters of various sizes. The network ends with a global average pooling layer, followed by a dropout layer and a dense layer with 1,000 neurons for output classification. This design allows InceptionV3 to excel in complex image classification tasks with improved efficiency.

- **Multi-Scale Feature Detection:** The Inception modules use multiple filter sizes in parallel to capture features at various scales, making it effective for detailed image analysis.
- **Computational Efficiency:** Designed to be computationally efficient, allowing it to handle complex tasks with reduced computational costs.
- **Object Detection and Segmentation:** Excels in tasks requiring the detection of objects of varying sizes within images.
- **Image Classification:** Provides strong performance in image classification tasks due to its ability to capture a wide range of features.

**TABLE 4. Architectural descriptions of the pre-trained CNN models used for our proposed work.**

Model	Layers	Parameters(M)	Input size	Output size
VGG-16	16	138.4	(224, 224, 3)	(7)
VGG-19	19	143.7	(224, 224, 3)	(7)
MobileNetV2	53	3.5	(224, 224, 3)	(7)
MobileNetV3	21	5.4	(224, 224, 3)	(7)
InceptionV3	42	23.9	(224, 224, 3)	(7)
ResNet-50	50	25.6	(224, 224, 3)	(7)
ResNet-34	34	21.8	(224, 224, 3)	(7)
EfficientNetB7	81	66.7	(224, 224, 3)	(7)
ConvNeXtXLarge	-	350.1	(224, 224, 3)	(7)

Finding the most effective deep learning [54], [55] model to achieve this research’s main goal is Fish Disease detection using the Freshwater Fish Disease Aquaculture dataset in South Asia. These findings can serve as a cornerstone for further research and the development of more efficient artificial intelligence remedies in the field of aquaculture and disease management.



**FIGURE 6.** Illustration of the major components of seven pre-trained CNN models with convolution blocks of different colors indicate filters of different sizes.

### C. PREDICTION USING ENSEMBLE LEARNING

After using transfer learning, we noticed that some models ('VGG-16, MobileNetV2, InceptionV3') [17], [18], [20], Performed well while others did not [56]. Then we selected three of the best-performing models and used EL to increase the accuracy of the final model.

Ensemble learning (EL) [57], is a technique that combines multiple models and strategies, and can address issues with computational intelligence such as classifiers as well as specialists. Enhancing the effectiveness of models in classification, prediction, and approximation of functions is the main objective of EL, as is lowering the possibility of choosing a subpar model. Error correction, combining data, incremental learning, non-stationary learning, choosing optimal or nearly ideal features, and granting confidence to the model's choice are just a few of the numerous uses for EL [58]. Traditionally Ensemble learning [57], is based on the integration of traditional machine learning models and their application in different contexts [59]. This approach significantly improved the prediction accuracy and robustness of the model. Many ensemble techniques such as averaging, bagging, random forests, stacking, and boosting are widely used in the literature, each offering unique advantages in different scenarios. Until now ensemble learning has been mainly limited to simple single models and

most efforts have been focused on combining these models effectively.

However, in recent years we have seen a shift towards combining ensemble learning and deep learning techniques [60]. This evolution is due to the growing popularity of deep learning and its remarkable performance in a variety of applications. Nevertheless, many early attempts at deep ensemble learning often used basic techniques such as average voting [61], to combine basic deep learning models. Although average voting is a simple approach it tends to favor learners with weak baselines and may not be the most efficient strategy for incorporating these learners [62]. Consequently, there is a need for more sophisticated clustering strategies that can be applied in deep learning. These advanced strategies aim to address generalization issues, training problems, and other challenges associated with traditional group techniques.

To perform EL, define a function called extract-features we take these three pre-trained models and a data directory as input, and then extract features from the images in the directory. Here's an explanation of how we perform the EL for Fish disease detection.

- **Initialization:**

- `feature_list`: Empty list to store extracted features.



- `label_list`: Empty list to store class labels of the images.
- **Iterating through Subdirectories:**
  - Loop through all subdirectories within the `data_directory`.
  - Skip hidden folders starting with "." (dot).
  - For each subdirectory (considered a class):
    - \* Create the path to the class folder.
    - \* Loop through all image files within the class folder.
    - \* For each image:
      - Load the image using an `image.load_img` function.
      - Convert the image to a NumPy array using `image.img_to_array`.
      - Expand the dimension of the array to add a batch dimension (suitable for model input).
      - Apply pre-process specific to the model using `preprocess_input_mobilenet` (this function needs to be adjusted based on the actual model being used).
      - Predict features from the image using the pre-trained model (`model.predict`).
      - Flatten the feature vector (convert from 2D to 1D array).
      - Append the flattened features to `feature_list`.
      - Append the subdirectory name (assuming it represents the class label) to `label_list`.
- Return two NumPy arrays:
  - `feature_list`: Array containing features extracted from all images.
  - `label_list`: Array containing class labels of the corresponding images.

#### Extracting features from train and test sets:

The code calls the `extract_features` function multiple times with different models (`base_model_mobile`, `base_model_vgg`, `base_model_inception`) and data directories (`train_data_dir`, `test_data_dir`). This extracts features for each image in the train and test sets using different pre-trained models.

#### Combining features

The code combines features extracted from different models using `np.hstack` (horizontal stack) [63]. We conducted an experiment with Principal Component Analysis (PCA) by setting `n_components` to 3 to reduce the dimensionality of the combined features. We also performed the experiment without using PCA. Our findings indicated that the model performed significantly better without PCA, albeit at the cost of increased processing time. Consequently, we decided to proceed with our experiment without employing PCA.

Overall, the snippet performs feature extraction from image datasets for training and testing purposes. It utilizes pre-trained models and combines features from three different models, potentially improving the overall representation.

Here, PCA is then applied for dimensionality reduction and then SVM used for classification [64], [65]. The proposed model is shown in Figure 7.

## IV. EXPERIMENTS AND RESULTS

This section showcases the findings derived from multiple experiments. We conducted an extensive experimental analysis to detect fish disease from Freshwater Fish Disease Aquaculture in South Asia dataset using seven pre-trained CNN models including VGG-16 [17], VGG-19 [36], MobileNetV2 [18], MobileNetV3 [19], InceptionV3 [20], ResNet-50 [21], ResNet-34 [22], EfficientNetB7 [23], ConvNeXtXLarge [24]. Table 5 here shows the results for all pre-trained CNN models.

### A. EXPERIMENTAL SETUP AND PERFORMANCE METRICS USED

We examined the influence of various hyper-parameters related to these models and conducted a comparative assessment among seven pre-trained CNN models. Here we used transfer learning. Transfer learning [51] accelerates model training, enhances performance on new tasks with limited data, and fosters generalization across domains. It leverages the pre-trained model's learned features, reducing training time and resources while offering state-of-the-art capabilities. This versatility aids in various applications and promotes accessibility to advanced machine learning techniques [50], [66].

### B. RESULTS PRE-TRAINED CNN MODELS

The training performance in terms of training loss, validation loss, and validation accuracy obtained by different networks at different epochs are listed in Table 5. Figure [8-14] illustrates the training and validation loss across different iterations for all networks. We presented the confusion matrices of all seven CNN models [21], [67] on the test data in Figure [15-18]. We also presented the F1 score for all pre-trained CNN models that are shown in Figure [19-22]. It can be observed that our proposed method with ConvNeXtXLarge [24], VGG-16 [17], and MobileNetV2 [18] are capable of classifying more than (80 %) cases accurately. The detailed classification results obtained from all networks are compared in terms of various metrics and are tabulated. It can be seen that the VGG-16 model achieved the highest performance 88.82% accuracy an f1 score of 88.20%, MobileNetV2 performance of 85.20% accuracy, and f1 score of 84.60%. ConvNeXtXLarge performance 85.20% accuracy and f1 score 85.10%.

### C. RESULTS COMPARISON WITH DIFFERENT OPTIMIZATION METHODS

Evaluating the impact of optimization methods on pre-trained deep learning models, we experimented with Adam, RMSProp, Adadelta, and SGD. Our results demonstrate that the performance of each optimizer varies significantly across different model architectures. The classification

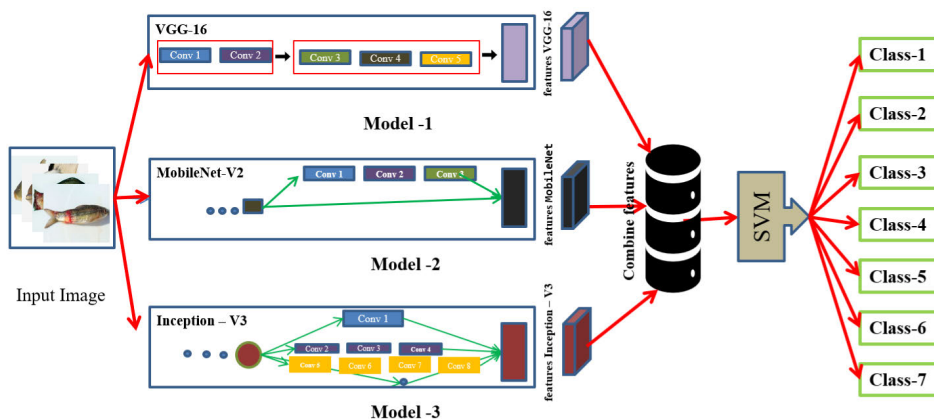


FIGURE 7. Proposed fusion model for classification of fish disease.

TABLE 5. Training performance of seven CNN models use for this experiment dataset-3.

Training Performance					
Model	Epoch	Train Loss	Train accuracy	Test Loss	Valid accuracy
VGG-16 [17]	1	5.3353	0.2867	2.2373	0.1714
	...	...	...	...	...
	29	0.3919	0.8805	0.9799	0.7143
	30	0.3615	0.8737	1.1881	0.7286
VGG-19 [36]	1	4.5435	0.1763	1.5423	0.1453
	...	...	...	...	...
	29	0.2724	0.75	0.8765	0.7542
	30	0.3615	0.7654	1.0.6787	0.7142
MobileNet-V2 [18]	1	9.1179	0.1572	7.8432	0.2386
	...	...	...	...	...
	29	6.2551	0.6450	6.1530	0.6932
	30	6.2137	0.6314	6.1257	0.6932
MobileNetV3 [19]	1	9.1179	0.1572	7.8432	0.2386
	...	...	...	...	...
	29	4.7352	0.6522	7.635	0.6327
	30	2.0821	0.6631	5.423	0.6732
InceptionV3 [20]	1	2.3484	0.3253	1.3809	0.5571
	...	...	...	...	...
	29	0.3634	0.8904	0.9521	0.7143
	30	0.3699	0.8801	1.0446	0.6714
ResNet-50 [21]	1	15.5708	0.2329	6.5496	0.4000
	...	...	...	...	...
	29	1.7959	0.3870	1.6685	0.4000
	30	1.7881	0.3870	1.6673	0.4000
ResNet-34 [22]	1	3.4316	0.2705	1.125	0.1000
	...	...	...	...	...
	29	1.2948	0.5240	3.0424	0.2571
	30	1.2898	0.5377	8.4655	0.1286
EfficientNetB7 [23]	1	103.2888	0.2358	10.3148	0.3977
	...	...	...	...	...
	29	1.8566	0.3821	1.8489	0.3977
	30	1.8539	0.3821	1.8459	0.3977
ConvNeXtXLarge [24]	1	28.8362	0.3252	6.8319	0.4545
	...	...	...	...	...
	29	0.8247	0.6477	1.4386	0.6136
	30	0.7644	0.6612	1.6133	0.6250

accuracy result of the various models like VGG-16, VGG-19, MobileNetV2, MobileNetV3, InceptionV3, ResNet-50, ResNet-34, EfficientNetB7 and ConvNeXtXLarge with Adam optimizer are 72.63%, 71.54%, 68.09%, 64.21%, 64.09%, 38.50%, 71.31%, 40% and 85.20% respectively.

Similarly the the models with RMSProp optimizer provides classification accuracy like 88.82%. The classification accuracy with SDG optimizer are 38.82%, 43.16%, 85.20%, 84.56%, 64.21%, 37.89%, 93.75%, 40.43% and 73.29. Accuracy with RMSProp optimizer are 88.82%, 61.08%,

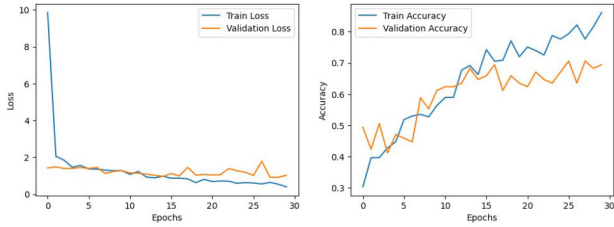


FIGURE 8. Loss convergence and accuracy plot obtained for dataset-3 with VGG-16 model.

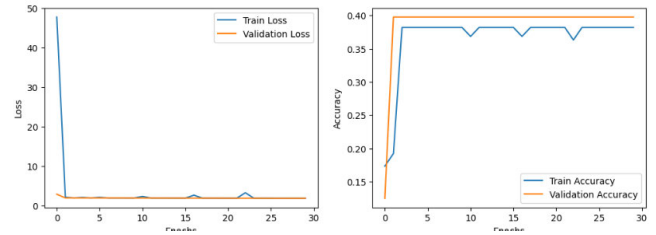


FIGURE 13. Loss convergence and accuracy plot obtained for dataset-3 with EfficientNetB7 model.

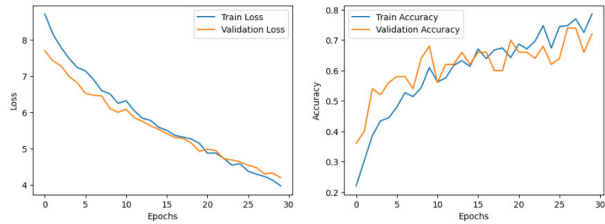


FIGURE 9. Loss convergence and accuracy plot obtained for dataset-3 with MobileNet-V2 model.

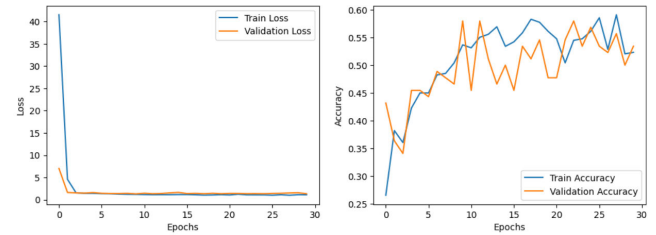


FIGURE 14. Loss convergence and accuracy plot obtained for dataset-3 with ConvNeXtLarge model.

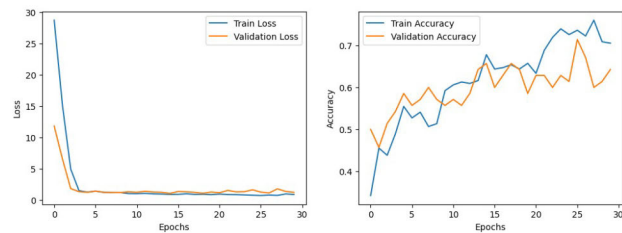


FIGURE 10. Loss convergence and accuracy plot obtained for dataset-3 with InceptionV3 model.

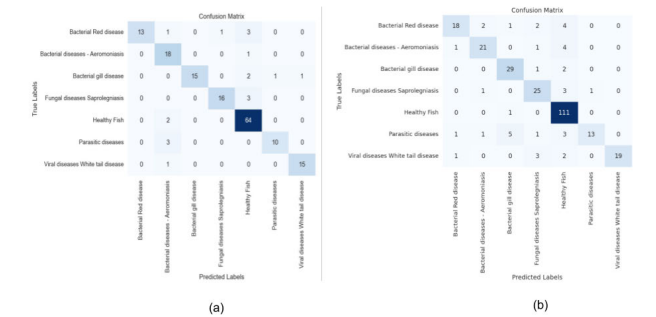


FIGURE 15. Confusion matrix for dataset-3 with (a) VGG-16, (b) MobileNetV2 models.

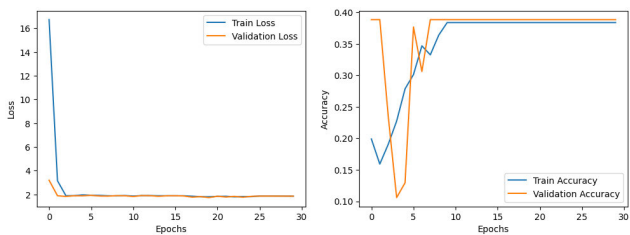


FIGURE 11. Loss convergence and accuracy plot obtained for dataset-3 with ResNet-50 model.

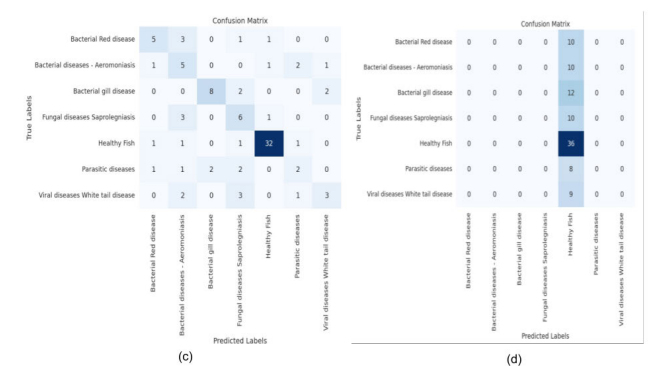


FIGURE 16. Confusion matrix for dataset-3 with (c) InceptionV3, (d) ResNet-50 models.

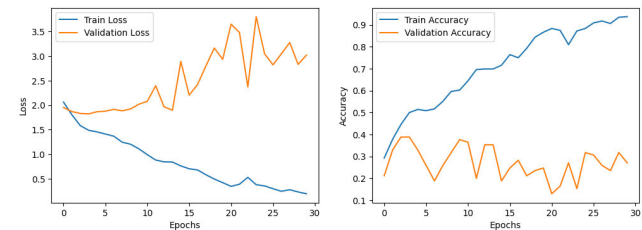


FIGURE 12. Loss convergence and accuracy plot obtained for dataset-3 with ResNet-34 model.

69.15%, 68.67%, 64.21%, 37.89%, 61.08%, 40.43% and 60.65%. Likewise accuracy with Adadelat optimizer 38.82%,

37.82%, 69.01%, 68.67%, 43.16%, 37.89%, 31.25%, 40.43% and 40.43%. For instance, Adam achieved the highest accuracy for ConvNeXtLarge, while RMSProp excelled with VGG-16. However, SGD demonstrated

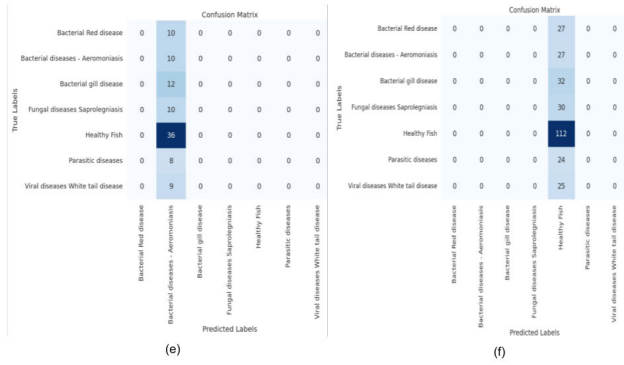


FIGURE 17. Confusion matrix for dataset-3 with (e) ResNet-34, (f) EfficientNetB7 models.

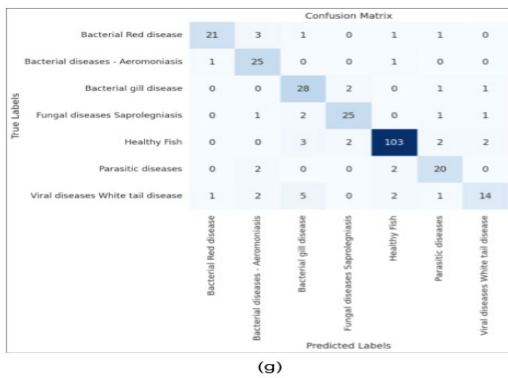


FIGURE 18. Confusion matrix for dataset-3 with (g) ConvNeXtXLarge model.

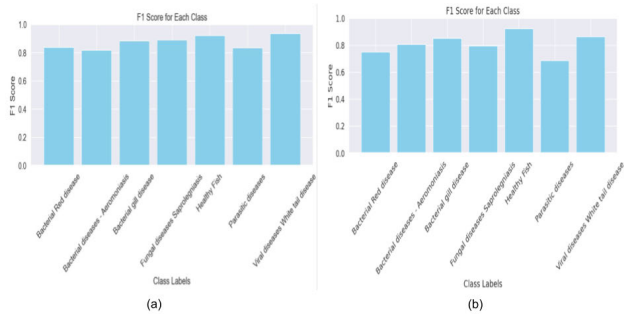


FIGURE 19. F1 Score obtained for dataset-3 with (a) VGG-16, (b) MobileNetV2 models.

superior performance for ResNet-34. Overall, our findings highlight the importance of carefully selecting optimization algorithms to maximize the potential of pre-trained models in specific application domains. Table 6 summarizes the classification results across all models and optimizers. Notably, VGG-16, MobileNetV2, and ConvNeXtXLarge consistently performed well with different optimization methods.

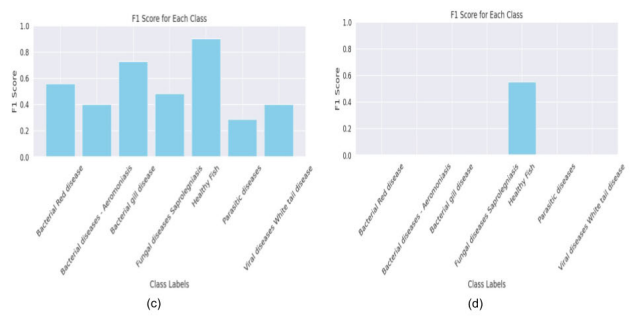


FIGURE 20. F1 Score obtained for dataset-3 with (c) InceptionV3, (d) ResNet-50 models.

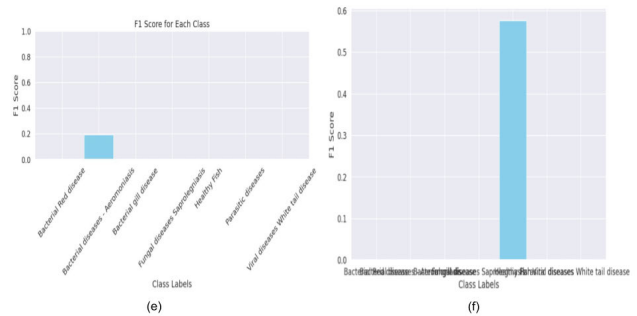


FIGURE 21. F1 Score obtained for dataset-3 with (e) ResNet-34, (f) EfficientNetB7 models.

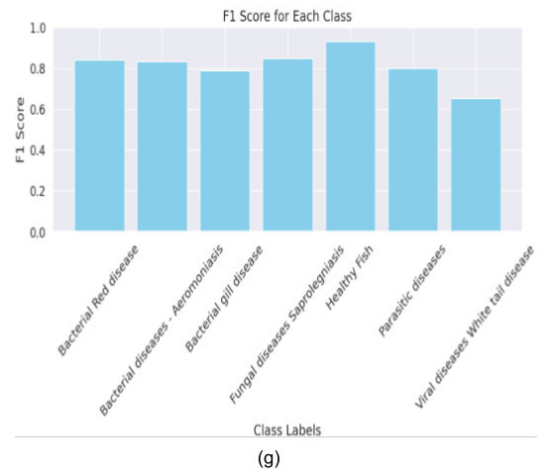


FIGURE 22. F1 Score obtained for dataset-3 with (g) ConvNeXtXLarge model.

**D. EXPERIMENTAL SETUP AND PERFORMANCE METRICS FOR ALL PRE-TRAINED CNN MODELS**

The models classified different types of fish skin disease from dataset-3. The details of the data splitting used in this study with augmentation are previously shown in Table 3.

The use of CNN models has provided excellent results for various image-processing applications. However, training these models from scratch to detect fish diseases is challenging due to the limited availability of image samples. In such

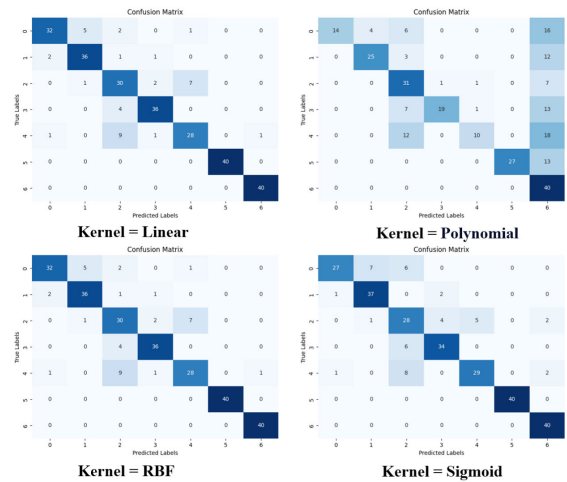
**TABLE 6. Classification performance (in %) comparison among different optimizers for dataset-3.**

Model	Optimizer	accuracy	f1 Score
VGG-16 [17]	ADAM	72.63	70.20
	SDG	38.82	28.43
	RMSProp	88.82	88.20
	Adadelata	38.82	37.23
VGG-19 [36]	ADAM	71.54	69.31
	SDG	43.16	36.41
	RMSProp	61.08	13.49
	Adadelata	37.82	35.23
MobileNetV2 [18]	ADAM	68.09	67.89
	SDG	85.20	84.60
	RMSProp	69.15	21.97
	Adadelata	69.01	19.82
MobileNetV3 [19]	ADAM	65.67	66.65
	SDG	84.56	83.67
	RMSProp	68.67	40.65
	Adadelata	68.67	40.65
InceptionV3 [20]	ADAM	64.21	64.65
	SDG	64.21	64.65
	RMSProp	64.21	62.10
	Adadelata	43.16	36.41
ResNet-50 [21]	ADAM	38.35	20.83
	SDG	37.89	20.83
	RMSProp	37.89	20.83
	Adadelata	37.89	20.83
ResNet-34 [22]	ADAM	71.31	6.25
	SDG	93.75	5.33
	RMSProp	61.08	13.49
	Adadelata	31.25	2.01
EfficientNetB7 [23]	ADAM	40.43	23.28
	SDG	40.43	23.28
	RMSProp	40.43	23.28
	Adadelata	40.43	23.28
ConvNeXtXLarge [24]	ADAM	85.20	85.10
	SDG	73.29	71.08
	RMSProp	60.65	58.64
	Adadelata	40.43	23.28

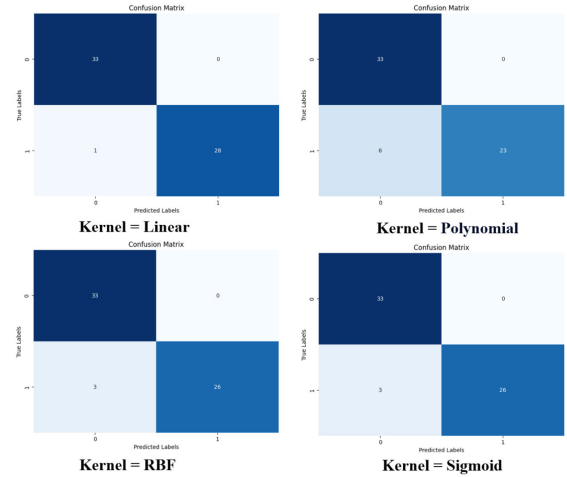
cases pre-trained models using Transfer Learning (TL) [51] may be useful. TL involves utilizing the knowledge gained by a deep learning model trained from a large dataset to solve a related task with a comparatively smaller dataset [68]. This eliminates the need for a large dataset and longer learning time required by deep learning methods trained from scratch. To classify fish diseases this study employed seven pre-trained models, including VGG-16 [17], [69], MobileNetV2 [18], InceptionV3 [20], ResNet-50 [21], ResNet-34 [22], EfficientNetB7 [23], ConvNeXtXLarge [24]. These networks have succeeded significantly in computer vision problems. It is worth noting that these models were originally trained on a large-scale labeled dataset. The last layer of these models was removed and a new Fully Connected (FC) layer with an output size of seven representing seven different classes (Bacterial diseases, Bacterial gill disease, Bacterial Red disease, Fungal diseases, Healthy Fish, Parasitic diseases, and Viral diseases White tail disease) was inserted. Only the last FC layer is trained in these resultant models, while other layers are initialized with pre-trained weights.

**E. EXPERIMENTAL PERFORMANCE FOR ENSEMBLE LEARNING**

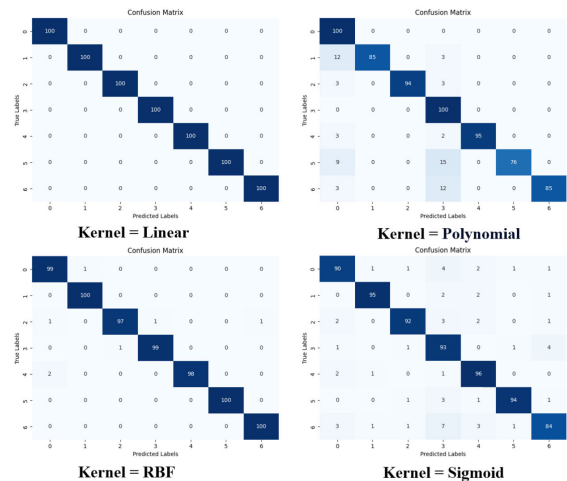
Explores the efficacy of ensemble learning methods utilizing popular deep learning architectures, including MobileNetV2 [18], VGG-16 [17], and InceptionV3 [20]. The research investigates both the performance of these ensembles with and without Principal Component Analysis(PCA) [28], [70]. We used to do experiments with dataset-1, dataset-2, and



**FIGURE 23. Confusion Matrix obtained for Ensemble learning with different kernels for dataset-1.**



**FIGURE 24. Confusion Matrix obtained for Ensemble learning with different kernels for dataset-2.**



**FIGURE 25. Confusion Matrix obtained for Ensemble learning with different kernels for dataset-3.**

dataset-3 to check the performance of the fusion model. For dataset-1 it has 7 classes. Figure 23 that shows the confusion

**TABLE 7. Classification results precision, recall, f1-score, support, accuracy, macro avg, weighted avg in fusion mode with dataset-1 for different kernels.**

Kernel = Linear				
	Precision(%)	Recall(%)	F1-score(%)	Support
Argulus	91.00	80.00	85.00	40
Broken antennae and rostrum	86.00	90.00	88.00	40
EUS	65.00	75.00	70.00	40
Healthy Fish	90.00	90.00	90.00	40
Redspot	78.00	70.00	74.00	40
THE BACTERIAL GILL ROT	100.00	100.00	100.00	40
Tail And Fin Rot	98.00	100.00	99.00	40
accuracy			86.00	280
macro avg	87.00	86.00	86.00	280
weighted avg	87.00	86.00	86.00	280
Kernel = Pynomial				
	Precision(%)	Recall(%)	F1-score(%)	Support
Argulus	100.00	35.00	52.00	40
Broken antennae and rostrum	86.00	62.00	72.00	40
EUS	53.00	78.00	63.00	40
Healthy Fish	95.00	47.00	63.00	40
Redspot	83.00	25.00	38.00	40
THE BACTERIAL GILL ROT	100.00	68.00	81.00	40
Tail And Fin Rot	34.00	100.00	50.00	40
accuracy			59.00	280
macro avg	79.00	59.00	60.00	280
weighted avg	79.00	59.00	60.00	280

**TABLE 8. Classification results precision, recall, f1-score, support, accuracy, macro avg, weighted avg in fusion mode with dataset-1 for different kernels.**

Kernel = RBF				
	Precision(%)	Recall(%)	F1-score(%)	Support
Argulus	91.00	80.00	85.00	40
Broken antennae and rostrum	86.00	90.00	88.00	40
EUS	65.00	75.00	70.00	40
Healthy Fish	90.00	90.00	90.00	40
Redspot	78.00	70.00	74.00	40
THE BACTERIAL GILL ROT	100.00	100.00	100.00	40
Tail And Fin Rot	98.00	100.00	99.00	40
accuracy			86.00	280
macro avg	87.00	86.00	86.00	280
weighted avg	87.00	86.00	86.00	280
Kernel = Sigmoid				
	Precision(%)	Recall(%)	F1-score(%)	Support
Argulus	93.00	68.00	78.00	40
Broken antennae and rostrum	82.00	93.00	87.00	40
EUS	58.00	70.00	64.00	40
Healthy Fish	85.00	85.00	85.00	40
Redspot	85.00	72.00	78.00	40
THE BACTERIAL GILL ROT	100.00	100.00	100.00	40
Tail And Fin Rot	91.00	100.00	95.00	40
accuracy			84.00	280
macro avg	85.00	84.00	84.00	280
weighted avg	85.00	84.00	84.00	280

matrix for dataset-1 and Table 7&8 shows the classification result. For dataset-1 we received highest accuracy 86.00% accuracy with Linear and RBF kernel. For dataset-2 it has 2 classes and we received highest accuracy 98.00%. Figure 24 that shows the confusion matrix for dataset-2 and Table 9 shows the classification result. Remarkably, they indicate a remarkable highest accuracy 100% for the ensemble models with dataset-3. For the Ensemble model in Table shows the classification of results precision, recall, f1-score, support, and accuracy and also shows classification performance comparison with different kernel in Table 10&11. Here, Figure 25 that shows the confusion matrices and Figure 26 shows the ROC curves for Dataset-3.

**F. DISCUSSION**

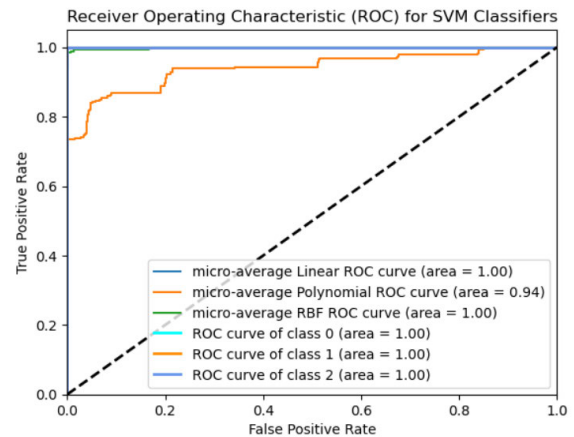
Identifying fish diseases in aquaculture is a pivotal research area that warrants utmost attention in the field of automated research. In this project, we present a novel dataset for aquaculture fish disease detection and carry out our research. Table 2 provides comprehensive information about our dataset, which we have allocated for our research experiments. Figure 2 represents a small segment of our dataset, showcasing images of both healthy and diseased fish specimens and here diseases are Bacterial diseases, Bacterial gill disease, Bacterial red disease, Fungal diseases, Parasitic diseases, Viral diseases shoaib2021fish. Table 12 presents a comparison between the proposed fish disease classification

**TABLE 9.** Classification results precision, recall, f1-score, support, accuracy, macro avg, weighted avg in fusion mode with dataset-2 for different kernels.

Kernel = Linear				
	Precision(%)	Recall(%)	F1-score(%)	Support
FreshFish	97.00	100.00	99.00	33
InfectedFish	100.00	97.00	98.00	29
accuracy			98.00	62
macro avg	99.00	98.00	98.00	62
weighted avg	98.00	98.00	98.00	62
Kernel = Polynomial				
	Precision(%)	Recall(%)	F1-score(%)	Support
FreshFish	85.00	100.00	92.00	33
InfectedFish	100.00	79.00	88.00	29
accuracy			90.00	62
macro avg	92.00	90.00	90.00	62
weighted avg	92.00	90.00	90.00	62
Kernel = RBF				
	Precision(%)	Recall(%)	F1-score(%)	Support
FreshFish	92.00	100.00	96.00	33
InfectedFish	100.00	90.00	95.00	29
accuracy			95.00	62
macro avg	96.00	95.00	95.00	62
weighted avg	96.00	95.00	95.00	62
Kernel = Sigmoid				
	Precision(%)	Recall(%)	F1-score(%)	Support
FreshFish	92.00	100.00	96.00	33
InfectedFish	100.00	90.00	95.00	29
accuracy			95.00	62
macro avg	96.00	95.00	95.00	63
weighted avg	96.00	95.00	95.00	63

**TABLE 10.** Classification results precision, recall, f1-score, support, accuracy, macro avg, weighted avg in fusion mode with dataset-3 for different kernels.

Kernel = Linear				
	Precision(%)	Recall(%)	F1-score(%)	Support
Bacterial Red disease	100.0	100.00	100.00	100
Bacterial diseases - Aeromoniasis	100.0	100.00	100.00	100
Bacterial gill disease	100.0	100.00	100.00	100
Fungal diseases Saprolegniosis	100.0	100.00	100.00	100
Healthy Fish	100.0	100.00	100.00	100
Parasitic diseases	100.0	100.00	100.00	100
Viral diseases White tail disease	100.0	100.00	100.00	100
accuracy			100.00	700
macro avg	100.00	100.00	100.00	700
weighted avg	100.0	100.00	100.00	700
Kernel = Polynomial				
	Precision(%)	Recall(%)	F1-score(%)	Support
Bacterial Red disease	77.00	100.00	87.00	100
Bacterial diseases - Aeromoniasis	100.0	85.00	92.00	100
Bacterial gill disease	100.0	94.00	97.00	100
Fungal diseases Saprolegniasis	74.0	100.00	85.00	100
Healthy Fish	100.0	95.00	97.00	100
Parasitic diseases	100.0	76.00	86.00	100
Viral diseases White tail disease	100.0	85.00	92.00	100
accuracy			91.00	700
macro avg	93.00	91.00	91.00	700
weighted avg	93.00	91.00	91.00	700



**FIGURE 26.** ROC curves in Ensemble learning for dataset-3.

approach and existing techniques from previous research. In [25], the method used NN and they got 86% accuracy. For this model need to upgrade the accuracy. In [1] they used the computer vision method and they got 98.79% accuracy. In [37] and [44] they used Convolutional Neural Network(CNN) method with respectably 3, 3 classes and they got accuracy gradually 96.7%, 94.4%. If they took more classes they would get better accuracy. In [42] the Convolutional Neural Network(CNN) method was used with 11 classes and they got a high number of accuracy and that is 98.94%. In [28] they used PCA and K-means clustering method with 11 classes and they got 91% accuracy. Although they used 11 classes, they still found relatively low accuracy.

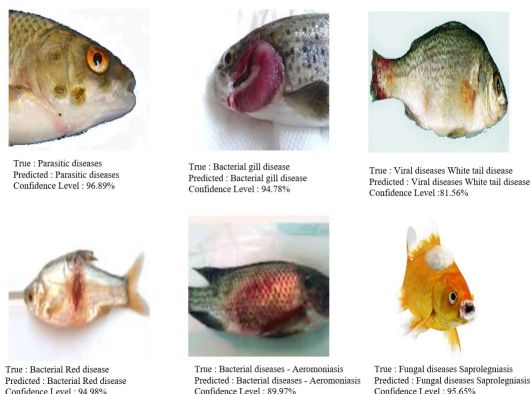
Therefore they should increase the accuracy of this model. In [25] they used PCA with HOG and FAST model with 2 classes and they got 86% accuracy. They should use more classes to get more accuracy. In [38] they used a popular method that is MobileNetV2 with 5 classes and they got a high accuracy which is 99.94%. In [13] they also got a high accuracy which is 94.64%. They used two popular methods that are YOLOV4 and MOBILENetV2. In [18] they have used MOBILENetV2 and LSTM with 8 classes but they got low accuracy which is 85%. For this model, they should upgrade their accuracy. For our research, we used Transfer Learning(TL) and Ensemble Learning(EL). In TL we used seven pre-trained CNN models, from here we applied

**TABLE 11.** Classification results precision, recall, f1-score, support, accuracy, macro avg, weighted avg in fusion mode with dataset-3 for different kernels.

Kernel = RBF				
	Precision(%)	Recall(%)	F1-score(%)	Support
Bacterial Red disease	97.00	99.00	98.00	100
Bacterial diseases - Aeromoniasis	99.0	100.00	100.00	100
Bacterial gill disease	99.0	97.00	98.00	100
Fungal diseases Saprolegniasis	99.0	99.00	99.00	100
Healthy Fish	100.0	98.00	99.00	100
Parasitic diseases	100.0	100.00	100.00	100
Viral diseases White tail disease	99.0	100.00	100.00	100
accuracy			99.00	700
macro avg	99.00	99.00	99.00	700
weighted avg	99.00	99.00	99.00	700
Kernel = Sigmoid				
	Precision(%)	Recall(%)	F1-score(%)	Support
Bacterial Red disease	92.00	90.00	91.00	100
Bacterial diseases - Aeromoniasis	97.0	95.00	96.00	100
Bacterial gill disease	96.0	92.00	94.00	100
Fungal diseases Saprolegniasis	82.0	93.00	87.00	100
Healthy Fish	91.0	96.00	93.00	100
Parasitic diseases	97.0	94.00	95.00	100
Viral diseases White tail disease	91.0	84.00	87.00	100
accuracy			92.00	700
macro avg	92.00	92.00	92.00	700
weighted avg	92.00	92.00	92.00	700

**TABLE 12.** Comparison of fish disease classification results with existing methods.

Existing Method	Number of Classes	Accuracy (%)
Customized CNN (15 Convolutional + 5 Dense layers) [44]	3	96.7
PCA + K-means [28]	11	91
PCA + HOG + FAST [25]	2	86
MobileNetV2 [38]	5	99.94
YOLOv4 + MobileNet [13]	4	99.64
MobileNetV2 + LSTM [18]	8	85
Proposed - VGG-16 + MobileNetV2 + InceptionV3 + SVM (Dataset-1)	7	86
Proposed - VGG-16 + MobileNetV2 + InceptionV3 + SVM (Dataset-2)	7	98
Proposed - VGG-16 + MobileNetV2 + InceptionV3 + SVM (Dataset-3)	7	100



**FIGURE 27.** Fish disease detection results of some samples.

EL with maximum accuracy 3 models and we got 99.59% accuracy.

Our primary aim in this study has been to distinguish between infected and fresh aquaculture fishes through classification. To ensure high accuracy, we conducted a thorough evaluation of the efficacy of the top seven CNN models such as VGG-16, MobileNet-V2, InceptionV3, ResNet-50, ResNet-34, EfficientNetB7, ConvNeXtXLarge and we also used Ensemble learning for detection of fish disease. The experimental findings and the comprehensive comparative analysis revealed the dominance of VGG-16, MobileNetV2, and ConvNeXtXLarge models. We achieved accuracy of 88.82%, 85.20%, and 85.20% for those models. However, by utilizing an Ensemble Learning model, we achieved a 99.59% accuracy. The output result of classification that shown in Figure 27. The models are economical and can support radiologists in validating their decisions. However, our future plans involve validating our approach with extensive datasets.

**V. SUMMARY AND CONCLUSION**

The paper represents a comprehensive approach to fish disease detection utilizing transfer learning techniques and a fusion of features from three deep learning models combined with support vector machine (SVM) classification. Through extensive empirical experimentation, we have demonstrated the effectiveness of our proposed model in accurately identifying and classifying fish diseases. By leveraging pre-trained deep learning models and integrating their learned features, we have achieved superior performance compared to traditional methods. Our results highlight the potential of transfer learning in fish disease detection, offering a promising avenue for further research and application in aquaculture management. In future work, we aim to further enhance the performance of our fish disease detection system by incorporating optimization techniques to fine-tune the



hyper-parameters of the deep learning models utilized in our framework. Overall, the findings contribute to advancing fish health monitoring systems, ultimately supporting sustainable aquaculture practices and the preservation of marine biodiversity.

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**SUBIR BISWAS** was born in Dhaka, Bangladesh. He is currently pursuing the B.Tech. degree with C. V. Raman Global University, Odisha, India, majoring in computer science and engineering. He is passionate about cutting-edge technologies, he specializes in machine learning and artificial intelligence. Beyond academics, he has hands-on experience in app development and data science projects, showcasing his versatility and dedication to staying ahead in the tech world. His journey is marked by a commitment to applying theoretical knowledge to real-world scenarios, making him a valuable asset to any project. His active involvement in diverse tech projects reflects his forward-thinking approach and potential to contribute significantly to the field. As he continues to excel both academically and professionally, he is poised to make a lasting impact in the ever-evolving landscape of technology.



**DEBENDRA MUDULI** (Member, IEEE) received the M.Tech. degree in computer science and engineering from the National Institute of Technology, Rourkela, in 2016, and the Ph.D. degree in computer science from the National Institute of Technology, Rourkela, in 2022. He is currently an Associate Professor with the Department of Computer Science and Engineering, C. V. Raman Global University, Bhubaneswar, India. His work has been published in numerous journals and international conferences. His research interests include cloud computing, pattern recognition, and medical image processing. He is actively involved in the academic community, serving as a reviewer for various reputable publications. He is a Life Member of the Indian Society for Technical Education (ISTE).



**MD ARIFUL ISLAM** was born in Dhaka, Bangladesh, in 2001. He is currently pursuing the Bachelor of Technology degree with the Department of Computer Science and Engineering, C. V. Raman Global University, Odisha, India. He has been working on machine learning, artificial intelligence, data science, and web development. His dedication and expertise in these domains have been showcased through his impactful contributions to various projects, highlighting his commitment to advancing the field. His academic pursuits and practical experience make him a promising individual in the ever-evolving landscape of technology.



**ANURADHA SHANTANU KANADE** received the B.Sc. and M.C.A. degrees in physics from Shivaji University, the M.B.A. (B.A.) and Ph.D. degrees from Savitribai Phule Pune University (SPPU), and the M.Phil. degree from BVDU. She is currently the Program Director of the Department of Computer Science and Applications, Dr. Vishwanath Karad MIT World Peace University, Pune. She is enthusiastic and passionate for teaching and research and works with dedication and positive approach. She has a vast experience of about 23 years including 21 years of teaching and about two years of industry experience. She is approved as a Ph.D. Supervisor with Dr. Vishwanath Karad MIT World Peace University. She authored more than 38 research articles in various national, and international journals and conferences, including IEEE and Springer, and UGC Care publications. There are eight patents in her name, including seven Indian and two U.K. patents. Three of her patents are granted, three are accepted, and two are published. She completed the BCUD-funded research project, in 2015, and has been working on sponsorship under the Innovation Funds Policy, since February 2022. She authored six books on different topics viz. Emerging Trends in Information Technology, R. Programming, Fundamentals of Data Science, Terminology and Technical Foundations of Blockchains, The Basics of AI, and the IoT-A Beginner's Handbook. Her research interests include databases, data science, blockchain technology, cloud computing, and algorithmics. She has also received best paper awards for her papers, in 2021 and 2022.



**ABU TAHA ZAMANI** has been a Lecture with the Department of Computer Science, Faculty of Science, Northern Border University, Arar, Saudi Arabia. He has several research articles in reputed International journals. His research interests include cloud computing, ad hoc networks, cyber security, AI, the IoT, machine learning, and data science. He serves as a reviewer of various journals. He is also a member of various international journals, such as IEEE and ACM. He is the Editorial Board Member of some reputed international journals in computer sciences.



**SHANTANU PANDURANG KANADE** (Member, IEEE) received the M.C.A. and B.Sc. degrees in chemistry from Shivaji University, Kolhapur, and the M.B.A. degree in finance and business analytics from SPPU, Pune. He is an approved Ph.D. Guide with the Symbiosis International Deemed University, Pune, with an interest in information systems, blockchain, and education technology. He has authored three books on blockchain, data science, and recent trends in IT. He is currently an Assistant Professor and a Program Coordinator with the Symbiosis School for Online and Digital Learning, Symbiosis International Deemed University, Lavale, Pune. He published ten papers in journals and conferences ranging on data science, blockchain, and education technology. His experience ranges from working as a Principal at Junior colleges, and a Manager at Customized Energy Solutions for Industry Academia Collaborator. He is a highly qualified and eminent academician with more than 20 years of experience in conducting subject related classes and managing administrative functions across diverse organizations, exploring challenging senior managerial assignments with a reputed organization. He was awarded a Ph.D. degree from MUIT Lucknow, and an M.Phil. degree from BVU, Pune.



**NIKHAT PARVEEN** received the B.Sc. degree in computer science and the M.C.A. degree from Andhra University, Andhra Pradesh, India, in 2000 and 2003, respectively, and the Ph.D. degree from the Department of Computer Application, Integral University, Lucknow, Uttar Pradesh, India. She is currently an Associate Professor with the Department of Computer Science and Engineering, Koneru Lakshmaiah Education Foundation, Guntur, India. She has more than 12 years of teaching experience and six years of research experience. She has six national patents. She is also working in the areas of soft computing, image analysis, big data analytics, and the IoT. Her research has been chronicled in more than 30 journal publications and international conferences. Her research and publication interests include artificial intelligence, machine learning, security software, security testing, software engineering, and requirement engineering. She is a Life Time Member of CSI, ACM, and IAENG, IACSIT.

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