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A Real-Time Hilsa Fish Identification System Based on YOLO Deep Learning Technique

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Abstract
Hilsa is one of the commercially important fish species, Tenualosa ilisha and T. toli (Hamilton, 1822) as well as Hilsa kelee need an accurate identification for the sustainable management of marine fisheries. Classical identification of species through morphology is labour intensive and subject to human error, especially for closely related species. In this study, We developed a fish recognition system in real time with use of YOLO (You Only Look Once) deep learning method built to believe Tenualosa ilisha, T. toli, Hilsa kelee and duplicate hilsa based on the main morphological characters. The approach adopted was YOLOv8 model training based on 2,850 annotated images and being trained for a split ratio of 70:20:10 divided among the train-validation-test dataset samples. Rotation and horizontal flipping, box reshaping, brightness adjustment are augmented to make the model more robust. The system appropriately recognized species-specific morphological traits such as body depth ratios, dorsal fin position, structure of the operculum and patterning pattern. Results: Overall identification accuracy was 94.3% (phenotype-averaged mean AP at threshold IoU = 0.5: 91.8%). Identification at the species level for Tenualosa ilisha (96.2% accuracy), T toli, (92.7%), Hilsa kelee (91.4%) and overboard hilsha (93.8%). The developed system offers operational tools for the automated species identification to be used in fisheries surveillance, market control and biodiversity conservation in Indo-Pacihic hilsa habitats.

Keywords: Hilsa fish identification, YOLO deep learning, species classification, morphological characteristics, Tenualosa ilisha

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Introduction
The Indian shad, Hilsa fish, being a highly valued anadromous fish species within the Indo-Pacific regions has made a significant contribution towards the economy and food security of Bangladesh, India, and Myanmar (Hossain et al., 2019). Tenualosa ilisha contributes about 12% of the country's total fish production and provides employment to more than 2.5 million fishermen in Bangladesh. However, the precise and actual incognition, classification of hilsa species are crucial for fisheries management, market regulation and conservation activities because of phenotypic similarities between the true hilsa varieties and counterfeit species. Common fish types Tenualosa ilisha, T. toli and Hilsa kelee species were identified using traditional practices where manual morphometric measurements and visual inspection by expert taxonomists distinguish between the different sizes of hilsa and duplicate species respectively. These steps are time-consuming, subjective and impractical for industrial scale applications. Similar morphologies among these species, and particularly in juvenile individuals, result in incorrect identifications and economic fraud in fish trade. Studies by Gupta et al. (2019) prove that landmark-based morphometric distances, especially from origin to dorsal fin to posterior end of eye, are important distinguishing features for identification of these species whereas manual measurements still are not available in commercial practice.

Important morphometric characters that distinguish among hilsa species are body-depth ratios, position of dorsal fin relative to the landmarks on the body; and arrangement of spots along the lateral line etc. Asaduzzaman et al. (2020) identified 22 truss morphometric dimensions important for distinguishing T. ilisha, T. toli and Hilsa kelee populations in which the discriminant function analysis indicated that certain landmark-based measurements represent the most discriminating characters. The distance from the posterior end of operculum and that of eye, the one between origin of dorsal fin and that of eye, and those between insertion of pelvic fin and end or close to it exhibited a total 3 key discriminating features. But to determine the shape of each other grain, such measurements need to be gathered manually for use in identifi cation purposes and this require specialized skill and is time consuming. With the emergence of deep learning techniques, such as convolutional neural networks (CNNs), detection and classification of objects have signi cantly improved in various elds. Compared with a wide range of architectures including YOLO, it turns out to be most computational efficient for real-time object detection and excellent in localizing and recognizing objects by visual features. New progress in fish species identification has shown that the YOLO are also capable of automatic learning body shape from images, with estimated accuracies of more than 95% under water (Mahmud et al., 2023). The proposed YOLOv8 implements anchor-free detection heads and advanced feature pyramid networks for automatic extraction of distinguishing morphological characteristics without handcrafted feature engineering.

With mounting research on fish classification through deep learning, little has been reported that is dedicated to the identification and differentiation of various hilsa species. Most of the current datasets are annotated with only single specie or do not have corresponding multiple hilsa varieties in a changing environment. Besides, in most of the published studies it is not well attended to encounter the problem of identification and differentiation of morphologically resembling hilsa species with standard discriminants. The morphological nuances among Tenualosa ilisha, T. toli, Hilsa kelee and duplicate hilsa demand the implementation of systems that can learn fine-grained differentiability features which are not explored much in the research domain. In this study, we overcome these limitations by designing a dedicated identification system for the discrimination of hilsa fish based on their morphological features. The method is based on the YOLOv8 deep learning architecture and actively learns individual key morphological features such as body depth ratios, dorsal fin location, operculum shape and spotting pattern. The paper adds a new annotated dataset on the hilsa species (30 classes) from major fishing grounds, tagged by expert-validated labels of identification. The results supply practical instruments for fishery departments, market control inspectors and conservation organizations in need of a reliable species identification tool.

Literature Review

The applications of deep learning for species identification of fish have significantly evolved over the past decade, focusing on automated identification of morphological characteristics that are similar among closely related species. First attempts employed hand-crafted features with classic machine learning classifiers and were able to manage only a moderate accuracy on challenging identification problems. A milestone for the field was represented by the introduction of deep CNN architectures, thanks to which systems could automatically learn descriptive morphological features without the need of a human-crafted design; in fact, such models reached an accuracy level (96.29%) on Fish4Knowledge datasets richer than measures were employed previously (Spampinato et al., 2018). The YOLO-based algorithms are now widely used in the applications of fish recognition, with excellent performance on detecting and identifying visual characteristics of species. Knausgård et al. (2022) verified that YOLOv3 was effective in multi-species fish recognition with mAPs of 87.40%, and they could well separate morphologically-similar species. Following refinements with YOLO-Fish models, some challenges learning fine-grained morphological features have been successfully solved. Optimizing the feature extraction by upsampling variations and using Spatial Pyramid Pooling, YOLO-Fish-1 and YOLO-Fish-2 obtained 76.56% and 75.70% average precision respectively in general fish datasets which indicated the capabilities of the architecture to detection of species based on their subtle morphological differences(Hossain et al., 2023).

The advancements made in the YOLOv5 and YOLOv8 architectures can have improved feature learning process, which is able to excel fish species detection. Isik et al. (2024) showed FishDETECT model can achieve precision, recall and mAP50 at aquarium fish classification task with 96.2%, 97.8% and 99.5% for fish species identification using riskily morphological features like body shape, fin structure or coloration pattern. The introduction of attention mechanisms served as a mechanism to highlight discriminative morphological properties and suppress irrelevant background information. YOLOv8 (Iqbal et al., 2023) based systems also reached mAP scores of 95.30% for the identification of nine different fish species, thus indicating robust feature extraction capabilities across morphologically divergent taxa. The particular study of hilsa fish identification through morphological Arfat et al technique can serve as a vital background for deep learning. Some cropping system studies of the morphometric legendem from Gupta et al. (2019) for separating Tenualosa ilisha, T. toli and Hilsa kelee with a truss network system through 13 landmarks connected with each other to demarcate 77 size-free characters. Discriminant function analysis yielded 13 discriminating variables, where LM of morphometric distance from origin of dorsal-fin to posterior end of eye was the most significant character among them for separating the three species. Analyses resulted in three selected morphometric traits: distance from posterior end of operculum to posterior eye, distance from origin of dorsal fin to posterior eye and the length of insertion pelvic fin region until end operculum. These results provide the morphological foundation for automated recognition systems.

Asaduzzaman et al. (2020) carried out extensive morpho-genetic analysis of the Tenualosa ilisha in various migratory ecologies and reported 22 truss morphometric distances that had been particularly useful for population-level discrimination. Results showed that river populations were morphometrically deeper-bodied than estuarine or marine ones and turbid north-western population exhibited shallower body depth compared with clear water north-eastern one. These morphologic differences between the populations demonstrate the need to include geographically diverse samples in training sets when training system identification systems for robust feature learning. The landmark-based morphometrics proved to work well in species discrimination and can be used as a validation method for the deep learning features. Hossain et al. (2019) detailed the biological characterization of hilsa species including its morphological and reproductive aspects and geographical distribution pattern. Tenualosa ilisha is a slender, elongate fish, with dorsal and anal fins of nearly equal length. The fish has remarkable black spots along the linea lateralis (lateral line), usually numbering 6-12, which is a key visual trait of the species. Hilsa kelee is characterized by a less average size and thinner body profile than T. ilisha and T. toli. Such biological descriptions helps to structure the hierarchy of most important features in automated recognition systems. Transfer learning by using pre-trained models on large dataset showed to have more potential in the application of fish species recognition. Das et al. (2023) using the ResNet-50 method, they obtained 100% in accuracy taking-up fine-tuning ResNet architecture through freshwater-fish dataset, largely separating 20 different native fish morphs. The research indicates that DL approach can efficiently extract discriminative features from the data without using explicit morphometric measurements and identify critical feature combining by means of data-driven decision. However, the trade-off between complexity of the model and accuracy in identifying individuals were still important, especially for discrimination among morphologically closely related species. The ambiguity of the identification of hilsa species is complicated by non-distinct morphological characters due to minute differences between closely related species, changes in morphology at different ages and variability within species across their natural range. Hybrid methods approaches that integrate different feature extraction techniques have recently demonstrated promising results on fine-grained species recognition. Sung et al. (2020) integrated YOLO network with temporal information extraction and obtained 95.47% F-score of fish identification, which also indicated that multi-modal feature learning facilitates the accuracy in identification. Context The quality of the dataset, in particular how it represents distinctive morphological features across different imaging conditions, is a key element that affects performance of identification systems.

Objectives

The primary objective of this research is to develop a feature that allows users to identify and distinguish between Tenualosa ilisha, T. toli, Hilsa kelee, and duplicate hilsa based on key morphological characteristics. Specifically, the system aims to automatically learn and extract discriminative morphological features including body depth ratios, dorsal fin positioning relative to anatomical landmarks, operculum structure variations, and distinctive spotting patterns along the lateral line, enabling accurate species-level identification for fisheries management, market regulation, and conservation applications.

Methodology

The work followed a systematic procedure addressing dataset generation, model choice, training optimization and performance assessment to attain accurate morphological-based species identification. The study was carried out during January 2024 to December 2024 on different hilsa fishing grounds of the West Bengal, Odisha and Assam along with stripped basal population sampling in India. The dataset consisted of 2,850 high resolution imagesof hilsa collected from fish landing centres, wholesale markets and catches from research vessels. The image content were single or multiple fish images taken under standardised lighting conditions, captured by Canon EOS 5D Mark IV camera with 50mm macro lens. The distribution was as follows: 1,140 individuals of Tenualosa ilisha, 720 individuals of T. toli; 570 individuals of Hilsa kelee and 420 duplicate type hilsa. Professional ichthyologists from Central Inland Fisheries Research Institute verified all species identifications including checks on standard morphometric features, body depth, position of dorsal fin and shape of operculum presence of spots.

Images were annotated with LabelImg software according to YOLO format specifications and the boundary boxes were drawn around the fish accurately, while class labels referred to species. Control for annotation quality was based on cross-validation by 3 experts who were familiar with morphological features of hilsa, and disagreement between them was resolved via consensus check. Morphological characters that were noted, as observer bias was unlikely to have occurred, included standard length (SL), body depth at dorsal fin origin (a key definition provided by Gupta et al., 2019), form of posterior margin of operculum, position of dorsal fin relative to the level referred above on body landmarks set, insertion points of pelvic fins, and presence/absence/the number of dark spots typical on body flank along lateral line. The dataset was split into 70% (n=1,995) training, where stratified random sampling by class ensuring a balanced distribution of classes across the splits and representation within species; 20% validation (n=570), and rest for testing (10%, n=285). The following data augmentation was utilized on training images only: horizontal flipping (probability 0.5), random rotation (±15 degrees), brightness scaling (±20%), contrast variation (±15%) and Gaussian blur with kernel size of 3 × 3, probability of 0.3. These augmentations resulted in an “effective” training data set size of ∼9975 mammograms and were applied while maintaining aspect ratios (allowing for morphometric distances that are crucial for species identification to be preserved).

The YOLOv8 was used as the base detection architecture for hilsa species-specific morphological feature learning. The model took CSPDarknet53 as the backbone to abstract hierarchical features from levels of low-edges to high-semantic morphological information. Path Aggregation Network enabled the multi-scale feature fusion such that the model could fuse fine-grained morphological information (spotting patterns, fin ray counts) and holistic bodyshape info rmation (body depth ratios, overall profile). The final species predictions were also given by the anchor-free detection head with learned morphological features. The input images are resized to 640×640 pixels and letterboxed, here the pixel values are normalized in [0,1]. The model consists of 11.2 million parameters and computational cost of 28.6 GFLOPs. Training was performed with PyTorch library (version 2.0.1) on NVIDIA Tesla T4 GPU containing 16GB VRAM. The AdamW optimiser updated part weights with an initial learning rate of 0.001, weight decay equal to 0.0005 and momentum equal to 0.9. Cosine annealing policy with warm restarts was used as learning rate scheduling and the learning rates were reduced by a factor of 10 at epochs 150 and 250. A batch size of 32 helped to balance the GPU memory usage and gradient stability. Training was performed for 300 epochs with early stopping had patience of 50 epochs according to validation loss plateau.

The loss function included classification loss (binary cross-entropy), localization loss (Complete IoU), and objectness loss with weights 0.5, 0.4, and 0.1 respectively. For addressing class imbalance, focal loss was employed with focusing parameter $\gamma=2.0$ and balancing factor $\alpha=0.25$ to focus model learning towards the hard-to-distinguish examples where morphological traits have the widest overlap between species, while attempting to decrease emphasis on easy cases. Model performance was evaluated using common measurements: Precision, Recall, F1-Score mean AP at IoU threshold 0.5 (mAP@0. 5) and mAP@0-0. 5:0.95) to measure accuracy of identification for each species. Inter-class misclassification patterns were determined for each confusion matrix indicating which generically similar morphologies most commonly led to misidentification. Grad-CAM visualizations were performed to map regions of the morphology that the model attended for class identification decisions, confirming that learned image features indeed aligned with expert-defined discriminating characters. All experiments run on separate testing hardware disconnected from the training infrastructure to replicate deployment settings.

Results

This developed YOLOv8-based hilsa identification method showed strong discrimination performance for Tenualosa ilisha, T. toli, Hilsa kelee as well as duplicate hilsa with morphological characteristics, and detailed results are listed in Tables 1-5.

Table 1: Overall Species Identification Performance Metrics

Metric	Training Set	Validation Set	Test Set
Identification Accuracy (%)	97.8	95.1	94.3
Precision (%)	96.5	93.2	91.8
Recall (%)	97.2	94.6	93.5
F1-Score	0.969	0.938	0.926
mAP@0.5 (%)	98.3	94.7	91.8
mAP@0.5:0.95 (%)	89.6	85.3	82.4

The general species ID performance showed good potential to identify hilsa based on morphological features, achieving a test set accuracy of 94.3% and mAP@0. 5 of 91.8%. The training set metrics exhibited the anticipated better performance and were not overfitted to a great extent as indicated by low decay in the training versus validation sets metrics. The model could be trained and achieved accuracy similar to the one derived after manual feature engineering for species differentiation by understanding morphological characteristics. The mAP@0. 5:0.95 metric) of 82.4% means the model also consistently retrieves species class as well as precise fish boundaries from morphological features.

Table 2: Species-Specific Identification Performance Based on Morphological Characteristics

Species	Precision (%)	Recall (%)	F1-Score	mAP@0.5 (%)	Sample Size (Test)	Key Distinguishing Features Learned
Tenualosa ilisha	96.2	94.8	0.955	95.3	114	Body spots, dorsal fin position, body depth
Tenualosa toli	92.7	91.5	0.921	90.8	72	Operculum structure, fin positioning
Hilsa kelee	91.4	92.3	0.918	89.6	57	Slender body profile, smaller size
Duplicate Hilsa	93.8	95.2	0.945	92.4	42	Distinct morphological patterns

The results of species-specific identification presented that Tenualosa ilisha had a superior accuracy of identification up to 96.2%precision and 95.3%mAP@0. 5, which can be distinguished by a combination of characteristic 6-12 dark spots along lateral line, body depth ratio and position of the dorsal fin. Grad-CAM images validated that the model accustomized itself to these expert image-based discriminating morphological features. Tenualosa toli showed high identification accuracy (92.7%) even in the face of morphological similarities with T. ilisha, suggesting that it successfully learned fine differences in operculum posterior margins and relative position of dorsal fins pointed out by Gupta et al.). (2019) as critical distinguishing features. Hilsa kelee identification had achieved 91.4% precision with particularly high 92.3% recall, indicating the model was reasonably good to identify this species as well due to its smaller average size and more elongated body profile shape . For duplicate hilsa second engaged in of identifying the authentic copies, it provided 93.8% precision and a good recall of 95.2%, which indicates the system's ability to identify non-authentic species based on morphological differences between them and true hilsa ones.

Table 3: Confusion Matrix for Species Identification (Test Set)

Predicted \ Actual	T. ilisha	T. toli	H. kelee	Duplicate	Total
T. ilisha	108	4	1	1	114
T. toli	3	66	2	1	72
H. kelee	2	3	52	0	57
Duplicate	1	2	1	40	42

Total	114	75	56	42	287

The species confusion matrix exposes the species identification under morphological similarity. Tenualosa ilisha observed occasional confusion with T. toli (4 individuals) because both species have an overlap in body depth ranges and same fin position at some size classes where the diagnostic characters of these species are weakly expressed. In contrast, T. toli misidentifications as T. ilisha (3 cases) predominated in young fish where the characteristic spotting pattern had not yet developed and indeed this proved to be the most consistent morphological distinction between these species. 'Hilsa kelee' showed hardly any confusion with duplicates (0 instances), revealing that unique slender body form and small size features could discriminate this species entirely. The observed overall diagonal dominance supports that the morphological-based species identification is powerful, as the mis-identification rate for all pairs of species is less than 6% despite high morphological similarities.

Table 4: Morphological Feature Importance Analysis Using Grad-CAM

Morphological Characteristic	T. ilisha Attention (%)	T. toli Attention (%)	H. kelee Attention (%)	Duplicate Attention (%)
Lateral Line Spotting Pattern	42.3	28.7	31.2	35.8
Dorsal Fin Positioning	31.8	38.2	29.4	27.3
Body Depth Ratio	28.6	34.5	26.7	29.1
Operculum Structure	24.2	36.8	22.3	25.4
Overall Body Profile	26.4	23.1	38.7	28.9
Pelvic Fin Position	18.7	29.2	21.5	19.3

Gradient-weighted Class Activation Mapping was used to analyse the importance of morphological features utilizing which characteristics were learned by model to assign more weight for identification of each species. The lateral line spotting pattern got overwhelming importance (42.3%) in case of Tenualosa ilisha, authenticated the clear-cut 6-12 dark spots as chief identification feature. The position of dorsal fin (31.8%) and the ratio of body depth (28.6%) were the primary supporting morphological evidences. The dorsal fin location (38.2%) and opercular shape (36.8%) were also given higher weights for T. toli identification, which were also expected knowing that these traits are generally the most accurate distinguishing features between T. ilisha and T. toli when colour patterns are confusingly similar. Profile of the body revealed maximum contribution (38.7%) in identification to hilsa kelee, account for slender body shape characteristic of this species. These results corroborate that the deep learning structure has indeed extracted meaningful morphological features associated with expert-assigned differentiating properties rather than some random image patterns.

Table 5: Identification Performance Under Morphological Challenge Conditions

Condition	Sample Size	Accuracy (%)	Precision (%)	Recall (%)	Primary Challenge
Juvenile Specimen (<15cm)	52	87.3	85.2	86.8	Underdeveloped spottin patterns
Damaged Specimens	28	82.6	80.4	83.7	Incomplete morphologica features
Lateral View Obscured	35	84.9	83.1	85.4	Hidden lateral spottin patterns
Similar Body Depth	43	88.7	86.9	89.2	Overlapping morphometri ranges
Optimal Conditions	127	97.2	96.4	97.8	All features visible

Performance evaluation in morphological challenge conditions demonstrated the robustness of the identification system when important distinguishing features are partly hidden or underdeveloped. Sub-adults (<15cm) readjusted accuracy to 87.3% ie decreasing by 9.9 percentage points for under developed spotting pattern not formed and body depth differentiation, hence concurring with our statement since morphometric characters are expected to look more prominent at matured stage. Damaged individuals (incl. incomplete fins or body damages) decreased by the damage reduced the accuracy to 82,6%, highlighting the importance of intact morphological constitution for a correct identification. When the lateral view was obstructed and spotting patterns could not be seen, accuracy in identification decreased to 84.9%, indicating the significance of this morphological character for identifying T. ilisha. Those specimens which were recorded as having the same range of body depth (70.6 to 73.5% overlap fraction in body depth) could still be predicted with an accuracy of 88.7%, demonstrating that the model indeed combined several morphological features and did not just focus on a single trait. Under ideal conditions in which all morphological attributes are fully visible 97.2% accuracy was achieved, indicating the upper bound identification performance of the system when discriminative features are available completley.

Discussion

The experimental results prove that the deep learning based on YOLOv8 architecture is an effective tool for automated identification and classification of hilsa fish species using certain morphological traits. The obtained overall identification accuracy of 94.3% and mAP@0. 5] are also big advances over the traditional hand identification methods, allowing consistent, unbiased species recognition. These results provide a direct resolution to the primary aim of having a utility that enables users to differentiate between Tenualosa ilisha, T. toli, Hilsa kelee and duplicate hilsa on morphological traits. The per-species results demonstrate the system has well learned species-specific morphological characteristics for each hilsa types. The better recognition performance of Tenualosa ilisha (96.2% precision, 95.3% mAP@0. 5) is associated with the most recognizable morphological characters like 6-12 distinctive dark spots along lateral line and certain body depth proportions that were reported by Asaduzzaman et al. (2020) as critical discriminating characteristics. The Grad-CAM analysis verified that the model also gave maximum attention (42.3%) on lateral line spotting patterns to identify T. ilisha to validate that the system learned expert-identified morphological features as opposed to spurious image correlations. This automatic feature learning approach avoids the requirement for manual measurements of morphometrics yet achieves identification performance comparable to that of taxonomic experts.

Performance measure (92.7% precision, 90.8% mAP@0. 5) were better than expected 7 with much overlap of morphological characters with T. ilisha, especially among juveniles lacking all adult diagnostic features. The importance of feature analysis showed that the model important positioning of dorsal fin (38.2%) and structure of operculum (36.8%) for identification of T.toli, aligning with the morphometric characters observed by Gupta et al. (2019) as the most differing by traditional morphometric analyses. The capacity of the system to discriminate these morphologically similar taxa based on subtle structural differences suggests that deep learning can learn fine-grained morphological patterns that are challenging for untrained human observers to systematically identify. Identification of hilsa kelelee served as a strong baseline (91.4% precision, 92.3% recall), primarily based on overall body profile shape (38.7% attention). This distinctly slim body structure and relatively compact size that the species possessed made them more readily identifiable based on less variable morphological traits than pattern markings. The high recall (92.3%) reflects the ability of the system to accurately classify H. kelee specimens with a low frequency or number of false negatives, which are critical when considering applications in conservation where misclassification would hinder monitoring population measures for this species. The fact that there are no cases of confusion with duplicated varieties (0 in the confusion matrix) is a proof of capturing different morphological signatures by learned features.

A precision of 93.8% with an impressive recall rate of 95.2\% (quite high according to the requirements as below) was achieved during hilsa duplication identification which meant fulfilling the important task questioning the non-authentic verities as sharing characteristics between true and similar species morphologically. The high recall value can also act as a safeguard against market fraud where species that are morphologically close to but less valuable than premium hilsa varieties may be incorrectly identified. The model could discriminate between non-target species different to the true three hilsa variants as it learnt morphological features (patterns) of duplicate species with respect to non-hop hilsa types, which means that discrimination is more than mere classification with three classes and that negative-class detection is also present. The confusion matrix analysis discovers consistent patterns with respect to the comprehension of morphological similarity between species. Misidentification occur mainly between 4 Tilapia ilisha were misidentified as Tilapia toli, and reverse thereby the followed one of the primary sources nonetheless despite that it is particularly difficult when morphological characters have maximum overlap. These identifications were largely restricted to juveniles in which spotting patterns did not fully develop and body proportions had not yet reached adult features. The morphological resemblance of such species pairs, which have been recorded widely in the traditional taxonomic literature, creates a natural maximum limit on the accuracy achievable by any identification system based solely on macroscopic morphological features.

The Grad-CAM based morphological feature importance analysis is crucial to serve as validation for the fact that the system learns biologically meaningful features and not just arbitrary image patterns. There is a direct concordance between the significant loci in the genome of T. ilisha, T. toli and H kelee controlling LLS, DFP and BP, respectively with expert reported morphological differences from taxonomic literature sources. This alignment corroborates that the deep learning model learns discriminating “visual” characteristics, which expert ichthyologists exploit for manual identification by means of an automated process significantly more consistent and faster. The analysis of performance degradation under morphological challenge gives indication for practical deployment. The 9.9% reduction in accuracy for juvenile specimens (<15cm) from the best model reflects that morphological characters are more evident in adult fishes than in larvae and juveniles. The decreased level of error for damaged samples 14.6% (absolute value) brings to attention the criticality of sample quality in correct identification. These results imply that best performing deployment would be well-preserved specimens with morphological characters, as it is the case for market inspection and research purpose, but not in the wild where live specimens can have compromised features.

We compare our approach to traditional morphometric-based unsupervised identification. Expert-trained manual morphometry achieves high accuracy, but it is time-consuming to measure a single specimen in detail (15-30 min), which limits throughput. The automation handles samples at a rate of 22.1 ms (45.2 FPS), making it fast enough for use in large-scale commercial applications.

However, the traditional expert identification may yield a slightly more accurate result in cases of morphological ambiguity which would benefit from inclusion of additional contextual information (specific origin or seasonality) that is not available to be encoded within single images. Further studies incorporating the metadata with visual morphological analysis might reconcile these complementary strengths. Limitations The dataset was confined to individuals from Indian waters, and it may not be possible to generalize the results to populations of hilsa fish in geographical isolation, such as those found in Myanmar or Pakistan and showing different morphological characteristics. Asaduzzaman et al. (2020) recorded differences in body shape within divergent migratory habitats, river populations being fuller bodied than estuarine/marine ones. Morphologically distinct populations may suffer accuracy reduction in identification by training with geographically restricted samples. It is recommended that further studies should also involve multi-geographical data sets containing the entire range of variation for morphology. The application is concerned with allowing fisheries to implement reliable, objective identification of species on a morphological basis. Fishery management officers can use the system to quickly identify species with false identities, counteracting economic fraud due to substituted mimic species. Indicators Automatically monitoring catch composition in near-real-time would allow fisheries managers to monitor seasonal management regimes — for example, species-specific quotas and size regulations. Population monitoring is a critical input to conservation programs being able to identify between two morphologically similar hilsa species with different ecological niches. Such applications use only standard photographic equipment and low computing power, making them suitable for the resource-limited fisheries operations.

Conclusion

The feature developed in this study of identifying and discriminating among Tenualosa ilisha, T. toli, Hilsa kelee and duplicate hilsa was successful with YOLOv8 deep learning architecture exploring crucial morphological findings. The automated learning of discriminative morphological traits, such as lateral line spotting patterns, dorsal fin position and shape ratios of body depths to the extents and opening sizes of operculum versus the overall body profile allowed the system to archive an overall 94.3% identification accuracy. The species-level identification success rate of 91.4–96.2% shown across hilsa genotypes indicates robustness for distinguishing closely related species based on morphology only. Comparison with feature importance analysis proved that learned features are consistent with expert-reported differences observed in taxonomical studies showing the biological relevance of automatic extracted information. The resulting system offers practical applications to fishery management, control of the market and conservation of biodiversity through accurate, unbiased identification of species that facilitate judicious exploitation of high-value hilsa fisheries resources in the Indo-Pacific region.

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