Transfer Learning-based Optimal Feature Selection with DLCNN for Shrimp Recognition and Classification

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Abstract: Shrimp is a main international food item with a significant economic value, as well as one of the most vital animal protein sources. The variety of shrimps can be found in aquaculture. Thus, it is necessary to categorize each shrimp. The conventional machine learning approaches are failed to classify the multiple classes of shrimp, which causes large economic losses in the shrimp farming industry. Therefore, this article proposes a hybrid mechanism for shrimp recognition and classification (SRC), which is named as transfer learning-based optimal feature selection (TLOFS) with deep learning convolutional neural network (DLCNN). Initially, transfer learning based AlexNet is used to extract the features from the shrimp samples. Then, machine learning based iterative random forest algorithm (IRFA) is utilized to select the optimal features from the AlexNet extracted features, which can also identify the relationship between various shrimp classes. Finally, DLCNN is trained and tested with the optimal features and classifies the various shrimp categories, hereafter the proposed hybrid model is named as TLOFS with DLCNN. Obtained simulations discloses the effectiveness of proposed TLOFS with DLCNN model with 99.98% of accuracy, and 99.97% of F1-score as compared to state-of-art SRC approaches.

Keywords: Image classification, Shrimp recognition, Convolutional neural networks, AlexNet architecture, Iterative random forest algorithm.

1. Introduction

As the need for food quality safety develops, people all across the world want high-quality, pollution-free food [1]. Non-destructive procedures are the most commonly used for determining food quality. Non-destructive techniques are used in several research domains, including vegetable freshness assessment, fruit exterior quality measurement, seafood quality grading, and fruit juice level categorization [2]. Food consumption is becoming increasingly important as the world's population expands rapidly due to the glasshouse effect and land degradation. Protein is an essential nutrient in the human diet. Fish and shrimp are also good sources of animal protein [3]. Shrimp is an important source of protein in fisheries and a major

economic item around the world. Furthermore, as natural fish sources have depleted and water pollution has increased, ocean fishing has been progressively superseded by ocean farming (or aquaculture), as illustrated in Fig. 1. A small percentage of faulty or ill shrimp is mixed in with healthy shrimp while harvesting fresh shrimp from shrimp production ponds [4]. In addition to shrimp that have been infected by germs or viruses, there are also shrimp that have been crushed, fractured, or perished as a result of a lack of oxygen in the water. If "dirty" shrimp are not identified and removed as soon as possible, they constitute a significant danger to the quality of fresh shrimp clusters and have the potential to degrade the overall quality of the shrimp product. According to data from the united nations food and agriculture organization, worldwide shrimp

Figure. 1 Various shrimps used for aquaculture.

production [5] exceeded 4.58 million metric tons in 2014, with a market value of US$23.5 billion. With an estimated production value of $30 billion by 2030, it is predicted to reach 5 million metric tons by that time. The white shrimp is the most widely cultivated species, accounting for 80 percent of total world shrimp production. As a consequence, shrimp is a potential breeding species with a high economic value, and it is becoming more popular. Shrimp cultivation, on the other hand, necessitates a significant investment in both manpower and time. As a result, intelligent shrimp farming benefits shrimp aquaculture greatly. Intelligent shrimp farming is strongly reliant on shrimp recognition, with the acquired results potentially being employed in other shrimp aquaculture applications [6, 7], increasing the value of shrimp aquaculture production. Typically, the white spot syndrOME Virus (WSSV) [8] is the casual virus that occurs in shrimps, causing major economic losses as well as harming consumer health. Currently, there are no effective preventive therapies for viral infections in shrimp and other crustaceans. Because of present era aquaculture procedures and WSSV's diverse intervention strategies, host range such as WSSV vaccine would be crucial to saving and protecting shrimp farming.

As a result, the proportion of faulty or sick shrimp [9] in sample can be utilized to define shrimp class to which it belongs. This operation was time-consuming, and uniformity across operators cannot be assured. As a result, it is required to define the various shrimp classes, which have the potential to distinguish disease-affected shrimp and normal shrimp. Recently, deep learning models are playing the major role in various fields of applications including aquaculture and these models are mostly utilized in the pattern identification and classification applications. Recently, shrimp farmers are capturing the photographs of shrimps and they are performing the diagnosis by help of experts. The productivity of

shrimp farming is always depending on the experience of farmers and disease identification rate also depending on the experience of experts. But, manual analysis of shrimp diseases with respect to multiple classes is a difficult task. Further, the productivity of shrimp food also depending on the recognition of best shrimp classes. But the farmers are unable to classify the shrimp classes with human eyes. Thus, artificial intelligence is an advanced alternative to the human intelligence. Furthermore, artificial intelligence [10] is one of the advanced technologies that can aid in the realization of intelligent shrimp farming. The major goal of any artificial intelligence approach has always been enhancing the performance of the systems by using deep learning models and it is frequently viewed as the closest technology to human intelligence. As a result, various works are attempted to enhance the quality of shrimp products and promote machine vision-based shrimp quality enhancement solutions. Machine vision is widely utilized in aquaculture product quality detection and assessment, notably for shrimp-related commodities, as a non-destructive method by identifying the various shrimp classes. The earlier works are focused on shrimp disease categorization that too most of the works were addressed only WSSV, but there are no works for performing the classification of shrimp categories. The shrimp classification process is suffering with many real time problems, such as there is no shrimp image database. The real-world shrimp images are suffering with the light illumination problems, water-based haze problems, noisy environment, artifacts, and visibility problems. There is lot of problems are associated with features of various shrimp classes and feature selection becomes crucial problem.

Thus, this article focuses on the solution to all these problems and the major contribution of this work is as follows:

- Utilization of AlexNet model is developed to extract the deep features from the given shrimp dataset i.e., the features with high seismic information with low computational complexity.
- Implementation of IRFA to identify the relationship between features of various shrimp classes extracted from AlexNet. This IRFA is a novel and robust algorithm for identifying the best features with high speed.
- Finally, DLCNN classifier is used to classify the various shrimp classes through the training and testing of optimal features.

Rest of the article is organized as follows: section 2 describes the related work done so far in the field of shrimp recognition. Section 3 discusses the proposed methodology with brief description of its internal operation. Section 4 explains the simulation results and analysis in terms of both quantitative and qualitative. Finally, section 5 concludes the article with possible future works followed by references.

2. Related work

This section provides a detailed examination of various shrimp segmentation and classification approaches. In [11], authors concentrated on the implementation of shrimp segmentation using the K-means clustering approach. This works mainly focused on WSSV segmentation of shrimp. The segmentation is the primary operation in the classification tasks, but this method is suffering with the inaccurate localization of segmented area. The difficulty of segmenting clustered flexional agricultural items grows increasingly complicated in [12]. The work is focused on the segmentation of various agriculture food products, including the shrimps. But this method is suffering with the high computational complexity. In [13], authors concentrated on the issues associated in recognizing and detecting shrimp disorders such as white spot syndrome since the circumstances involved in image capture and the technologies employed in development are more complicated than in other disciplines. As a result, adoption of computer vision systems for disease detection in aquaculture has been slow. Combining techniques like image processing, computer vision, and expert systems increases the level of automation. In [14], authors presented an algorithm that automatically evaluated the shrimp form completeness, and it also provided an evolutionary perspective. A features-based strategy was built to improve the performance of the system. This work utilized the AdaBoost model to extract the deep features. But this method suffering with color illumination problems during the preprocessing operation, which reduced the performance of the system. The original method of shrimp categorization described in [15] has been done by physical labor, which was prone to a large amount of subjectivity and variation. Based on the GLCM and the interactive micromixer version 3, this study suggests a revolutionary efficient technique. To begin, raw shrimp images were mechanically segmented into minimal circumscribed rectangles to create areas of interest, after which GLCM was used to compute moment of inertia, inverse difference mark, entropy, and angular second moment from four directions:

horizontal (0°), diagonal (45°), vertical (90°), and inverse diagonal (135°). An overall decision tree structure based on ID3 was developed based on the textural characteristic values of the training samples, and then the test samples were made to traverse the entire decision tree. When the eigenvalues of the testing samples fall within the range of the leaf node, they are certified as normal shrimp samples; otherwise, they are contaminants.

The freshness of the shrimps was assessed using a computer vision approach based on color changes in the head, legs, and tail in [16]. Hue, chroma, yellowness, redness, lightness, chroma component, luma component, luma information, value, saturation, lightness hue, blue, green, and red were among the 36 color qualities assessed. The computations of 36 features are significantly more sophisticated, increasing the computing cost of the classification procedure. The fuzzy based approaches also providing the better performance in classification operations with low computational complexity [17]. These fuzzy approaches were used to check the quality of the shrimps, which can be further extended with the shrimp class classification. The findings show a positive response, with four degrees of water quality classification: excellent, good, regular, and bad. Better management approaches, combined with suitable growth monitoring and shrimp feed control, can boost agricultural profitability, according to [18]. Manual shrimp growth measurement on a large population is a time-consuming and difficult task that requires the use of back propagating artificial neural networks. Underfeeding produces slower development rates, whilst overfeeding pollutes the ecosystem. As a result, non-invasive, continuous, and automated technologies such as computer vision are gaining traction. On the other hand, existing research on vision-based growth parameter monitoring has yet to be applied to shrimp feed management. In [19], authors utilized a machine learning-based sparse auto encoder (SAE), with promising results in a range of domains. However, this approach was mainly suffering with the higher training time and reduced speed of classification of soft-shell shrimps.

In [20], a joint feature extraction method that is associated with a single classifier is addressed, which has a low classification rate. This work mainly focused on classification of impurities presented in the fresh shrimps. The majority voter is used to classify the various features of fresh shrimp, but this method is suffering with the feature synchronization issues. In [21], authors developed an image-based approach for recognizing shrimp that have been deveined wrongly. Before extracting essential characteristics from grayscale images, basic filtering

operation is performed to remove the haze artifacts and noises. Among these characteristics are pixel value measurements and shape measurements derived from an image histogram. In this study, two classification approaches were used to identify rejected shrimps: linear discriminant analysis and support vector machine (SVM).

Further, hybrid version of machine learning using SVM [22] are used to detect the snapping shrimps. This method resulted better performance for plain background but suffering with complicated backgrounds. Further, the advanced deep learning based AlexNet model is used to extract the deep features from soft shell shrimps, and they also performed the shrimp food classification operation [23]. However, this approach was focused on single class classification and failed to classify the multiple classes of the shrimp. Liu et al. [24] presented deep CNN-based approach for shrimp segmentation and recognition to overcome the inefficiency of traditional algorithms of shrimp recognition. However, the classification accuracy still needs to improve. The work addressed in [25] proposes a method for integrating shallow and deep features and producing feature maps from different layers based on shrimp characteristics using the classification model of CNN. The conventional methods are focusing on detection and classification of multiple items from underwater image. These methods were also focused on shrimp feed type classification, but they were unable to classify the multiple classes of shrimp. Recently, ShrimpNet was proposed in [26], which is used to identify the multiple classes of shrimp, that encompasses not only shrimps and lobsters residing in the sea, but also certain freshwater shrimps, in order to simplify future shrimp-related research. The "ShrimpNet" collection contains shrimp photos retrieved from image search engines. ShrimpNet consists of two CNN layers and two fully connected layers. Shrimp aquaculture, on the other hand, is a labor-intensive and time-consuming profession. As a result, intelligent shrimp farming is extremely beneficial to shrimp aquaculture. Shrimp recognition [27] is a critical component of intelligent shrimp aquaculture. The acquired results can be used in additional shrimp aquaculture applications, which can help to increase the value of shrimp aquaculture production.

3. Proposed methodology

Shrimp classification is a critical stage in the realm of commercial aquaculture. This section describes the computer-aided detection mechanism for classifying shrimp classes. As a result,

aquaculture growers are quickly discovering different types of shrimp with low efforts. Another objective of shrimp classification is that it can also be used to classify the diseases associated with shrimps.

Fig. 2 depicts the proposed TLOFS with DLCNN model's architecture, which consists of three stages: feature extraction, feature selection, and classification. The AlexNet algorithm was developed first to extract deep properties from a synthetic shrimp dataset. It is a transfer learning model capable of extracting features from high-resolution seismic data with low processing effort. The IRFA technique is then utilized to determine the relationship between AlexNet properties for different shrimp classes. The IRFA is a novel, robust algorithm capable of swiftly selecting the best qualities. Finally, the DLCNN classifier is used to categories the distinct shrimp classes after training and evaluating optimum features.

3.1 Pixel locator

Recently, deep learning playing the major role in variety of applications with the advanced image analysis.

The deep learning based AlexNet model capable of extracting the detailed spatial, spectral, texture, and color features from the images with high correlation. The AlexNet model also capable of identifying the relationship between various pixels of images and extracts the inter dependent relationships as the features. Fig. 3 shows the feature extraction based AlexNet architectures, which used to extract the various features from shrimp images and differentiate the features based on shrimp classes. Table 1 listed with the detailed information of each layer presented in AlexNet model. The performance of deep learning models is purely relay based on the number of layers and activation units. The AlexNet model consisting of the five number of convolution layers and three fully connected layers. The color shrimp input image is applied as input to the convolution layer 1 (conv1). The convolution layer contains the kernel or filter-based feature detectors, which extracts the features by performing the convolution operation between input to the kernel matrix. Here, feature detectors are used to extract the edges, horizontal lines, boundaries, bends, and vertical lines, etc. Further, feature maps are activated (selected) by using Rectified linear unit (ReLU). In addition, convolution layers also perform the pooling of data, which is used to convert the invariance to translation.
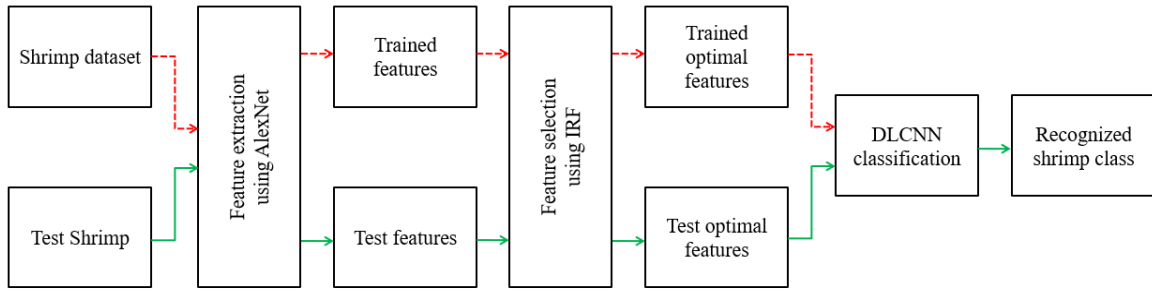
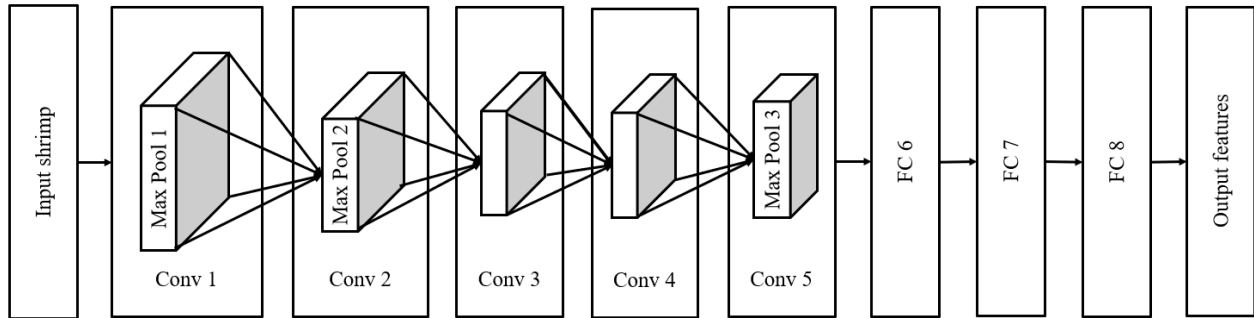Figure. 2 Block diagram of proposed SRC system using TLOFS with DLCNN

Figure. 3 The AlexNet architecture

Table 1. Layers of AlexNet model.

Layer	Number of Filters	Filter size	stride	Padding	Feature map size	Activation function
Conv 1	96	11 x 11	4	-	55 x 55x 96	ReLU
Max Pool 1	-	3x3	2	-	27x27x96	-
Conv 2	256	5x5	1	2	27x27x256	ReLU
Max Pool 2	-	3x3	2	-	13 x 13x 256	-
Conv 3	384	3x3	1	1	13 x 13x 384	ReLU
Conv 4	384	3x3	1	1	13 x 13x 384	ReLU
Conv 5	256	3x3	1	1	13 x 13x 256	ReLU
Max Pool 3	-	3x3	2	-	6 x 6 x 256	-
FC 6	-	-	-	--	1 x 4096	ReLU
FC 7	-	-	-	--	1 x 4096	ReLU
FC 8 (output)	-	-	-	--	1 x 1000	SoftMax

The unique property of convolution layer is that, even though the size of input is changed from layer to layer, but the pooled outcome was not change. The initial convolution layers contain the smaller number of filters and extracts the deeper features. As the layers are increases, the number of filters is increases as compared to preceding layer, which are capable of extracting the higher ordered features.

$$f(i,j) = \sum_m^M \sum_n^N I(i-m, j-n) * W(m,n) \quad (1)$$

Here, $I(m,n)$ represents the input image with "m" number of rows and "n" number of columns. $W(m,n)$ represents the weight matrix with kernel properties and $f(i,j)$ represents the output feature. The output features of Conv1 are applied to Conv2, like these five convolution layers are connected in serial manner. Then, conv 5 output

features are connected to the fully connected layer 6 (FC6). The FC layer is a flatten layer, which connects all the neurons with equal probability mapping. The input features are connected in a linear transformation manner to get the output feature. Totally, three FC layers are used to generate the robust features of shrimp images based on various classes.

3.2 Feature optimization using IRFA

The IRFA algorithm is used to identify the best features, which contains three fundamental operations. The IRFA algorithm looks for high-order feature interactions in three phases as shown in Fig. 4. The first phase is iteratively reweighted RF, here the input features are applied to the system. The features are assigned to iterative manner with each feature allotted to a Gini importance score. Here, the
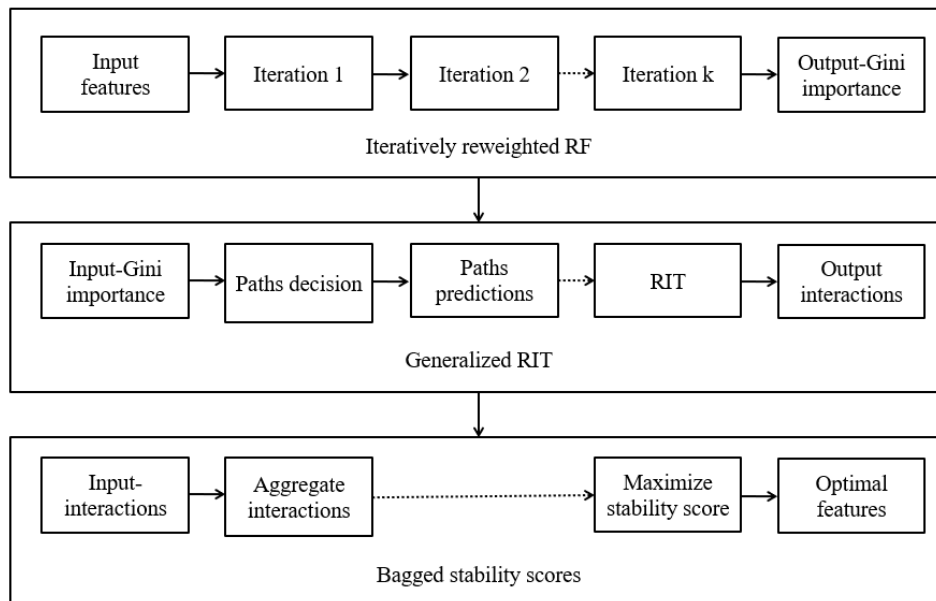
Figure. 4 Optimal feature selection using IRFA

Gini score is the relation aware feature score, which holds the probability levels of each feature, and these probabilities are updated with the iterative process.

The second phase is generalized random intersection trees (RIT), here a tree-based decision mechanism is developed among the input Gini importance scores. This phase mainly utilizes the tree-based decision architecture, and each Gini score is allotted with the tree branches. Then, the best path decisions and predictions are placed between each Gini score, which are used to estimate the interactions between multiple scores. These interactions were holding the optimal feature properties with high correlations and the interactions are changed based on shrimp-to-shrimp class.

The final phase is bagged stability scores, here the optimal features are generated by assigning the stability scores to each interaction. The input interactions may contain the properties of multiple shrimp classes, which leads reduction of stability score and causes to reduction of classification performance. Thus, the stability scores play the major role in improving the classification accuracy by selecting the best features. During this phase, the aggregation of interactions was performed and finally the stability score of each feature is maximized. Based on this score, the optimal feature set is generated from the available features by focusing on variation between shrimp classes.

Feature-Weighted RF and RIT: The IRFA introduces iterative weighted property to RF for reduction of feature space dimensionality. The major advantage of the IRFA is that it won't delete the insignificant features during the iterative process, but

it will merge the properties of insignificant features to others for higher order intersections. Consider $RF(w)$ as optimal feature generated using IRFA, here w is the group of non-negative weights denoted as $w = (w_1, \ldots, w_p)$ with p number of total feature maps. The $RF(w)$ chooses the highest probability based jth feature based on their weight levels. This joint feature and weight property is called as the "enriched random forests" and weights are utilised in genomic data processing for feature selection and generates the new probabilities as $RF(\frac{1}{p}, \ldots, \frac{1}{p})$.

Based on these probabilities, the higher order interactions will be generated and forms the RIT between various inter dependent features in a deterministic way. Here, RIT searches for the similar set of features, interactions presented in the single classification class. Finally, the updated probability between various interactions was identified with lower computational complexity.

Let the constraint optimization problem is generated in the binary classification with p binary properties and n observations. The input data is $(I_i, Z_i), i = 1, \ldots, n$ with each $Z_i \in \{0, 1\}$ indicates the binary level. The active features in the subset are denoted as $I_i \subseteq \{1, 2, \ldots, p\}$. Finally, the predominance of an interaction is calculated by using gene's promoter region with low to high feature enrichments.

$$P_n(S|Z = C) := \frac{\sum_{i=1}^n 1(S \subseteq I_i)}{\sum_{i=1}^n 1(Z_i = C)} \qquad (2)$$

Here, empirical probability distribution is given by P_n. Apply the thresholding region with optimal boundary conditions $0 \leq \theta_0 < \theta_1 \leq 1$ in the empirical distribution, which generates a new set of distributions as follows:

$$P_n\ (S|Z\ =\ 1)\ \geq\ \theta_1,\ P_n\ (S|Z\ =\ 0)\ \leq\ \theta_0 \quad (3)$$

Further, the IRFA utilizes the properties of supervised learning, here the Gini impurity criterion index is used to measure the significance of a variable and provides information on the prediction potential of a feature. In order to determine the relevance of unconditional permutation, data is sent down each tree in the forest and the accuracy of predicting between the actual and synthetic data is recorded for each tree in the forest. A permutation is carried out in order to disrupt the relationship between the feature and the label in question. By averaging the difference in accuracy before and after the permutation, an unconditional RIT is calculated. A conditional permutation importance framework is used to evaluate the relevance of variables in complicated data sets with connected characteristics. One at a time, the values of a feature are conditionally permuted based on the groupings of each and every other feature, resulting in a disruption of the dependent structure of the connected features. In order to achieve a real variable significance measure, one must measure the partial correlation of one feature while simultaneously adjusting for the influence of another feature.

We collect all leaf nodes in the output tree ensemble of an RF for each tree $t\ =\ 1, \dots, T$ and index them by $j_t\ =\ 1, \dots, J(t)$ Each feature–response pair (x_i, y_i) is represented with respect to a tree t by (I_{i_t}, Z_{i_t}) where Iit is the set of unique feature indexes falling on the path of the leaf node in the tth tree containing (x i,y i). As a result, each (x_i, y_i) generates T such index set and label pair pairings, corresponding to the T trees. As a result, we aggregate these pairs across observations and trees.

$$\text{R} = \{(I_{i_t}, Z_{i_t}) : \ x_i \text{ falls in leaf node it of tree } t\} \quad (4)$$

and then run RIT on this modified dataset R to get a list of interactions.

1) Iteratively reweighted RF: Using a bootstrapping sample process, determine the optimal number of trees to be planted. When the data splitting procedure was completed at all internal nodes, the optimal number of leaves (node size) was determined as a stated stop condition to be reached. The terminal nodes of a tree are the points at which the tree's development is halted. The trees' depth may become too varied if they are allowed to grow to their full potential (i.e., result in relatively high variance and low bias and a possible overfitting of the data). As a result, the tree's pruning is accomplished by determining the ideal number of leaves to have. The number of input variables (i.e., the number of individual bands or VIs) utilized for the split choices were picked at random from the total at each node of the tree at every node of the tree. In our technique, the stop condition for each tree's development was established by determining the optimal number of leaves on the tree. The number of trees and the number of leaves were optimized by reducing the root mean square error.

2) Generalized RIT: RF model training was completed, and the relative relevance of the input characteristics was determined at the end of the process. The notion of variable significance is founded on the premise that if the omission of a variable is linked with a significant drop in prediction accuracy, then that variable is regarded to be significant in the forecast. As a result, a subset of traits is chosen depending on the significance values assigned to them. When rating variable significance, the strategy used in this research is referred to as "permutation accuracy importance," and it is regarded to be one of the most helpful ways available. It is necessary to divide the operation into two parts in order to simplify the IRFA model while maintaining forecasting accuracy. In the first stage, the model is trained using all of the predictors as input features, and the model is refined in the second step. By gradually decreasing the number of predictors and performing an iterative removal of the less essential predictors, the second phase aims to evaluate whether or not the RF model has a positive impact on model performance. The predictive accuracy of the RF model is determined in this stage. In accordance with this criterion, the amount of input characteristics was gradually decreased, iteratively, until it reached 50 percent of the total at each iteration, and this process was repeated until the error did not grow noticeably.

3) Bagged stability scores: The bootstrap sampling technique does not need exclusive training and validation sets, as does the optimal feature selection with sampling approach. However, rather than dividing the data into distinct portions, the procedure involves dividing the dataset into K number of folds and then going through an iterative process where it first trains on the random subset size $(K-1)/K$ of the observations ($K-1$ of the folds), and then evaluates performance on the random subset size $1/K$ of the observations ($K-1$ of the folds)
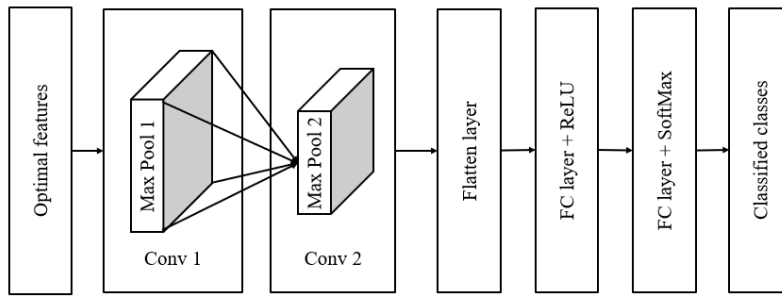
Figure. 5 DLCNN model for classification

Table 2. Layers of DLCNN model

Layer	Number of Filters	Filter size	Feature map size	Activation function
Conv 1	12	56 x 56	56 x 56x 12	ReLU
Max Pool 1	-	28 x 28	28 x 28 x 12	-
Conv 2	28	28 x 28	28 x 28 x 28	ReLU
Max Pool 2	-	14 x 14	14 x 14 x 12	-
FC1	-	-	1 x 5488	ReLU
FC2	-	-	1 x 6	SoftMax

(Kth fold). The procedure is performed a total of K times. When the bootstrap sampling procedure is completed, the final performance metric is calculated by taking the average of the validation metrics for each of each of the K rounds. Although the out-of-bag performance of an IRFA model is quite comparable to that of a cross-validation model, it is highly proposed that a rigorous validation using an independent test dataset be performed.

3.3 Classification using DLCNN

This work utilizes the DLCNN model to predict and classify the various classes of shrimp. Fig. 5 presents the DLCNN model, which is trained by using optimal features selected by using IRFA. Table 2 presents the detailed layer analysis of DLCNN model. The deep learning model developed with the multiple sequential layers for the classification operation.

Convolution layer: Convolution layers consisting of feature detectors for extracting the features by using the multi-data kernels. Eq. (5) shows the process of feature detection with x as input and w is the weighted kernel. Further, the convolutional layers also contain the pooling and activation function. Here, MaxPooling is used to select the maximum region of available features. Thus, the resultant data contains the maximum available features based on the length of stride and filter size. Eq. (6) represents the ReLU activation

function, which is a piecewise linear activation mapping module. If the input feature is positive, then the output will generate, otherwise output becomes zero. The ReLU activation functions are used to eliminate the vanishing gradient problem, which improves the training accuracy by enhancing the training speed. The ReLU activations utilize the probability of data manipulation with accurate feature analysis.

$$x_i^l = f\left(\sum_{j=1}^k w_{i,i}^l * x_j^{l-1}\right) \quad (5)$$

$$f(x) = \max(0, x) = \begin{cases} 0, & if \ x < 0 \\ x, & if \ x \geq 0 \end{cases} \quad (6)$$

Fully connected layer: The FC layers are dense output layers, which interconnects the various feature neurons with all possible combinations. Thus, the output node contains the direct paths from all the input features. The final FC layer utilizes the SoftMax classifier to generate the final output. These FC layers are the flatter layers with unidirectional data analysis.

$$loss = -\sum_{j=1}^k y_i' \log(y_i) \quad (7)$$

Usually, the deep learning models are suffering with the cross-entropy loss as presented in Eq. (7). Here, y_i is the output feature with classified outcome. The proposed DLCNN model reduces the loss by using stochastic gradient decent optimization. The SoftMax classifier assigns the probabilities to each shrimp classes. Further, the test images probabilities are checked with trained probabilities under marginal conditions and results the classified outcome.

4. Results and discussion

This section describes the performed simulations on shrimp dataset using existing SRC systems and proposed TLOFS with DLCNN model with both qualitative and quantitative analysis. Since there is no

Figure. 6 Recognized and classified shrimp classes using proposed TLOFS with DLCNN model

Table 3. Collected shrimp dataset

Category of shrimp	Samples
Panulirus ornatus	120
Peacock mantis shrimp	120
Procambarus clarkia	119
Marsupenaeus japonicus	120
Giant river shrimp	119
White shrimp	120
Total	718

standard dataset for the applications of SRC, the dataset is prepared by authors from Google imaging sources. Table 3 listed the information of shrimp dataset collected from internet sources, where the 1st column gives the category of shrimp, and the 2nd column describes the number of sample shrimps considered for the given category.

4.1 Dataset

The simulations are run on a synthetic dataset that includes the six shrimp species listed in Table 3 with Panulirus ornatus, Peacock mantis shrimp, Procambarus clarkia, Marsupenaeus japonicas, giant river shrimp, and white shrimp classes. Fig. 6 depicts the several recognized and categorized shrimp classes based on the proposed TLOFS with DLCNN model.

4.2 Quantitative assessment

This section contains a detailed examination of simulation findings as well as comparisons with state-of-the-art methodologies. Confusion matrices are created for calculating the various performance metrics such as accuracy, precision, recall, F1-score, sensitivity, and specificity. The confusion matrices of HML [27], ShrimpNet [26], and Proposed TLOFS with DLCNN are shown in Fig. 7. According on the
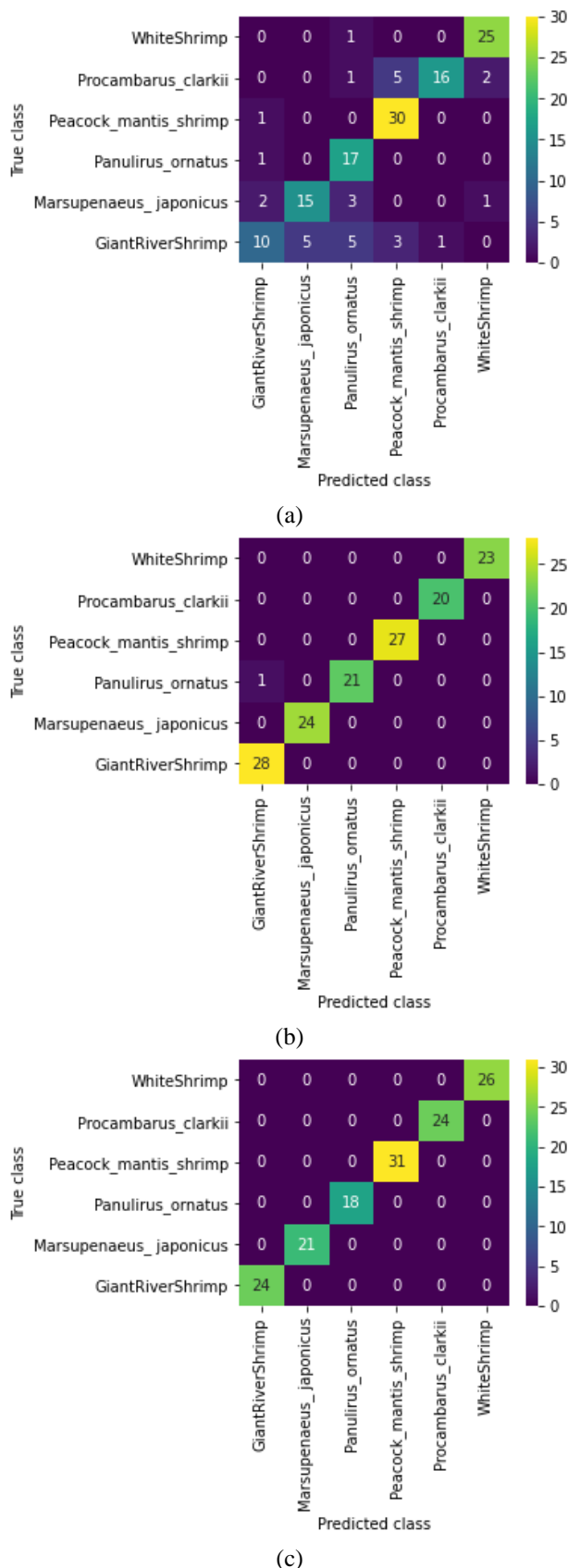

(a)

(b)

(c)

Figure. 7 Confusion matrix: (a) HML [27], (b) ShrimpNet [26], and (c) Proposed TLOFS with DLCNN

confusion matrix values, the proposed TLOFS with DLCNN model has greater true positive values and

Table 2. Performance comparison of proposed TLOFS with DLCNN with state-of-art SRC approaches

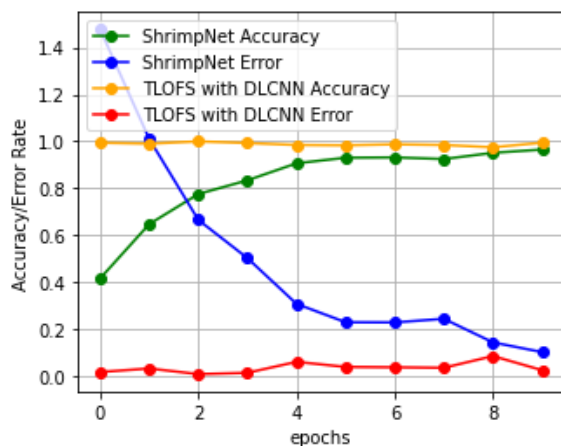| Method	Accuracy (%)	Precision (%)	Recall (%)	F1-score	Sensitivity (%)	Specificity (%)
HML [27]	77.77	78.76	77.27	76.64	80	81.35
AlexNet [23]	85.644	85.736	85.238	82.923	83.235	81.957
CNN [25]	86.103	89.669	87.089	88.464	91.342	83.395
ShrimpNet [26]	99.30	99.33	99.01	99.15	100	100
Proposed TLOFS with DLCNN	99.98	99.97	100	99.97	100	100

Figure. 8 Performance comparison of accuracy and error rate of existing ShrimpNet and proposed TLOFS with DLCNN models

lower true negative values than the state-of-the-art techniques. Similarly, the proposed TLOFS with DLCNN model has low false positive and false negative values, resulting in higher sensitivity and specificity metrics when compared to conventional approaches.

Table 2 shows that the proposed TLOFS with DLCNN outperformed traditional approaches such as HML [27], AlexNet [23], CNN [25], and ShrimpNet [26] in terms of accuracy, precision, recall, F1-score, sensitivity, and specificity.

These present approaches have feature extraction and feature selection issues, which have resulted in worse subjective and objective performance. Fig. 8 shows a graphical representation of the accuracy/error rates in relation to the various epochs. Fig. 8 shows that the proposed TLOFS with DLCNN outperformed the previous ShrimpNet model in terms of accuracy-error rate trade-off performance. Furthermore, when compared to the previous ShrimpNet model, the proposed TLOFS with DLCNN has higher accuracy and lower error rates for all epochs.

5. Conclusions

Shrimp is a prominent international food item with a great economic value, as well as one of the most essential animal protein sources. This paper introduced the proposed TLOFS with DLCNN model as a hybrid technique for shrimp identification and classification. Initially, the feature properties from the shrimp database are extracted using AlexNet, a transfer learning-based algorithm. The best features from the AlexNet-retrieved characteristics are then chosen using machine learning-based IRFA, which also identifies the link between different shrimp classes. Finally, using these top features, DLCNN is created and tested to classify the various shrimp classes. The simulations were done on a synthetic dataset, and the results revealed that the proposed TLOFS with DLCNN outperformed state-of-the-art approaches across all performance criteria. To reduce complexity, this technique may be extended to implement bio-optimization-based feature selection with transfer learning categorization.

Conflicts of interest

The authors declare no conflict of interest.

Author contributions (Mandatory)

"Conceptualization, G. Tej Varma; methodology, G. Tej Varma; software, G. Tej Varma; validation, G. Tej Varma; formal analysis, G. Tej Varma; investigation, G. Tej Varma; writing—original draft preparation, G. Tej Varma; writing—review and editing, G. Tej Varma, A. Sri Krishna;

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