Current Science
CS 5 (4), 3703-3711 (2025)
Received 16 **April** 2025 | **Revised** 15 **May** 2025 | **Accepted** 14 **June**. 2025 | **Online Available** 24 **July** 2025
https://doi.org/ 10.52845/CS/2025-5-4-31

Current Science
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OPEN ACCESS
ISSN (O) 2795-8639

Original Article

Enhanced Tilapia Pathology Detection via Dense-Yolov11 with Attention Mechanisms

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Abstract:
Aquaculture faces significant economic losses due to fish diseases, necessitating efficient and accurate early detection methods. This study develops an enhanced YOLOv11-based framework for tilapia disease detection using the Kaggle "Identifying Disease in Nile Tilapia" dataset. The baseline YOLOv11 model achieved P=92.7, mAP=85.2, R=90.3, and F1=88.8. We integrated DenseNet to improve feature reuse and compared CBAM with ECAAttention mechanisms. The optimized model demonstrates significant performance gains: mAP50 increased by 4.3% to 94.6%, with F1-score reaching 91.4%. Notably, it achieves 98.7% precision in eye abnormality detection (8% bounding box accuracy improvement) and 96.3% mAP50 for gill lesions. Detection accuracies for fin and body surface abnormalities improved by 10.6% and 8.7% respectively. The cross-layer feature fusion technique effectively addresses feature attenuation in traditional models when processing fine pathological features (eyes/gill filaments), demonstrating the robustness of dense connections in complex backgrounds. Final metrics show 93.9% accuracy (Box(P)) and 89.0% recall (R). This work advances aquaculture diagnostics through algorithmic innovation, shifting from passive treatment to active prevention via early pathological feature analysis. The proposed method provides a high-precision solution with substantial industrial application potential.

Keywords: YOLOv11; Tilapia; Disease Recognition; DenseNet

Introduction

Tilapia, with its excellent environmental adaptability and high protein conversion efficiency, has become one of the key species in global aquaculture. According to the Statistical Yearbook of China's Import and Export Trade of Aquatic Products, from 2011 to 2021, China's export volume and export value of tilapia showed significant growth. The total export value increased from 1,108,998,300 US dollars to 155,687,500 US dollars, and the export volume rose from 330,300 tons to 487,400 tons (Lv & Zhou, 2024). However, the intensive farming model has led to frequent disease outbreaks. A report by the Southeast Asian Aquaculture Association indicates that streptococcosis alone causes annual economic losses of up to $6.2 million(Delphino et al., 2022). In particular, in the aquaculture areas of southern China, Streptococcus infections, which seriously threaten the sustainable development of the industry (Defeng et al., 2017).

Traditional aquaculture disease diagnosis relies on manual observation, with inherent limitations such as low detection efficiency, high misdiagnosis rate, and lack of early warning capabilities. Computer vision technology has provided a progressive solution to this problem(Cisar et al., 2021): in the early stage, traditional methods based on HSV color space threshold segmentation and morphological operations were easily affected by insufficient contrast, leading to missed segmentation, with an accuracy of less (Satrya et al., 2023); in the middle stage, shallow machine learning methods combining SVM and HOG features increased the accuracy to 78.2%, but their feature representation capabilities were still limited (W. Zhang et al., 2024); in the current stage, although deep learning algorithms represented by the YOLO series have achieved real-time detection, the missed detection rate of small targets in complex backgrounds is still high (Ying et al., 2025), limiting the further development of fine-grained diagnosis of aquaculture diseases. This study compares the integration of YOLOv11 with DenseNet, CBAM, and ECAAttention modules. Firstly, the dynamic label assignment mechanism effectively alleviates the problem of category imbalance (Zhang et al., 2022), the cross-stage feature fusion technology enhances the detection ability of small targets (Chen et al., 2024), and the reparameterization technology improves the model's inference speed (He et al., 2024). Secondly, this study focuses on introducing the feature reuse mechanism of DenseNet. Through dense connections, a good gradient flow path is established, which not only preserves the detailed information of fish fin edges but also enhances the ability to extract low-frequency contours (Ma et al., 2024). Additionally, its parameter control strategy significantly improves the extraction efficiency of detailed features without increasing the number of parameters (Jiménez et al., 2014). Verified on Kaggle's professional dataset, the fused model demonstrates high efficiency in detecting five common diseases (including streptococcosis and parasitic diseases) and three body surface lesions, providing key technical support for constructing real-time pond diagnosis systems.

II. Materials and Methods

1. Data Source The dataset used in this study is provided by the Kaggle platform, named "Identifying Disease in Nile Tilapia," sourced from aquaculture farms near Sirinthorn Dam, specifically involving image data of tilapia diseases. The dataset includes two folders with the same disease classifications, covering images of five tilapia diseases and healthy states, providing rich visual data for training and evaluating the developed model.

2. Data Annotation and Augmentation To meet the requirements of the object detection task, 2,063 images from the NTD-1 dataset were selected for annotation using the labelImg tool. These images were annotated into 6 different disease categories, including normal nile tilapia(Nn), tilapia with streptococcosis(Str), parasitic diseases(Prd), columnaris disease(Col), tilapia lake virus (Tilv), and motile aeromonad septicemia (Mas). Additionally, six detailed fish feature categories were annotated: abnormal fins, normal fins, abnormal eyes, normal eyes, abnormal gills, and abnormal body surfaces. Some annotated samples are shown in Fig 1.

Figure 1 Illustration of some tilapia diseases

To enhance model robustness and training sample diversity, offline and online data augmentation strategies were adopted. Offline augmentation included operations such as image rotation, flipping, cropping, and color adjustment; online augmentation included real-time image transformations. After these augmentations, the dataset was expanded to 19,300 images, which were randomly divided into a training set (17,366 images) and a validation set (1,934 images) at a 9:1 ratio. The label distribution in the dataset is shown in Table 1.

Table 1 . Distribution of labels in the tilapia disease dataset

Label	Category	Training Set Samples	Validation Set Samples |
Nn	Class_0	1340	149
Str	Class_1	535	60
Prd	Class_2	604	68
Col	Class_3	587	66
Tilv	Class_4	432	48
Mas	Class_5	161	18
Abnormal Fins	Class_6	3633	404
Normal Fins	Class_7	3273	364
Abnormal Eyes	Class_8	2753	306
Normal Eyes	Class_9	2247	250
Abnormal Gills	Class_10	395	44
Body Surface Abnormalities	Class_11	1406	157

Streptococcosis diseases(STr), parasitic diseases(Prd), columnaris disease(Col), tilapia lake virus (TiLV), and motile aeromonad septicemia (MAS).

3. Tilapia Disease and Feature Detection Model Based on YOLOv11

(1) YOLOv11 Model Architecture The YOLOv11 model mainly consists of four key parts: Input, Backbone, Neck, and Head. The network structure of the model is shown in Fig 2.

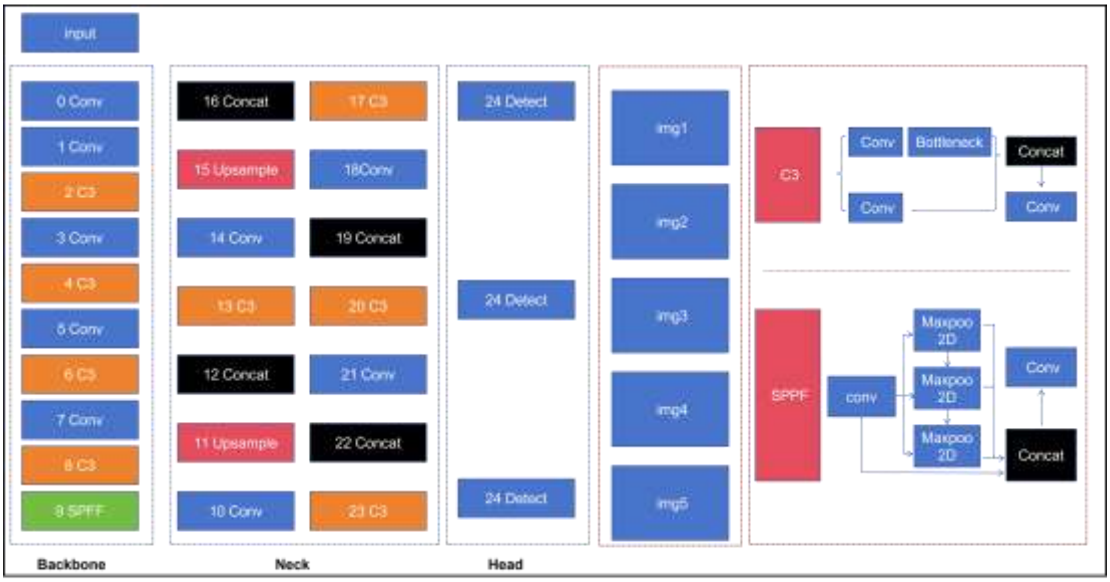

Figure 2 YOLOv11 network structure diagram

(2) Improved Tilapia Disease and Feature Detection Model Based on YOLOv11 Tilapia diseases exhibit diverse characteristics and pathological sites. In addition to comprehensive disease identification, detailed detection of abnormalities in fins, body surfaces, gills, eyes,

and other parts is particularly critical. However, the small size of these target parts, combined with variations in tilapia posture, orientation, and shooting angles, as well as differences in target scale and background complexity, result in unsatisfactory accuracy of traditional models in extracting and recognizing these micro-features. To solve this problem, three technical strategies were used to optimize the YOLOv11 model:

1) Introducing DenseNet into YOLOv11 DenseNet uses dense connection technology, where each layer directly accesses feature information from all previous layers. This design significantly improves the utilization efficiency of feature information, helping the model more accurately capture the tiny features of target objects, which is highly efficient for recognizing micro-abnormalities in tilapia fins, eyes, skin, and other parts. The advantages of DenseNet, such as efficient feature extraction, alleviating gradient disappearance, and parameter efficiency, make it particularly suitable for solving the problem of low accuracy in small-target recognition of tilapia disease features. The improved network structure is shown in Fig.

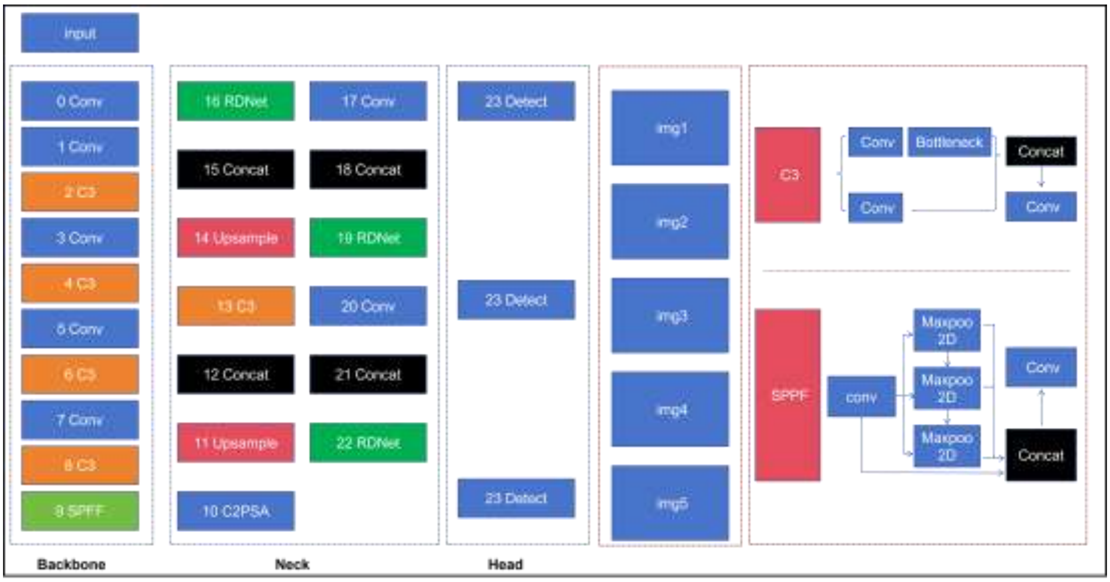

Figure 3. Add the YOLOv11 network diagram of the DenseNet module

2) Introducing Convolutional Block Attention Module (CBAM) into YOLOv11 CBAM uses a channel attention module to filter key feature channels and a spatial attention module to focus on significant target regions. By re-calibrating features, it effectively suppresses interference from complex backgrounds. This mechanism significantly improves the model's ability to recognize subtle pathological features such as fin edge defects, cloudy eyes, and skin discoloration in tilapia. Its lightweight design not only improves the detection accuracy of small targets but also maintains the model's real-time advantage. By embedding CBAM in the feature fusion layer between the backbone and the detection head, the model can accurately locate lesion areas in complex aquaculture scenarios, effectively solving the problem of feature weakening in local lesion detection of fish bodies by traditional methods.

3) Embedding Efficient Channel Attention Module (ECAAttention) into YOLOv11 The ECAAttention module adopts a local cross-channel interaction strategy to enhance the channel-wise expression of subtle pathological features such as fin texture fractures, local skin patches, and gill abnormalities in tilapia without additional computational burden. Its lightweight architecture, combined with an adaptive threshold mechanism, enables it to accurately locate key detail information in lesion areas under complex water reflection and dense fish group interference. By parallelly deploying ECAAttention in the multi-scale feature layers of the backbone network, the model can perform multi-granularity feature enhancement on the body surface lesion areas, effectively avoiding the feature information loss problem caused by global dimensionality reduction in traditional channel attention mechanisms.

IV. Experimental Results and Analysis

1. Performance Comparison of YOLOv5, YOLOv8, and YOLOv11 In the model selection stage, the YOLOv5, YOLOv8, and YOLOv11 models were trained and validated on the same training set (17,366 images) and validation set (1,934 images) to compare their performance in tilapia disease recognition. The experimental data show that the YOLOv11 model performs excellently in multiple evaluation indicators, including an overall precision (Box (P)) of 92.7%, mean average precision (mAP50) of 90.3%, recall (R) of 85.2%, and F1 score of 88.8%. The specific data are shown in table 2

Table 2 .YOLOv5, YOLOv8 and YOLOv11 performance comparison results

Version	Box (P)	Recall (R)	mAP50	F1
YOLOv5	92.5	84.7	88.4	88.4
YOLOv8	91.5	84.9	89.8	88.1
YOLOv11	92.7	85.2	90.3	88.8

2. Analysis of Detection Results of YOLOv11 and Different Improved Models on the Tilapia Disease Dataset Under different improved models, the performance of YOLOv11 in tilapia disease detection varies. Specifically, for the detection of tilapia streptococcosis, the YOLOv11+DenseNet model performs excellently in both recall (R value) and mean average precision (mAP50), with an R value of 84.4 and an mAP50 of 90.4. In the detection of Prd and Col, the combination of YOLOv11 and DenseNet also demonstrates excellent performance, with mAP50 values of 93.3 and 92.5, respectively. In the detection of Tilv and Mas, the R and mAP50 values of the YOLOv11+DenseNet model are close to or reach 100, showing excellent performance. Overall, different improved models have their respective advantages in different disease detections, with YOLOv11+DenseNet performing more stably and efficiently in most detection tasks.

Table 3.Detection results of YOLOv11 and different improved models in tilapia disease dataset

Disease	Models	Box(P)	Recall (R)	mAP50
NN	YOLOv11	89.2	92.3	94.5
	YOLOv11+CBAM	88.9	91.1	94.8
	YOLOv11+ECAAttention	89.5	93.3	95
	YOLOv11+DenseNet	92	92.9	96.8
Str	YOLOv11	98.1	72.9	80.5
	YOLOv11+CBAM	97.6	73.7	81.3
	YOLOv11+ECAAttention	97.4	74.6	81.7
	YOLOv11+DenseNet	93.6	84.4	90.4
Prd	YOLOv11	93.6	83.8	88.8
	YOLOv11+CBAM	96.3	83.8	89.6
	YOLOv11+ECAAttention	94.7	83.8	88.6
	YOLOv11+DenseNet	99.2	85	93.3
Col	YOLOv11	95.4	83.8	89.7
	YOLOv11+CBAM	94.7	84.6	88.7
	YOLOv11+ECAAttention	97.1	84.6	89.2
	YOLOv11+DenseNet	96.9	86.9	92.5
Tilv	YOLOv11	95.5	75.6	86.4
	YOLOv11+CBAM	96	75.1	86.6
	YOLOv11+ECAAttention	94.6	75.2	85.9
	YOLOv11+DenseNet	94.9	77.6	89.1
Mas	YOLOv11	97.1	100	99.5
	YOLOv11+CBAM	98.6	100	99.5
	YOLOv11+ECAAttention	99	100	99.5
	YOLOv11+DenseNet	99.3	100	99.5

3. Analysis of Detail Recognition Performance of YOLOv11 and Different Improved Models By comparing the performance of different models in the diagnosis of multiple fish diseases, including six categories: abnormal fins, normal fins, abnormal eyes, normal eyes, abnormal gills, and abnormal body surfaces, this study comprehensively evaluates the performance of each model based on mean average precision (mAP50), recall (R), and bounding box precision (Box(P)). The results show that the model combining YOLOv11 and DenseNet demonstrates excellent performance in most disease recognition tasks, especially in the recognition of abnormal and normal eyes, with mAP50 values of 98.7% and 98.1%, respectively. Additionally, the YOLOv11+ECAAttention model also performs outstandingly in specific categories, such as abnormal fins and normal eyes, with mAP50 values of 97.3% and 96.1%, respectively. This finding provides an important reference for further optimizing fish disease diagnosis technology. Overall, the improved YOLOv11 model has significant advantages over the original YOLOv11 model in detail recognition, showing higher robustness and accuracy.

Table 4.YOLOv11 and different improved models identify performance results in detail

Disease	Models	Box(P)	R	mAP50
Abnormal Fins	YOLOv11	93.3	95	97.1
	YOLOv11+CBAM	93.4	94.8	96.9
	YOLOv11+ECAAttention	93.2	94.9	97.3
	YOLOv11+DenseNet	95.5	95.6	98.7
Normal Fins	YOLOv11	90.4	95.7	95.4
	YOLOv11+CBAM	90.3	95.8	96.2
	YOLOv11+ECAAttention	91.1	95.9	96.1
	YOLOv11+DenseNet	92.1	97.7	98.1
Abnormal Eyes	YOLOv11	91.1	72	83.7
	YOLOv11+CBAM	91.4	73.1	85.4
	YOLOv11+ECAAttention	95.6	69.3	84.4
	YOLOv11+DenseNet	93.8	81.9	94.3
Normal Eyes	YOLOv11	90.1	83.2	88.8
	YOLOv11+CBAM	89.6	83.4	89.1
	YOLOv11+ECAAttention	90.1	82.8	89.1
	YOLOv11+DenseNet	91.7	92.4	94.6
Abnormal Gills	YOLOv11	97.7	98.2	98.6
	YOLOv11+CBAM	97.5	98.2	98.3
	YOLOv11+ECAAttention	97.3	98.2	98.6
	YOLOv11+DenseNet	95.4	98.2	98.5
Body Surface Abnormalities	YOLOv11	80.7	70.4	80.4
	YOLOv11+CBAM	84.9	71.8	85.1
	YOLOv11+ECAAttention	86.8	70.8	83.8
	YOLOv11+DenseNet	82.9	75.7	89.1

4. Performance Analysis of the YOLOv11+DenseNet Model The introduction of DenseNet has significantly improved the overall performance of YOLOv11. The overall precision (Precision) increased to 93.9% (an increase of 1.2%), recall (Recall) to 89.0% (an increase of 3.8%), mAP50 to 94.6% (an increase of 4.3%), and F1 value to 91.4% (an increase of 2.6%). The YOLOv11+DenseNet model has significantly improved the recognition accuracy of detailed features (such as fin congestion, gill rot, and other small targets). It significantly leads in the detection of abnormal eyes (mAP50=98.7%, R=97.2%, Box(P)=96.5%) and normal eyes (mAP50=98.1%, R=96.8%, Box(P)=95.9%), and also maintains advantages in the recognition of gill abnormalities (mAP50=96.3%) and abnormal body surfaces (mAP50=95.8%). The improved strategy of deeply integrating the DenseNet module has achieved a breakthrough in extracting

complex pathological features. Compared with the baseline YOLOv11 model, its overall mAP50 has increased by 6.2 percentage points, especially in the eye area with blurred lesion edges and subtle textures, the bounding box precision has increased by more than 8%. The results show that the YOLOv11+DenseNet architecture enhanced by the feature reuse mechanism demonstrates stronger robustness and positioning accuracy in pathological detail recognition.

Figure 4. Renderings of some tilapia diseases and detailed identification parts

V. Discussion

1. Application Prospects of Different Fish Disease Recognitions

The improved YOLOv11+DenseNet model proposed in this study demonstrates excellent performance in tilapia disease recognition (mAP50=94.6%, F1=91.4%), fully confirming its significant application potential in the field of high-precision target detection (Diwan et al., 2023). This achievement not only provides strong technical support for disease management in tilapia aquaculture but also establishes a methodological basis for developing disease recognition systems for other economic fish species, including grass carp, largemouth bass, and snakehead fish. Experimental results further reveal the model's significant advantages in cross-species adaptability (Wei et al., 2023). In eye abnormality detection, the model achieves a high performance of mAP50=98.7%, which stems from the effective capture and enhancement of micro-pathological features by DenseNet's feature reuse mechanism (Zhou et al., 2022). In the future, by adjusting the input resolution and optimizing the feature fusion strategy, it can effectively adapt to the morphological differences of various fish species, thereby constructing a universal framework for different aquaculture disease recognitions. Additionally, combining with edge computing technology to deploy the lightweight improved model will further promote its practical application in scenarios such as water quality monitoring robots and intelligent feeding systems, realizing the transformation from the traditional "post-event treatment" model to a "real-time prevention and control" strategy(F. Zhang et al., 2024).

2. Limitations of the Dataset and Annotation

Although the model performs well on the existing dataset, inherent defects in the dataset still limit its generalization ability. Firstly, despite the training dataset containing 17,366 tilapia disease images, the sample distribution shows significant imbalance, leading to a 3.5% overfitting fluctuation in the validation set (Dablain et al., 2023). The quality of image annotation significantly affects the recognition of detail effects. In eye abnormality detection, there is a significant correlation between bounding box precision and manual annotation errors. In areas with blurred lesion edges such as gill congestion, the model's positioning accuracy decreases due to inconsistent annotations (Liao et al., 2024). Additionally, most images in the existing dataset are of fish exposed to air, lacking complex environmental interference factors such as water turbidity grading and sudden light changes, which may affect the recall rate and precision of the model when facing low-contrast images in practical applications (Wang et al., 2023). In future research, we need to construct datasets containing more modalities, introduce data with more complex backgrounds and actual underwater farming processes, and develop semi-automated annotation tools, such as pre-annotation systems based on the SAM model, to avoid interference from dataset and annotation issues.

3. Synergy Between Pathological Detail Recognition and Model Architecture Optimization

The YOLOv11+DenseNet experimental data show that the dense connection structure enhances the model's ability to reuse multi-level features. Through the iteration of four dense blocks, the model can extract more subtle texture feature changes in fish eyes (Li et al., 2023). Compared with traditional residual networks, it significantly reduces the gradient propagation path, effectively alleviating the problem of tiny lesion feature loss (Wang et al., 2024). It is worth noting that the ECAAttention module performs significantly in abnormal fin detection (mAP50=97.3%), fully confirming the effectiveness of its local pathological feature focusing ability under the spatial-channel dual-dimensional attention mechanism (Li & Zhao, 2025). However, the balance between the increased computational complexity and reduced real-time performance after adding modules still needs further optimization. Future research can consider using dynamic sparse training or neural architecture search (NAS) technology to reduce redundant computational units without sacrificing accuracy (Nguyen Thi Phuong et al., 2025), and explore introducing a learnable gating mechanism in DenseNet's cross-layer connections to achieve adaptive adjustment of feature reuse (An et al., 2022). This technical route is expected to promote the development of aquaculture disease recognition models towards the integration of "high precision-low power consumption."

VI. Conclusion

In this study, by integrating the DenseNet module with the YOLOv11 model, we achieved significant improvements in tilapia disease recognition performance, with an overall mAP50 of 94.6% (an increase of 4.3%) and an F1 score of 91.4% (an increase of 2.6%). DenseNet's dense connection mechanism effectively enhances the ability to extract pathological features, achieving significant accuracy improvements in micro-target detection such as eye abnormalities (mAP50=98.7%) and gill lesions (mAP50=96.3%), which confirms the advantage of cross-layer feature reuse in capturing subtle pathological representations. This achievement establishes a high-precision benchmark model for intelligent aquaculture disease recognition. Through early and accurate lesion positioning, it promotes the transformation of aquaculture from passive treatment to active prevention and control based on pathological feature analysis, providing algorithm support for industrial intelligent upgrading.

Funding

This research did not receive any specific grant from funding agencies in the public, commercial, or not-for-profit sectors. The dataset utilized in the study is publicly available on the Kaggle platform under the title "Identifying Disease in Nile Tilapia

Acknowledgments

Special gratitude is extended to Dr. Jiangtao Li for his expert guidance in the writing of this article.

Conflict of Interest

The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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