

Enhancing Fish Disease Classification in Bangladeshi Aquaculture through Transfer Learning, and LIME Interpretability Techniques

Nuzhat Noor Islam Prova

*Pace University, Seidenberg School of CSIS
One Pace Plaza, New York City, NY 10038, USA
nuzhatnsu@gmail.com*

Sadia Hossain

*Internet of Things and Robotics Engineering
Bangabandhu Sheikh Mujibur Rahman Digital University
Gazipur, Bangladesh
sadiaupoma540@gmail.com*

Abstract—Fish disease classification is an essential component of aquaculture management and is essential to preserving the sustainability and health of fish populations. Research on fish diseases has been done sparingly, and each study has certain limitations. There isn't a single study that uses an image classification approach and cutting-edge methods like transfer learning from a Bangladeshi perspective. We classified the freshwater image diseases in Bangladesh through research using the Inceptionv3, ResNet-50, DenseNet-121, and EfficientNetB3 transfer learning models. We have customized the model in light of our findings. Among all models, the Inceptionv3 model performed well. The validation and testing accuracy of the model is, accordingly, 95.51% and 82.51%, which shows the highest testing accuracy. The model also performed better in terms of precision, recall, and f-score than others; the performance is 83%, 82%, and 82%, respectively. The collected dataset applied here is limited and imbalanced. We performed a data augmentation technique to increase the dataset in our research. Further investigation to evaluate the model for imbalanced data are kappa and MCC, both of which serve as insightful indicators of classification robustness and efficacy. The best Kappa and MCC values obtained by the InceptionV3 model are 0.8006 and 0.8018. Furthermore, we explore the integration of explainable AI techniques, such as LIME (Local Interpretable Model-agnostic Explanations), to enhance the transparency and trustworthiness of classification models in aquaculture.

Index Terms—Deep Learning, Transfer Learning, Augmentation, Fish Diseases, LIME, Image Classification

I. INTRODUCTION

Aquaculture is a crucial aspect of ensuring global food security by providing a significant portion of the world's seafood demand. In Bangladesh, the aquaculture industry contributes significantly to the national economy. Fish production is a major source of food and employment for millions of people. However, the emergence and rapid spread of diseases in the fish population pose a significant challenge to the sector. These diseases threaten crops and cause economic losses, which can affect the country's food security. This paper aims to explore the critical area of fish disease diagnosis in Bangladesh, examining the results, implications, and unique challenges faced by the country's fish species.

Detecting fish diseases is an essential aspect of aquaculture. With the increasing world population and the subsequent rise in demand for fish and seafood, the need for higher production is crucial. To meet the demand, aquaculture has expanded rapidly, leading to more intensive fishing practices. However, these practices come with additional challenges, including greater susceptibility to diseases due to stocking densities and environmental pressures. In this context, the timely and accurate detection of fish diseases is a cornerstone of the industry's sustainability.

Manual identification is always time-consuming and sometimes can be wrong. With the advancements in technology, artificial intelligence is applied in this field. Various approaches have been proposed by several studies for the classification of fish diseases. Using Multi-Support Vector Machines (M-SVMs) for classification and K-means and C-means fuzzy logic clustering techniques for segmentation, Juel Sikder et al. developed a system that achieved high accuracy rates of 96.48% and 97.90%, respectively [1]. By utilizing machine learning algorithms, feature extraction with HOG and FAST descriptors, and image segmentation, Shaveta Malik et al. were able to identify Epizootic Ulcerative Syndrome (EUS) disease with a higher degree of accuracy than they could with other techniques [2].

For this study, we used a strong classification technique to identify freshwater fish diseases in Bangladesh. By combining a traditional CNN model with cutting-edge deep learning models, such as ResNet-50 [3], DenseNet-121 [4], InceptionV3 [5], and EfficientNetB3 [6], we were able to improve disease identification efficacy and accuracy. Owing to the limitations of a small dataset, we used data augmentation methods to increase the training set's diversity and strengthen the models' capacity for generalization. As an XAI technique, we implemented LIME to enhance the interpretability of our models and provide confidence in their predictions. This enhances our classification framework's transparency and reliability while also making it easier to comprehend how decisions are made within the models. Our research aims to address the particular challenges presented by a limited dataset by offering a thorough and dependable tool for the

classification of freshwater fish diseases through the use of this transfer learning approach.

The contribution of our research :

- We have applied the data augmentation techniques here to increase the dataset.
- The study focused on Bangladeshi Aquaculture, where we applied various artificial intelligence techniques to classify fish diseases.
- Various transfer learning models were employed in our research to compare the performance and find the suitable model for fish disease classification.
- To ensure the model's trustworthiness and robustness, we applied the Explainable artificial intelligence framework LIME.

The rest of the paper is organized as follows: the background and previous study are described in section II. The research steps and the proposed model are described in section III. We have presented the outcomes of our research in section IV.

II. RELATED WORK

Recent advancements in image processing have significantly contributed to the detection of fish diseases. This literature review explores various studies in this domain, focusing on different methodologies and their outcomes.

Ahmed et al. showed how Machine Learning(ML) can be used in aquaculture by using a Support Vector Machine(SVM) to find pathogens in salmon. They were able to get 91.42% accuracy. In contrast, Mia et al. expanded the study by using different classifiers. Random Forest (RF) did better than the others, correctly identifying 88.87% of fish diseases class [7]. Xu et al. did more research on classifying fish species using Transfer Learning and SE-ResNet152. Even though the dataset was not balanced, they were able to get a 98.8% success rate [8]. Whatever, when the dataset is imbalanced, calculating just accuracy is not a trustworthy evaluation.

In the field of Neural Networks(NN), Waleed et al. looked into how different Convolutional Neural Network(CNN) architectures could be used to find diseases [9]. They found a link between network performance and learning rate, but they did not give any specific accuracy metrics. Chakravorty proposed a faster diagnosis method for Epizootic Ulcerative Syndrome(EUS) using Principal Component Analysis(PCA) and NN [10]. Rachman et al. improved EUS detection to 98.75% by using the DL techniques along with MobileNet and Unet transfer learning model [11].

Nayan et al. looked into the link between fish health and water quality. They used gradient boosting to predict diseases in fish based on water quality and were 92% accurate on average [12]. Malik et al. compared their PCA, FAST, and NN methods for EUS detection with other methods that were already out there, but they did not say how accurate their methods were [13].

According to Huang et al., they made a Multilayer Fusion Network with an attention mechanism that could find places with infected fish 94.28% of the time. However, this model

lacked a comparative analysis with other Attention-Based Models [14]. Barik et al. utilized Unsupervised Learning to detect diseased spots on fish but did not provide comprehensive accuracy results or dataset details [15].

Hasan et al. used CNNs to find diseases in fish and got a 94.44% success rate, even though they only had a small dataset to work with [16]. Malik et al. showed that neural networks and KNN algorithms are used for EUS identification. They had success rates of 96.67% and 93.33%, respectively, but they did not say which datasets they used [1]. Sikder et al. suggested using K-means and C-means clustering techniques with M-SVMs. These methods worked 96.48% and 97.90% of the time when Fuzzy Logic was added, but the study did not look at how well they worked in other situations [2].

Comparatively, both Ahmed et al. [17] and Mia et al. [7] applied the ML models for classification effectiveness. Mia et al.'s study was more comprehensive, involving eight different classifiers, providing a broader perspective. Both studies utilized SVM, but Mia et al. also incorporated ensemble methods like Random Forest, which showed slightly lower accuracy than Ahmed et al.'s augmented SVM. However, Ahmed et al.'s study lacked a comparative analysis with existing methods.

Xu et al. [8] and Rachman et al. [11] both reported high efficacy with their deep-learning approaches. Xu et al. employed SE-ResNet152, while Rachman et al. combined MobileNet and Unet. These studies addressed dataset challenges differently: Xu et al. focused on class imbalance, and Rachman et al. on dataset quality. Deep learning methods like transfer learning by Xu et al. and architecture combination by Rachman et al. were used. This shows how flexible these methods are for identifying fish diseases.

In a broader context, Malik et al. [10], Nayan et al. [12], and Barik et al. [15] contribute diverse perspectives to image processing and disease detection. Malik et al. emphasized speed and efficiency; Nayan et al. explored the predictive relationship between water quality and disease; and Barik et al. investigated unsupervised learning techniques. Each study adds to the understanding of factors influencing fish health and the potential of machine learning in this field.

We have listed some of the limitations in fish disease classification:

- Most of the work had been done on the small dataset, and the classes of the dataset were a maximum of four. So, the existing research worked on a few diseases of fish.
- Most of the time, the dataset was unbalanced. The researchers used only the accuracy terms to evaluate the model where calculation precision, recall, f-score, and kappa evaluation metrics are necessary for the imbalance dataset to check the model effectiveness.
- The implementation of the eXplainable Artificial Intelligence (XAI) technique, which enhances the trustworthiness of predictions, has not been applied. Interpretability and model trustworthiness are pivotal factors in fortifying the robustness of the model.

III. METHODOLOGY

A. Data Collection and preprocessing

The Fish Dataset was collected from the Kaggle website and uploaded in 2022. This image data was collected from Tangor haor and Kaptai Lake and comprises a total of 133 images, categorized into seven distinct classes, namely Argulus, Broken Antennae and Rostrum, EUS, Healthy Fish, Redspot, Tail and Fin Rot, and The Bacterial Gill Rot. The dataset has 23 images of the Argulus class, 7 images of the Broken antennae and rostrum class, 26 images of the EUS class, 30 images of the Healthy Fish class, 31 images of the Redspot class, 9 images of the Tail And Fin Rot class, 6 images of the The bacterial gill rot class. The purpose of the dataset is to facilitate research and analysis related to fish health and diseases.

Data Augmentation :As our dataset was limited, we used data augmentation techniques in our research. Data augmentation is used to apply different transformations to already-existing data, increasing the diversity of a dataset and improving the robustness of the model. Keras's ImageDataGenerator class was used to augment our data. This is because it provides a quick and easy way to augment images. Additionally, the following settings techniques were used: `horizontal_flip=True` to increase variability by flipping images horizontally, `vertical_flip=True` to increase variability by flipping images vertically, `rotation_range=20` to enhance model robustness to rotations within ± 20 degrees, `fill_mode='nearest'` to fill empty regions after transformations with the nearest pixel value, `brightness_range=[0.5,2.0]` to simulate different exposure levels to handle lighting variations, `rescale=1/255` to normalize pixel values to $[0, 1]$ for deep learning models, `shear_range=0.2` to improve the model's perspective invariance through shearing, and `zoom_range=0.2` to augment the dataset with zoomed images to handle different scales. After augmenting the dataset, the total data samples are reached to 2031 samples. Where 10% data is used for validation, 10% for testing and the rest of the data samples were used for training. The input image was preprocessed (299*299) size. The number of images per class after data augmentation is shown in Figure 1. The weight of all the classes is shown in Table I, which is used during the training of the model.

TABLE I: Class Weights

Class	Weight
0	0.98
1	0.98
2	1.12
3	0.98
4	0.98
5	0.98
6	0.98

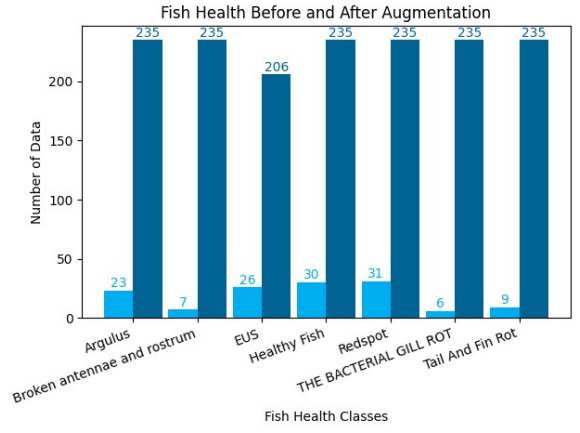


Fig. 1: Number of images per class before data augmentation and after data augmentation



Fig. 2: Samples of an image after performing augmentation

B. Proposed Model

In the research, we have applied different transfer learning models to classify fish diseases. For the deep learning algorithms to train the millions of parameters and various weights in the deep network, a sizable dataset and a considerable amount of time are needed. This makes it possible to represent knowledge precisely. First off, the data augmentation technique is a way to make datasets bigger. In order to prevent overfitting, it employs image transformation. Transferring knowledge from one domain to another through Artificial Intelligence (AI) is known as transfer learning. The ability of a system to identify and apply knowledge and skills from earlier tasks to new tasks and domains is known as transfer learning. In the context of Deep Convolutional Neural Networks, the transfer learning approach is especially crucial for classification and noise reduction using multiple trained deep architectures. Deep neural networks can learn incredibly

complex relationships through transfer learning, which can result in overfitting—learned models with more parameters than necessary. Regularization and dropout are two techniques that can help reduce overfitting. To provide a consistent adaptation, we suggested an architecture based on features. Our fundamental architecture is a deep learning model that uses a pre-trained model such as Inceptionv3, DensNet-121, ResNet-50, and EfficientB3. The network parameters for the second step are initialized in the first step. Pre-trained from ImageNet, VGG16, Resnet-50, and DenseNet-121 exhibit strong performance in image recognition and classification. Since the final fully connected layers were utilized to categorize ImageNet’s 1,000 classes, they have been eliminated. A modification is made by freezing all of the pre-trained layers’ weights in order to tackle the new classification challenge. The model is extended by the addition of two fully connected layers. The fully connected back layer’s output provides the classification for every class. Next, we expanded our model to include a Global Average Pooling (GAP) layer. It keeps important spatial information while reducing dimensionality. In contrast to conventional fully connected layers, GAP preserves spatial details necessary for tasks like object localization by calculating the average of each feature map. This greatly lowers the number of parameters in the model, improving translation invariance while also increasing parameter efficiency. A dropout layer with a value of 0.2 was applied to reduce the overfitting. As a result, the target dataset is used to train each layer of the new model, and the softmax function is used in the final layer to perform multiclass classification. The hyperparameters used for training the pre-trained models are shown in Table II.

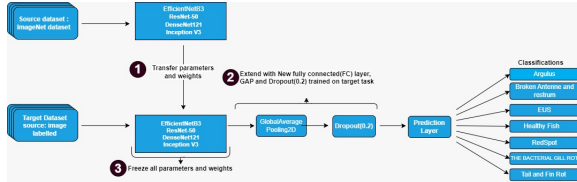


Fig. 3: Proposed transfer learning schema

TABLE II: Hyperparameters used for training the pre-trained models

Hyperparameters	Value
Optimizer	Adam
Learning Rate	0.001
Loss	Categorical Crossentropy
Verbose	2
Class Weight	class_weight
Epochs	50
Use multiprocessing	True

IV. RESULT & DISCUSSION

To evaluate our model, firstly, we have calculated the training, validation and testing accuracy, which is shown in Table III. The intention was to evaluate the validation and testing accuracy to see if there was any overfitting or

underfitting presented and how the model performed on unseen data. Notable accuracy rates were achieved by Inceptionv3, one of these models: 99.57% on the training set, 95.51% on the validation set, and 82.91% on the testing set. With training accuracy of 97.46%, validation accuracy of 96.63%, and testing accuracy of 81.91%, ResNet-50 likewise showed good performance. DenseNet-121 displayed a distinct pattern with comparatively higher testing (77.89%) and validation (86.52%) accuracy than training (75.31%). With 98.51% accuracy during training, EfficientNetB3 did well, but its testing accuracy dropped to 79.90%. Therefore, these outcomes show that Inceptionv3 performed well in terms of accuracy in our study. Further, we have evaluated our model using precision, recall and f-score that is shown in Table IV.

TABLE III: Training, Validation and Testing accuracy of all models

Model	Training	Validation	Testing
Inceptionv3	99.57%	95.51%	82.91%
ResNet-50	97.46%	96.63%	81.91%
DenseNet-121	75.31%	86.52%	77.89%
EfficientNetB3	98.51%	95.51%	79.90%

TABLE IV: Precision, Recall and F-score of all models

Model	Precision	Recall	F-score	Kappa	MCC
Inceptionv3	83%	82%	82%	0.8006	0.8018
ResNet-50	81%	82%	82%	0.7889	0.7868
DenseNet-121	78%	78%	77%	0.7420	0.7408
EfficientNetB3	80%	80%	79%	0.7655	0.7640

The performance of Inceptionv3 is well-balanced, with accuracy, recall, and F-score all at 82%. This suggests that the model captures a high proportion of true positive instances (recall) and is effective at accurately identifying positive instances (precision). The F-score illustrates the model’s dependability in the classification task for fish diseases by displaying the pleasing harmony between precision and recall. ResNet-50 consistently achieves an 82% F-score, recall, and precision. The model’s recall and f-score performance are comparable to that of the Inceptionv3 model, albeit marginally worse. DenseNet-121 continues to perform admirably, maintaining 78% precision, 78% recall, and 77% F-score. The model efficiently detects positive examples while limiting the amount of false positives and false negatives. The model’s performance was inferior to that of ResNet-50 and Inception V3. Ultimately, EfficientNetB3 outperforms DenseNet-121 and underperforms InceptionV3 and ResNet-50 in terms of precision, recall, and F-score, with respective values of 80%, 80%, and 79%. The InceptionV3 model outperformed the others in terms of f-score, recall, and precision. The model also outperformed the others when we calculated accuracy. As our dataset is unbalanced, we have also measured the kappa and MCC values. With a high MCC (0.8018) and Kappa (0.8006), Inceptionv3 shows that there is a good degree of agreement between the model’s predictions and the actual classifications. ResNet-50 exhibits strong agreement, as evidenced by its MCC of 0.7868 and Kappa of 0.7889. Taking into account

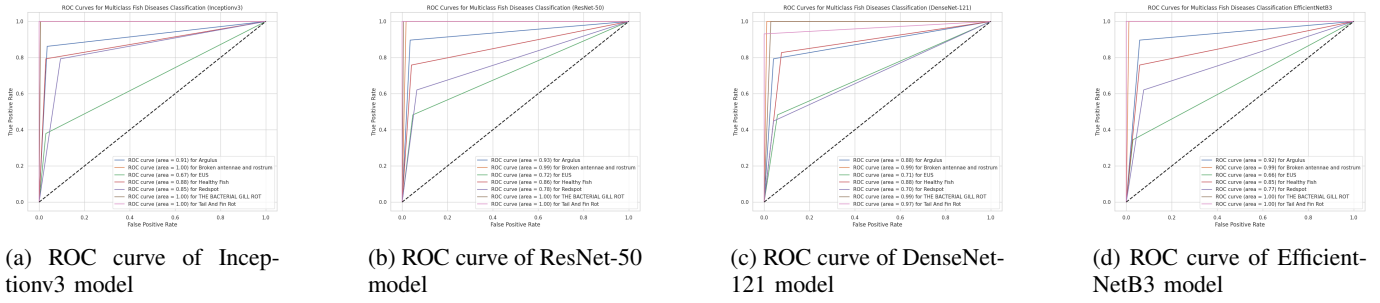


Fig. 4: Roc Curve.

the possibility of random chance, these values highlight the model's predictability. DenseNet-121 has an MCC of 0.7408 and a Kappa of 0.7420. EfficientNetB3, with an MCC of 0.764 and a Kappa of 0.7655, shows a strong degree of agreement. Taking into account the possibility of chance agreement, Kappa and MCC offer additional insights into the models' performance. High agreement metrics are exhibited by all models. The presented tables III and IV indicate that Inceptionv3 performed best by every criterion of evaluation. Finding the Area Under the Receiver Operating Characteristic (ROC) Curve (AUC) in multiclass classification is essential to comprehending a model's ability to discriminate between different classes. AUC offers important information about how well the model differentiates between various classes, enabling performance evaluations based on class. In addition to facilitating overall model comparison and robust evaluation in the presence of imbalanced class distributions, macro- and micro-averaging AUC provides a thorough understanding of the model's multiclass classification capabilities. The AUC values of all classes are shown in Figure 4a-4d. For the argulus class, the highest value (0.93) is achieved by the ResNet-50 model. On the other hand, the broken antennae and rostrum class InceptionV3 model performed well (1.00). The EUS class has achieved a much lower AUC value compared to other classes. This class's highest and lowest AUC values are 0.72 and 0.66, achieved by the ResNet-50 and EfficientNetB3 model accordingly. DenseNet-121 and Inceptionv3 performed well for the healthy fish class. They performed a 0.88 AUC value for this class. The Inceptionv3 model performed well for the remaining 3 classes accordingly, 0.88, 1.00 and 1.00, respectively, among all models. This analysis also showed that for the maximum class, the best value is achieved by the Inceptionv3 model. Another graphical evaluation was performed in our research confusion matrix. The confusion matrix breaks down predictions into true positives, true negatives, false positives, and false negatives for each class, giving a clear and comprehensive picture of a model's classification performance. Particularly in multiclass scenarios, this visual representation helps pinpoint areas of strength or weakness and provides insight into the model's accuracy in classifying instances within each class. The confusion matrix is shown for all classes in Figure 5a-5d.

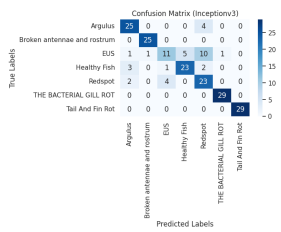
A. Explaining the Results with LIME

When it comes to image classification using transfer learning, LIME is invaluable. LIME can be applied to different model architectures because of its model-agnostic approach. By creating streamlined, intelligible models that roughly represent the behaviour of the underlying complex models, it offers local interpretability for individual predictions. In image classification applications, ethical considerations like bias and fairness are critical, and this local perspective helps with validation, debugging, and handling these issues. To investigate which aspects of the image influence the outcome of the model's predictions, the LIME library version 0.2.0 was utilized. The images used for evaluation are separated into superpixels in accordance with the weights in the model using the LimeImageExplainer function in this library and are then visualized. The given Figure 6 shows the original fish image first and then uses the QuickShift algorithm to generate superpixels that create perceptually meaningful regions. Superpixel boundaries are superimposed on the original image to visualize this segmentation. Superpixels enable meaningful perturbations when using LIME to interpret the model's decision. Superpixels are areas of the image with similar properties; by varying them separately, one can observe how sensitive the model is to particular features. In this case, the superpixel boundaries serve as borders for the areas depicted in Figure 7. The model makes the prediction correct by identifying these superpixels.

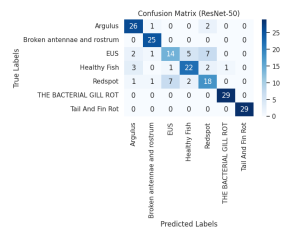
The other Lime analysis is shown in Figure 8 and 9. The original Figure is shown first. When the model is classified as an actual class, it depends on the specific region of the original image. The place is extracted and shown in Figure 9. The original image shows that a specific region carried out the disease. When our model makes a prediction, it considers that specific area which is actually responsible for differentiating the class from other image classes. So, the analysis helps us to trust the prediction system of our model.

V. CONCLUSION

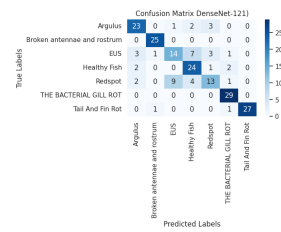
We have explored the field of fish disease classification in this research paper, using sophisticated transfer learning models to improve accuracy and dependability in the aquaculture setting. The models under investigation, which



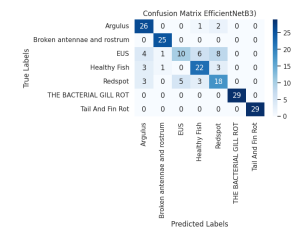
(a) Confusion matrix of Inceptionv3 model



(b) Confusion matrix of ResNet-50 model



(c) Confusion matrix of DenseNet-121 model



(d) Confusion matrix of EfficientNetB3 model

Fig. 5: Confusion Matrix.

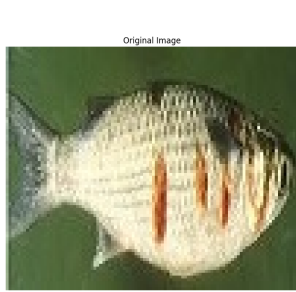


Fig. 6: Original image

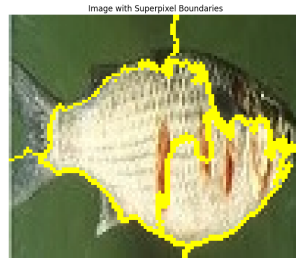


Fig. 7: Image with superpixels boundaries



Fig. 8: Original image

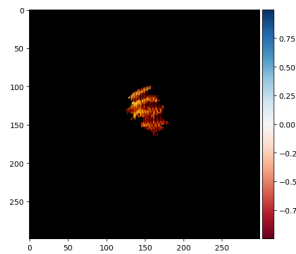


Fig. 9: Important part is extracted (LIME)

comprised Inceptionv3, ResNet-50, DenseNet-121, and EfficientNetB3, demonstrated differing levels of efficacy. Notably, Inceptionv3 demonstrated exceptional performance throughout the training, validation, and testing stages. Complex fish disease patterns and scarce datasets have presented significant challenges that have been successfully addressed by combining advanced architectures with methods like data augmentation and transfer learning. Furthermore, by using interpretability tools—most notably, LIME—these models' decision-making processes have become more transparent, highlighting the significance of individual features and promoting confidence in their forecasts.

REFERENCES

[1] S. Malik, T. Kumar, and A. K. Sahoo, "Image processing techniques for identification of fish disease," *2017 IEEE 2nd International Conference on Signal and Image Processing (ICSIP)*, Aug 2017. [Online]. Available: <http://dx.doi.org/10.1109/siprocess.2017.8124505>

[2] J. Sikder, K. I. Sarek, and U. K. Das, "Fish disease detection system: A case study of freshwater fishes of bangladesh," *International Journal of Advanced Computer Science and Applications*, vol. 12, no. 6, 2021. [Online]. Available: <http://dx.doi.org/10.14569/ijacsa.2021.01206100>

[3] B. Koonce and B. Koonce, "Resnet 50," *Convolutional Neural Networks with Swift for TensorFlow: Image Recognition and Dataset Categorization*, pp. 63–72, 2021.

[4] S. Nandhini and K. Ashokkumar, "An automatic plant leaf disease identification using densenet-121 architecture with a mutation-based henry gas solubility optimization algorithm," *Neural Computing and Applications*, pp. 1–22, 2022.

[5] C. Wang, D. Chen, L. Hao, X. Liu, Y. Zeng, J. Chen, and G. Zhang, "Pulmonary image classification based on inception-v3 transfer learning model," *IEEE Access*, vol. 7, pp. 146 533–146 541, 2019.

[6] A. A. Nafea, M. S. Ibrahim, M. M. Shwaysh, K. Abdul-Kadhim, H. R. Almamoori, and M. M. AL-Ani, "A deep learning algorithm for lung cancer detection using efficientnet-b3," *Wasit Journal of Computer and Mathematics Science*, vol. 2, no. 4, pp. 68–76, 2023.

[7] M. J. Mia, R. B. Mahmud, M. S. Sadad, H. A. Asad, and R. Hossain, "An in-depth automated approach for fish disease recognition," *Journal of King Saud University - Computer and Information Sciences*, vol. 34, no. 9, p. 7174–7183, Oct 2022.

[8] X. Xu, W. Li, and Q. Duan, "Transfer learning and se-resnet152 networks-based for small-scale unbalanced fish species identification," *Computers and Electronics in Agriculture*, vol. 180, p. 105878, Jan 2021. [Online]. Available: <http://dx.doi.org/10.1016/j.compag.2020.105878>

[9] A. Waleed, H. Medhat, M. Esmail, K. Osama, R. Samy, and T. M. Ghanim, "Automatic recognition of fish diseases in fish farms," *2019 14th International Conference on Computer Engineering and Systems (ICCES)*, Dec 2019. [Online]. Available: <http://dx.doi.org/10.1109/icc48960.2019.9068141>

[10] H. Chakravorty, "To detection of fish disease using augmented reality and image processing," *Advances in Image and Video Processing*, vol. 7, no. 6, Jun 2020. [Online]. Available: <http://dx.doi.org/10.14738/aivp.76.7503>

[11] F. Rachman, M. Akbar, and E. Putera, "Fish disease detection of epizootic ulcerative syndrome using deep learning image processing technique," *International Conference on Fisheries and Aquaculture*, Jan 2023. [Online]. Available: <http://dx.doi.org/10.17501/23861282.2023.8102>

[12] A.-A. Nayan, J. Saha, A. N. Mozumder, K. R. Mahmud, A. K. Al Azad, and M. G. Kibria, "A machine learning approach for early detection of fish diseases by analyzing water quality," *Trends in Sciences*, vol. 18, no. 21, p. 351, Oct 2021. [Online]. Available: <http://dx.doi.org/10.48048/tis.2021.351>

[13] S. Malik, T. Kumar, and A. Sahoo, "A novel approach to fish disease diagnostic system based on machine learning," *Advances in Image and Video Processing*, vol. 5, no. 1, Feb 2017. [Online]. Available: <http://dx.doi.org/10.14738/aivp.51.2809>

[14] Y.-P. Huang and S. P. Khabusi, "A cnn-oselm multi-layer fusion network with attention mechanism for fish disease recognition in aquaculture," *IEEE Access*, vol. 11, p. 58729–58744, 2023. [Online]. Available: <http://dx.doi.org/10.1109/access.2023.3280540>

[15] R. C. Barik, "Spot disease identification using unsupervised machine learning based image segmentation with its remedial solution in aquatic fauna," *Journal of Survey in Fisheries*

- Sciences*, vol. 10, no. 2, 2023. [Online]. Available: <https://sifisheressciences.com/index.php/journal/article/view/1030>
- [16] N. Hasan, S. Ibrahim, and A. Aqilah Azlan, "Fish diseases detection using convolutional neural network (cnn)," *International Journal of Nonlinear Analysis and Applications*, vol. 13, no. 1, pp. 1977–1984, 2022. [Online]. Available: https://ijnaa.semnan.ac.ir/article_5839.html
- [17] M. S. Ahmed, T. T. Aurpa, and M. A. K. Azad, "Fish disease detection using image based machine learning technique in aquaculture," *Journal of King Saud University - Computer and Information Sciences*, vol. 34, no. 8, p. 5170–5182, Sep 2022.