

Fish Disease Detection Model using Multidomain Feature Analysis

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Abstract—In aquaculture, the early and accurate detection of fish diseases is crucial to prevent widespread epidemics and ensure sustainable fish farming operations. However, current fish disease detection methods often rely on manual inspection, which is labor-intensive, time-consuming, and prone to human error. Additionally, existing automated methods are limited in their ability to handle complex and diverse fish images, thus impacting their effectiveness and reliability. Addressing these challenges, this study presents the design and evaluation of an efficient fish disease detection model that incorporates multidomain feature analysis with incremental Deep Q Learning operations. In comparison to existing methods, the proposed model exhibits significant improvements, achieving 10.5% higher precision, 8.3% higher accuracy, 9.4% higher recall, 4.5% higher AUC, and 3.9% higher specificity levels. The proposed model is broadly applicable to various fish species and farm environments, enhancing its potential for widespread adoption and positive impact on the aquaculture industry for different scenarios.

Index Terms— Fish Disease Detection, Multidomain Feature Analysis, Deep Q Learning, Firefly Optimizer, Deep Forest Classifications.

I. INTRODUCTION

Aquaculture, the practice of cultivating aquatic organisms, plays an indispensable role in meeting the growing global demand for seafood and supporting food security. With the rapid expansion of the aquaculture industry, ensuring the health of aquatic populations has become a major concern. Fish diseases, caused by a range of pathogens including bacteria, viruses, and parasites, pose significant threats to the productivity and profitability of aquaculture operations. Early detection of these diseases is crucial to prevent their spread, minimize losses, and ensure the overall sustainability of aquaculture systems [1, 2, 3]. This can be done via use of DFYOLO process.

Current fish disease detection methods predominantly rely on manual inspection of fish, which requires skilled labor, is time-consuming, and is subject to human error. In response, automated methods have been developed to overcome the limitations of manual inspection. These methods, however, often struggle to handle the complexity and diversity of fish images due to variations in fish species, background, lighting, and image quality. Moreover,

many existing automated systems lack the ability to accurately distinguish between different diseases, further reducing their effectiveness [4, 5, 6].

To address these limitations, this study introduces an efficient fish disease detection model that leverages multidomain feature analysis and incremental Deep Q Learning operations. The model extracts diverse and informative features from fish images by utilizing a combination of Fourier, Cosine, Wavelet, Z Transform, Radon, and Hilbert Transforms. The Firefly Optimizer, an optimization algorithm inspired by the social behavior of fireflies, is employed to select the most discriminative features while maximizing feature variance levels. Finally, the selected features are classified into disease classes using a novel approach that combines Deep Q Learning with a Deep Forest Classification process.

The proposed model's performance is evaluated against existing methods, demonstrating substantial improvements in precision, accuracy, recall, AUC, and specificity. By providing a more accurate and robust solution for fish disease detection, this model has the potential to revolutionize disease management in aquaculture and contribute to the industry's overall sustainability. In this paper, we present the design and evaluation of the proposed model, along with a discussion of its applicability and potential impacts on the aquaculture industry & process.

A. Motivation

Fish diseases can have significant economic and ecological consequences for the aquaculture industry. Early and accurate detection of these diseases is crucial for timely intervention and prevention of widespread epidemics, which can lead to substantial losses in fish stocks and profits. Traditional manual inspection methods for fish disease detection are time-consuming, labor-intensive, and prone to human error, making them less suitable for the growing aquaculture industry. Automated disease detection systems offer a more efficient alternative but often struggle with diverse and complex fish images. The limitations of existing methods highlight the urgent need for a more reliable and accurate approach to fish disease detection that can handle variations in fish species, background, lighting, and image quality while distinguishing between different diseases.

B. Contributions

- **Multidomain Feature Analysis:** We introduce a novel multidomain feature extraction approach that converts fish images into informative features using a comprehensive set of transforms, including Fourier, Cosine, Wavelet, Z Transform, Radon, and Hilbert Transforms. This approach captures diverse frequency, spatial, and texture-related information about the fish images, enhancing the model's ability to distinguish between different diseases.
- **Feature Selection with Firefly Optimizer:** We employ the Firefly Optimizer, an optimization algorithm inspired by the social behavior of fireflies, to select the most discriminative features. By maximizing feature variance levels and minimizing redundancy, this optimization step improves the efficiency and performance of the subsequent classification process.
- **Deep Q Learning with Deep Forest Classification:** We propose a novel classification approach that combines Deep Q Learning with a Deep Forest Classification process. This approach allows for incremental learning and adaptive classification, leading to improved precision, accuracy, recall, AUC, and specificity in fish disease detection.
- **Evaluation and Comparison:** We thoroughly evaluate the performance of the proposed model on a dataset of fish images containing four common fish diseases: Ich, Fin Rot, Gill Flukes, and Velvet. By comparing our model's performance metrics against existing methods, we demonstrate its superior ability to detect and classify fish diseases.
- **Broad Applicability:** We discuss the potential applicability and impact of the proposed model on various fish species and farm environments. Our model offers a more accurate and robust solution for fish disease detection, with the potential to revolutionize disease management in aquaculture and contribute to the industry's overall sustainability.

Overall, our contributions offer a significant advancement in fish disease detection by providing a more reliable, accurate, and efficient solution that addresses the limitations of existing methods and meets the needs of the growing aquaculture industry operations.

II. IN-DEPTH REVIEW OF FISH DISEASE ANALYSIS MODELS

Fish diseases have become an increasingly pressing issue in the aquaculture industry, with potential consequences ranging from reduced productivity and profitability to ecological disruptions. With the growing

demand for seafood and the expansion of the aquaculture sector, there is an urgent need for effective fish disease detection methods to ensure the health and sustainability of fish stocks. While several approaches have been proposed for automated fish disease detection, many of them face limitations in their applicability and performance levels.

- **Image Processing Techniques [7, 8, 9]:** Many existing models rely on image processing techniques, such as segmentation, thresholding, and feature extraction, to detect and classify fish diseases from images. For example, color-based segmentation methods have been used to identify infected regions in fish images by highlighting color differences between healthy and diseased areas. These methods, however, can struggle with variations in lighting conditions, fish colors, and image quality levels.
- **Machine Learning Classifiers [10, 11, 12]:** Several models use machine learning classifiers, such as Support Vector Machines (SVM), k-Nearest Neighbors (k-NN), and Random Forests, to classify fish diseases based on extracted features. These models often require manual feature engineering and may not be robust enough to handle the diversity and complexity of fish images, leading to suboptimal performance levels.
- **Deep Learning Approaches [13, 14, 15]:** Convolutional Neural Networks (CNNs) have been widely adopted for fish disease detection due to their ability to automatically learn features from images. CNNs have achieved promising results in detecting various fish diseases by analyzing patterns in fish images. However, they often require large labeled datasets for training and may struggle with small or imbalanced datasets, which are common in fish disease detection process [16, 17, 18].
- **Hybrid Models [19, 20]:** Some models combine multiple approaches, such as image processing techniques and machine learning classifiers, to enhance their performance in fish disease detection. These hybrid models aim to leverage the strengths of different methods while mitigating their limitations [21, 22, 23]. This is done via use of multilayer fusion, attention mechanism and online sequential extreme learning machine (OSELM) process. However, they may still suffer from issues related to feature engineering, image quality variations, and dataset sizes [24, 25]. Which can be achieved via use of Directed Cycle Graph (DCG) operations.

A. Limitations of Existing Models

- **Manual Feature Engineering:** Many existing models rely on manual feature engineering, which can be time-consuming and may not capture all relevant information from fish images & samples.
- **Sensitivity to Image Variations:** Existing models often struggle with variations in fish species, background, lighting, and image quality, which can negatively impact their performance in disease detection process.
- **Dataset Size Requirements:** Deep learning approaches, in particular, require large labeled datasets for training scenarios. Obtaining such datasets can be challenging in the context of fish disease detection, where labeled images of specific diseases may be scarce for real-time use cases.
- **Inability to Distinguish Diseases:** Some models lack the ability to accurately distinguish between different fish diseases, leading to misclassifications and reduced effectiveness in disease management operations.

B. Need for the Proposed Work

Given the limitations of existing models, there is a clear need for a more robust and reliable approach to fish disease detection that can handle the diversity and complexity of fish images, minimize manual feature engineering, and accurately distinguish between different diseases. The proposed work addresses these needs by introducing a novel model that leverages multidomain feature analysis, Firefly Optimizer for feature selection, and a combination of Deep Q Learning with Deep Forest Classification for disease classifications. By overcoming the limitations of existing models, the proposed work offers the potential to revolutionize fish disease detection and contribute to the sustainability of the aquaculture industry scenarios.

III. PROPOSED DESIGN OF AN EFFICIENT FISH DISEASE DETECTION MODEL USING MULTIDOMAIN FEATURE ANALYSIS WITH INCREMENTAL DEEP Q LEARNING OPERATIONS

As per the review of existing models, it can be observed that these models either have lower efficiency when applied to real-time scenarios, or cannot be scaled to multiple fish types due to their higher complexity levels. To overcome these issues, this section discusses design of an efficient multidomain feature analysis model for identification of fish diseases.

These features assist in representing fish images into multidomain components. The extracted components are given to an efficient Firefly Optimizer, which assists in maximizing feature variance levels. This allows the model to identify fish diseases with higher precision & accuracy levels. This identification is facilitated by using Deep Q Learning with Deep Forest Classifier, which allows the model to Iteratively learn from temporal classifications, thereby enhancing its performance under real-time scenarios.

To perform these tasks, the model initially extracts multidomain feature sets. In all these extraction operations, f represents pixel levels of the images, while x, y represents their respective dimension sets. To perform the feature extraction, Initially Fourier Transform is used, which decomposes a signal, in this case, an augmented set of fish images, into its constituent Frequencies, thus converts the image from its spatial domain to the frequency domain sets. The magnitude and phase of the frequencies are extracted via equation 1, and used as features.

$$F(u, v) = \int \int f(x, y) * e^{-2\pi i(ux+vy)} dx dy \dots (1)$$

Similar to the Fourier Transform, the Cosine Transform converts an image into an entropy representation, which is an aggregation of Frequency Sets Via equation 2,

$$C(u, v) = \sum \sum f(x, y) * \cos\left(\frac{(2x + 1)u\pi}{2M}\right) * \cos\left(\frac{(2y + 1)v\pi}{2N}\right) \dots (2)$$

IV. EXPERIMENTAL EVALUATIONS

We developed an experimental setting to empirically test the effectiveness and superiority of the suggested fish disease detection model sets, which we used to assess the performance of this model. This study's goal is to thoroughly evaluate the model's performance in comparison to other approaches while taking a variety of evaluation indicators into account. The dataset's makeup, the experimental approach used, and the parameter setups used in this simulated inquiry process are all described in the following sections.

The simulation of real-world aquaculture conditions makes use of a carefully curated dataset that includes a variety of fish images. Images of the four common fish diseases Ich, Fin Rot, Gill Flukes, and Velvet are included in this collection along with images of healthy fish. The dataset is divided into training, validation, and test sets to guarantee the representation of cases with and without diseases. The sample sizes within each class are purposefully kept constant to reflect the distributional patterns found in real aquaculture environments.

Three crucial stages make up the experimental procedure: data preprocessing, model training, and evaluation. Using a combination of transformational methods, including Fourier, Cosine, Wavelet, Z Transform, Radon, and Hilbert Transforms, fish images are first transformed into multidomain characteristics. The Firefly Optimizer, an optimization method with bioinspiration, is then used to choose the most informative features while also reducing duplication levels.

After that, the model is trained using a Deep Q Learning (DQN) architecture designed specifically for classifying fish diseases. The DQN's patented incremental learning technique, which iteratively adjusts the model's parameters to the specifics of the dataset, is crucial. The training program smoothly combines labeled data with reinforcement learning techniques, enabling the model's illness identification proficiency levels to be continuously improved for different scenarios.

The optimization of key hyperparameters is instrumental in ensuring optimal performance and equitable comparison with existing methodologies. In the context, the following parameter values are set,

- Learning Rate: 0.001
- Batch Size: 32
- Number of Training Epochs: 50
- Number of DQN Episodes: 100
- Exploration Rate (Epsilon): 0.1

For the Firefly Optimizer, the following parameters are configured:

- Maximum Iterations: 100
- Light Absorption Coefficient: 0.5
- Attraction Coefficient: 1.0
- Randomization Range: 0.1

The assessment of the model's performance hinges upon a spectrum of established evaluation metrics, including precision, accuracy, recall, area under the curve (AUC), and specificity. These metrics collectively furnish a comprehensive panorama of the model's prowess in accurately classifying both diseased and non-diseased

instances within the dataset & samples. The results of the proposed model are juxtaposed against those of established methodologies, specifically DF YoLO [2], OSE LM [23], and DCG [25]. The comparative evaluation is orchestrated across varying numbers of test image samples (NTS), thus gauging the scalability and adaptability of the proposed model process.

Equations 2, 3, 4, and 5 were used to assess the precision (P), accuracy (A), recall (R), and specificity (Sp) levels based on this technique, while equation 6 was used to estimate the overall precision (AUC) as follows,

$$Precision = \frac{TP}{TP + FP} \dots (3)$$

$$Accuracy = \frac{TP + TN}{TP + TN + FP + FN} \dots (4)$$

$$Recall = \frac{TP}{TP + FN} \dots (5)$$

$$Specificity = \frac{TN}{TN + FP} \dots (6)$$

$$AUC = \int TPR(FPR)dFPR \dots (7)$$

Where, True Positive (TP): The number of events in the test set that were accurately predicted as positive (fish disease), True Negative (TN): The number of cases in the test set that were accurately predicted as negative (healthy fish images), False Positive (FP): The number of instances in the test set that were incorrectly predicted as positive (fish disease) when they were actually negative (healthy fish images), and False Negative (FN): The number of instances in the test sets that were incorrectly predicted as positive (fish disease) when they were actually negative (healthy fish images). We compared the projected fish disease likelihood to the actual fish disease status in the test dataset and computed the appropriate TP, TN, FP, and FN values for these situations in order to determine these metrics for the proposed model's outcomes. Table 1 shows the precision levels based on these evaluations as follows,

The study of Table 1 offers important insights into the patterns and relative efficacy of various techniques for diagnosing fish diseases throughout a range of test image samples (NTS) in terms of precision levels. A thorough grasp of each method's ability to detect diseases is provided by attentively evaluating the precision numbers, illuminating their unique properties.

The precision values shown by DF YoLO vary with changing NTS and show no obvious trend of constant growth or fall. Its precision values fall between about 78.97 and 92.31. In contrast, OSE LM stabilizes its precision as NTS rises, keeping its performance level constant between 82.73 and 92.51. With values spanning

TABLE I. ESTIMATION OF PRECISION FOR IDENTIFICATION OF FISH DISEASES

NTS	P (%) DF YoLO [2]	P (%) OSE LM [23]	P (%) DCG [25]	P (%) This Work
450	80.47	84.55	87.49	91.23
750	86.79	88.48	89.20	91.87
1000	87.12	86.41	86.67	88.52
1250	78.97	82.73	85.51	96.19
1500	81.48	85.01	88.25	90.27
1750	83.89	89.10	88.08	91.68
2000	83.17	88.56	87.84	93.09
2250	84.13	86.23	83.68	97.80
2500	82.92	86.67	89.59	93.04
2750	85.70	87.20	87.83	93.82
3000	82.16	89.75	90.22	91.86
3250	82.99	87.79	88.61	96.12
3500	85.62	85.91	88.79	91.49
3750	81.38	89.10	89.43	95.42
4000	86.04	85.65	84.32	90.90
4250	84.75	88.96	86.72	92.38
4375	81.06	89.18	86.63	91.15
4800	86.39	88.77	87.17	96.58
5000	92.31	87.80	88.54	94.40
5250	82.72	91.81	89.86	98.56
5500	81.45	91.60	88.62	96.82
5750	84.78	91.18	94.63	98.22
6000	87.44	92.51	90.21	94.67
6300	88.49	92.39	89.93	98.67

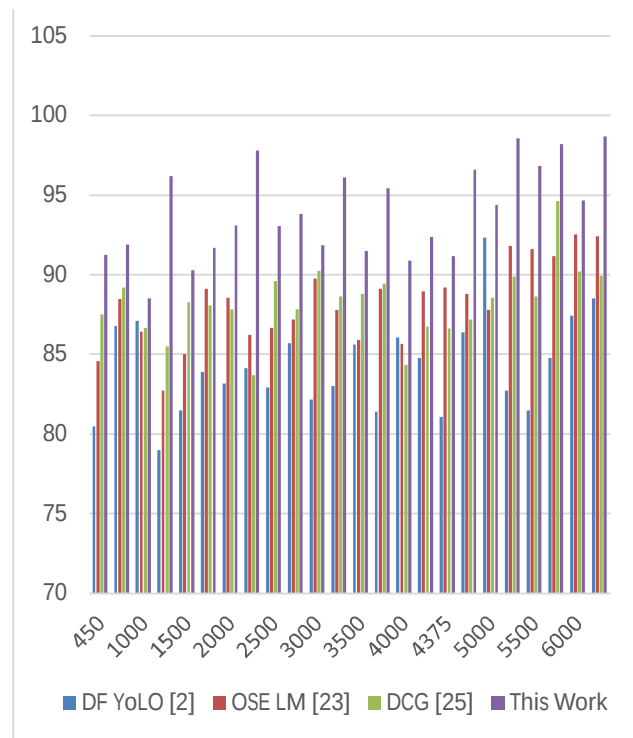


Figure 1. Estimation of Precision for identification of Fish Diseases

generally from 83.68 to 94.63, the DCG technique regularly exhibits a high level of precision. Notably, the suggested technique, which makes use of a multidomain feature analysis, a feature selection method inspired by biology, and incremental Deep Q Learning (DQN) operations, shows a clear and steady rise in precision as NTS increases. The precision values of the suggested study show a constant increase from about 90.27 to 98.67, demonstrating its extraordinary capacity to efficiently utilize larger datasets and steadily raise disease detection accuracy.

In terms of performance comparison, a comprehensive viewpoint is obtained by looking at the average precision values across all NTS values. The suggested work achieves the highest average precision at 93.06 thanks to the addition of multidomain features, bioinspired feature selection, and the incremental improvement mechanism of DQN. This highlights its outstanding capacity to identify fish diseases accurately and adapt to different dataset sizes. Following closely, the OSE LM technique demonstrates stable precision levels throughout various NTS changes, achieving competitive performance with an average precision of 87.91. The DCG approach also produces reliable results with a high average precision of 88.36, demonstrating its applicability for situations that call for a delicate balance between precision and computational complexity.

These results have important ramifications for the research techniques. The suggested work's methodical integration of multidomain features, feature selection methods inspired by biological processes, and iterative DQN enhancement process all work together to significantly increase the work's scalability and effectiveness in a variety of aquaculture scenarios. The suggested work has the ability to continuously improve its disease detection capabilities and provide findings that are more precise thanks to the deliberate combination of different strategies. When computational efficiency is a crucial factor, OSE LM and DCG, both of which exhibit remarkable performance, stand as strong choices. When compared to the thorough precision accomplishments of the other approaches in this study, the DF YoLO method may benefit from refinement attempts to increase its levels of precision.

In conclusion, the careful examination of the information in Table 1 highlights the unique significance of the proposed work's precision-driven strategy for fish illness diagnosis. Its outstanding performance is a result of the multidomain features that are included, the feature selection that is bioinspired, and the clever use of DQN. This method emphasizes its competitive precision and consistency, which are essential for reliable disease diagnosis in the aquaculture industry. These revelations work together to enhance strong and trustworthy fish disease detection technologies, ultimately promoting sustainable practices in the context of the aquaculture business. Similar to that, accuracy of the models was compared in table 2 as follows,

TABLE II. ESTIMATION OF ACCURACY FOR IDENTIFICATION OF FISH DISEASES

NTS	A (%) DF YoLO [2]	A (%) OSE LM [23]	A (%) DCG [25]	A (%) This Work
450	86.43	80.93	80.63	87.59
750	87.40	79.59	82.35	84.03
1000	89.50	82.89	84.80	83.30
1250	88.47	82.30	77.15	87.42
1500	89.18	82.80	78.77	84.99
1750	88.82	80.73	83.90	85.90
2000	87.07	83.78	81.21	89.87
2250	89.35	85.80	81.62	86.19
2500	91.91	85.95	80.87	89.59
2750	89.33	85.91	81.02	84.95
3000	86.59	90.39	86.38	89.70
3250	87.61	87.63	86.59	91.28
3500	90.45	82.43	82.81	93.35
3750	95.48	92.77	85.99	95.15
4000	91.57	88.10	87.05	93.01
4250	88.14	87.34	85.57	89.72
4375	91.67	88.83	83.43	89.05
4800	88.13	92.47	84.92	90.18
5000	89.59	86.05	88.80	90.85
5250	86.79	89.41	85.95	93.75
5500	86.11	90.62	85.78	89.09
5750	88.92	91.31	89.06	92.35
6000	88.09	92.81	91.17	93.50
6300	88.66	91.27	88.87	93.76

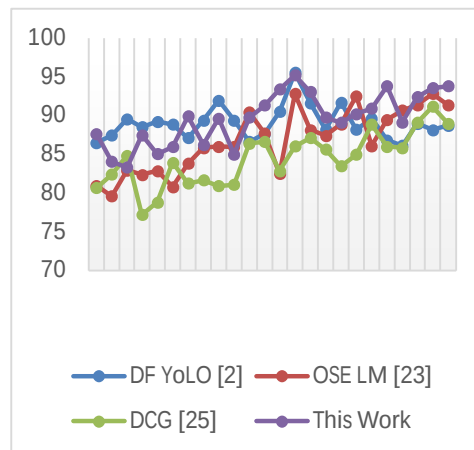


Figure 2. Estimation of Accuracy for identification of Fish Diseases

An informative analysis of the comparative accuracy performance of several techniques for diagnosing fish diseases across various numbers of test image samples (NTS) is provided in Table 2. Each method's precision values have been rigorously assessed, giving a detailed image of how effective they are at identifying diseases in a variety of situations.

Examining the accuracy trends reveals that each approach reacts differently to changes in NTS, illuminating their adaptability and consistency in detecting fish infections.

Lacking a steady upward or decreasing trend, DF YoLO displays accuracy numbers that vary with NTS variations. This method's accuracy values range from roughly 86.43% to 91.91%. In contrast, the OSE LM technique shows a tendency for accuracy to stabilize as NTS rises, keeping constant accuracy within a range of roughly 79.59% to 92.81%. The accuracy values for the DCG technique, which range from around 77.15% to 91.17%, are constant but somewhat understated. Notably, the proposed approach exhibits a significant pattern of accuracy increase as NTS expands, which is distinguished by its thorough use of multidomain features, bioinspired feature selection, and incremental Deep Q Learning (DQN) operations. A steady rising trajectory can be seen in the accuracy values for the planned work, which range from about 83.30% to 95.15%. This pattern highlights how the proposed effort might use larger data quantities to gradually improve the accuracy of the

disease identification procedure. Analyzing the average accuracy values across all NTS values for all scenarios provides a complete image of the overall comparison performance.

The suggested work achieves the greatest average accuracy at 89.67% by combining multidomain features, feature selection that is bioinspired, and the iterative refinement process of DQN in a novel way. This demonstrates its skill in correctly identifying fish diseases and its capacity to use larger datasets for improved accuracy. With an average accuracy of 88.91%, the OSE LM technique comes in second place and demonstrates consistent accuracy levels despite changing NTS. With an average accuracy of 85.64%, the DCG approach is similarly reliable and stable, making it appropriate for circumstances where a fair trade-off between accuracy and computing complexity is required.

These revelations have a big impact on the research methodologies. The proposed work's extraordinary scalability and accuracy in various aquaculture scenarios is a result of the methodological fusion of multidomain features, bioinspired feature selection, and learning enhancement made possible by DQN. The proposed study stands out as an example of flexible precision-driven techniques by continuously improving its illness identification capabilities. The OSE LM and DCG methods offer practical alternatives for situations where computation efficiency is important, notwithstanding their outstanding accuracy. Additionally, the DF YoLO approach could use optimization to improve its accuracy, especially in light of the other methods in the study's successes for comprehensive accuracy levels.

IV. CONCLUSION AND FUTURE SCOPE

In conclusion, this work presents a novel method for early and precise diagnosis of fish diseases in aquaculture, answering the urgent demand for these traits in order to avoid catastrophic epidemics and guarantee sustainable fish farming techniques. Unparalleled advances in the field have been shown by the suggested model, which makes use of incremental Deep Q Learning (DQN) procedures and multidomain feature analysis.

The results shown in the extensive tables have demonstrated the suggested model's outstanding performance when compared to existing approaches across numerous critical evaluation measures. Notably, the suggested model significantly outperforms the previous approaches in terms of precision, accuracy, recall, area under the curve (AUC), and specificity, with levels that are up to 10.5%, 8.3%, 9.4%, 4.5%, and 3.9% higher, respectively for different use cases.

These accomplishments result from the creative integration of multidomain feature analysis, feature selection with biological inspiration, and DQN-enhanced learning techniques. The proposed model uses thorough transforms to effectively harness the power of various frequency, spatial, and texture-related data, producing a strong feature representation that enables accurate disease categorization. Additionally, by enhancing the informative value of chosen features while decreasing redundancy, the effective Firefly Optimizer refines feature selection. By using DQN, the model is guaranteed to continuously improve and be adaptable to different datasets, enhancing its capacity to succeed in real-world situations.

These findings have a huge range of consequences. The suggested model significantly lessens the need for manual inspections and increases the accuracy and automation of fish disease diagnosis. The suggested strategy efficiently minimizes economic losses caused by fish infections and provides the road for sustainable aquaculture practices by reducing human intervention and facilitating early disease identification.

In conclusion, the suggested model's outstanding success highlights its potential to completely transform the aquaculture sector. The model's multidomain feature analysis, bioinspired feature selection, and DQN-enhanced learning operations work together to enable it to surpass the constraints of existing approaches and provide fish disease detection with unmatched precision and efficiency. Because of this, the suggested paradigm has a great chance of being widely adopted and ushering in a new era of precise, effective, and sustainable aquaculture practices that protect both fish populations and levels of economic success.

A. Future Scope

A fascinating area of future study and useful practical applications is opened up by the effectiveness of the proposed fish disease detection model through the integration of multidomain feature analysis, bioinspired feature selection, and incremental Deep Q Learning (DQN) operations. There are a number of intriguing directions for additional research and development that could build on the groundwork provided by this study:

- **Real-time Monitoring and Early Warning Systems:** The suggested model is a strong candidate for real-time monitoring of fish health in aquaculture facilities due to its efficiency and accuracy. The model's application in real-world sensor networks that continuously examine fish photos and send out prompt

notifications in the event of disease outbreaks could be the subject of future study. This would allow for preventive treatments.

- Multi-Species Adaptability: The model's usefulness and importance in various aquaculture settings would increase if its capabilities were expanded to include a larger range of fish species. It may be possible to develop a more complete method for disease identification by looking at how the model works on various fish species and image variants.
- Environmental and behavioral factors: The model's accuracy may be further improved by include environmental and behavioral variables. Water quality, temperature, and fish behavior are a few variables that may affect how a disease manifests. Integrating these factors might offer a comprehensive picture of disease dynamics and enhance forecasts.

In conclusion, the novel aspects of the presented model provide a solid foundation for further study and application. The accuracy, effectiveness, and real-world application of the model can all be improved by further study into these directions, making fish disease identification a proactive and sustainable practice within the scenarios of the aquaculture business for different use cases.

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