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Feature Engineering and Hybrid Deep Learning for Gender Classification of *Bombyx mori* Pupae

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Abstract— *In sericulture, the gender classification of silkworm pupae is particularly important since it has an impact on the amount and the quality of silk seeds produced.This paper presents a hybrid deep learning framework that combines CNN-based feature extraction with handcrafted morphological features for gender classification of ventral silkworm pupae images. The model uses highly specific morphological features of the pupal body, such as the presence of a vertical line in female pupae and the dot-like structure in male pupae in posterior abdominal region ,the handcrafted morphological descriptors were integrated with CNN-derived deep features for binary classification.This work achieved 100% accuracy,recall, precision, and F1score on an independent test set. Statistical tests confirmed the robustness of these results: the Wilson score 95% CI for accuracy was [0.981, 1.000], the AUC was 1.00 (95% CI: [1.000, 1.000]), and the binomial test against chance yielded* $p < 0.000001$*. By combining handcrafted morphological features with CNN-derived features, the model achieved 100% accuracy in five-fold cross-validation. Five-fold stratified cross-validation further demonstrated consistency, with a mean accuracy of 1.000 ± 0.000. Additional reliability metrics (MCC, Kappa, specificity, and Brier score) consistently supported perfect agreement between predictions and ground truth. Such high accuracy is not only important from a scientific standpoint but is quite important in prac tical applications in the silk seed production process, where slight inaccuracies might result in huge economic impact and loss of yield quality.*

Keywords— *Silkworm Pupae, Gender Detection, Image Processing, Statistical Validation, CNN.*

I. Introduction

Sex identification in silkworm pupae is one of the most essential tasks in the silk seed production process (Fig. 1). The examination process of male and female pupae has to be carried out to obtain the best breeding ratios. This is crucial to ensure the best silk yield and quality silk seed is achieved. The work of sex separation is usually done manually, which appears to be tedious, takes a lot of time, and is also prone to errors. This has negative effects on the entire silk seed production process [1]. Thus, there is an increasing need for a faster, non-invasive, and more accurate method of sex classification.Although several destructive and non-destructive techniques have been explored, such as optical penetration, spectroscopy, imaging, and computer vision, relatively few reliable non-destructive methods are available for silkworm sex identification [2].

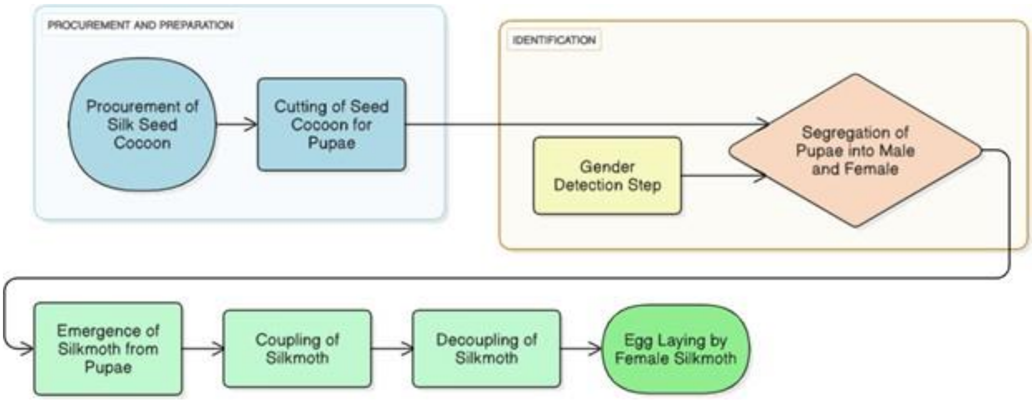

Figure 1. Basic Steps in silk seed production process

This study presents a hybrid deep learning framework for automatic gender classification of silkworm pupae. [3] .The purpose of the work is to examine the ventral side images of the pupae, focusing on the special structures found in the posterior abdominal region segments of the pupae. The primary features used for this classification include the presence of a vertical line in the center of one of these segments for females and a dot-like mark for males. The proposed model reaches an outstanding value of 100% accuracy without defects, cross-validated 5 times, demonstrating the effectiveness of the proposed approach.The information acquired on the sex of the silkworm pupae is of great importance in the course of silk seed production to ensure the proper breeding and production quality.

A. Problem Statement:

The classification of gender in silkworm pupae is critical in the silk industry for effective breeding and silk seed production. Manual inspection of these pupae is a tedious process and sensitive to human error, which requires an expert laborer for this work. Being a living material, there is a need for a non-invasive, cost-effective, and automated solution to accurately classify

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silkworm pupae based on morphological features. This proposes a hybrid deep learning that combines CNN and hand-crafted characteristics extracted from the segments of the posterior region (8th, 9th, and 10th) to classify male and female pupa with high precision.

B. Objective:

This research will combine CNN based feature extractions with morphologic features from the 8th-10th abdominal segment of silkworm pupae with the intention of creating a deep learning framework. More specifically, this research attempts to:

- The construction and execution of a hybrid CNN model that integrates deep features with biologically insightful handcrafted features with a high level of accuracy without misclassifications, which is essential in silk seed production.
- Establish rigorous and impartial performance through extensive statistical validation, which includes the binomial test, Wilson confidence intervals, McNemar's test, MCC, Kappa, Brier score, and calibration analysis.
- Demonstrate the consistency and generalizability of the model through 5-fold cross-validation.

II. Review literature

Identifying silkworm pupae genders falls under two categories: destructive and non-destructive. However, the Non-destructive method is very important with respect to live specimens as it does not cause injury. In grainage areas, observers determine the sex of silkworm pupae by finding particular marks: females are identified by a vertical line feature in the eighth segment of the abdomen, while males are identified by a dot lesion in the ninth segment. At present, mostly trained personnel carry out this sex separation, which is tedious and error prone processes. The literature review includes the creation of a T2 relaxation model aimed at differentiating the intrinsic water content of silkworm silk glands using magnetic resonance imaging. This model helped to determine the sex of silkworms due to tissue contrast [4]. Proposed the relation of enhanced optical pattern recognition in near-IR wavelength to non-destructive degree of silkworm gender determination, which was achieved through improved classification of images that included processing techniques [5]. Implemented a region of interest (ROI) approach to light classification to diminish noise interference, thus increasing image processing speed[6] .Implemented a normalized cross correlation technique that introduces cross correlation of images to help improve both image analysis and the gender determination of the silkworm. Attachment of spectra for gender identification [7].Attachment of spectra for gender prediction looked at the absorption spectra of gender differentiation and reported that green and red were the best wavelengths for sex tissues [8]. The internal and external features of the cocoons were combined in what is called count sex classification, which incorporated external methods of X rays in conjunction with decision trees such as SVM, KNN and LDA algorithms, with high accuracy being observed[9]. When using red and white multifunctional lights to obtain female pupa in dual-wavelength optical architect, it was observed that the identification efficiency was greatly improved [10]. Who offered a possibility to improve the accuracy of automatic region selection [11].Proposed a system for automatic determination of silkworm gender based on computer vision and SVM and neural networks and significantly improved silkworm breeding technologies [12]. Who studied Bombyx mori in relation to sex determination, more particularly piRNA mediated interaction [13]. Proposed a sorting system in which near infrared spectroscopy is utilized to protect the live silkworm chrysalis against disturbance by noise [14]. MLGBP with neural networks was further enhanced by introducing feature extraction based on MLGBP coupled with machine learning and increasing the precision of classification[15] [16][17]. Employing hyperspectral imaging technology[19][20].Proposed a multisensory system with weight and image data for automated sex classification employing SVM[18]Improved gender classification from a very simple but accurate light penetration method [21].Successfully used transfer learning in seed classification with a resulting precision of 99% [22]. Spectral data with over 98% precision distinguishing between male and female cocoon pupae employing algorithms including PC and LDA [23] [24].Used LDA, CNN, and SVM for gender classification employing diffuse transmission spectra from NIR and depicted the success of machine learning techniques [25] Although these methods used X-ray imaging and high accuracy female sex classification without invasive procedures using machine learning models such as AdaBoost [26] [27].Performed automated seed detection. An analysis of various techniques and classification systems to determine the appropriate sex in silkworms brought his attention to the classical manual and refinement of the machine learning technology of hyperspectral imaging, NIR spectroscopy [28].A non-destructive X-ray and GRNN-based method for precise cocoon classification, achieving 94.56% accuracy. Reduce human bias and improve fairness in estimating silk yields, benefiting the silk industry[29]. However, the approach requires specialized X-ray equipment, which may be costly for smaller producers, and its accuracy might vary with different cocoon types, warranting further validation for broader use (Table 1).

III. Research Methodology

The essential steps included in the proposed methodology are: dataset preparation, image pre-processing, extraction of regions of interest (ROI), feature extraction procedures, model architecture and development, model training and evaluation, and analysis of model interpretability (Fig. 2).

A. Dataset Preparation

The data set used for this research consists of primary data, totaling 996 ventral side images of silkworm pupae of bivoltine races P1 (SH6 and NB4D2), collected from the Silk Seed Production Center in Palampur, Himachal Pradesh, India. The data set is evenly distributed, with 498 images of male pupae and 498 images of female pupae, ensuring balanced representation for training and evaluation. All images were captured with a standard camera under ordinary light conditions.The dataset comprised 996 individual silkworm pupae (498 male and 498 female), with one ventral image acquired from each specimen.Before image acquisition, each pupa was identified by experienced sericulture experts using established ventral morphological markers. These expert annotations were used only to generate the ground-truth labels for supervised learning.No duplicate images or repeated acquisitions of the same pupa were included. Each image therefore represents a unique biological sample.

B. Image Pre-processing

Resizing and Normalization: All images were resized with 128 × 128 pixels to keep the input size constant for the CNN model. The pixels were normalized between [0, 1] as shown in Eq.1:

$$I_{norm} = \frac{I_{pixel}}{255} \tag{1}$$

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Table 1. Comparison of existing classification methods.

Technique	Advantages	Limitations
Magnetic Resonance Imaging (MRI)	Non-destructive and accurate tissue characterization	Expensive equipment and limited practical use
Near-Infrared (NIR) Spectroscopy	Rapid and non-destructive classification	Requires specialized spectroscopic instruments
X-ray Imaging	High classification accuracy with internal feature analysis	High equipment cost and radiation-based system
Hyperspectral Imaging	Rich spectral information with high accuracy	Computationally intensive and expensive
Optical Imaging	Simple, non-invasive image acquisition	Sensitive to illumination variations
Classical Machine Learning (SVM, KNN, LDA, ANN)	Effective with handcrafted features and moderate datasets	Performance depends on feature engineering
Deep Learning (CNN, Transfer Learning)	Automatic feature extraction with high classification performance	Requires large annotated datasets and higher computational resources
Proposed Hybrid CNN Framework	Combines deep features with biologically meaningful ventral morphological features for robust non-destructive gender classification under ordinary natural daylight conditions	Requires validation on larger datasets acquired under diverse environmental conditions

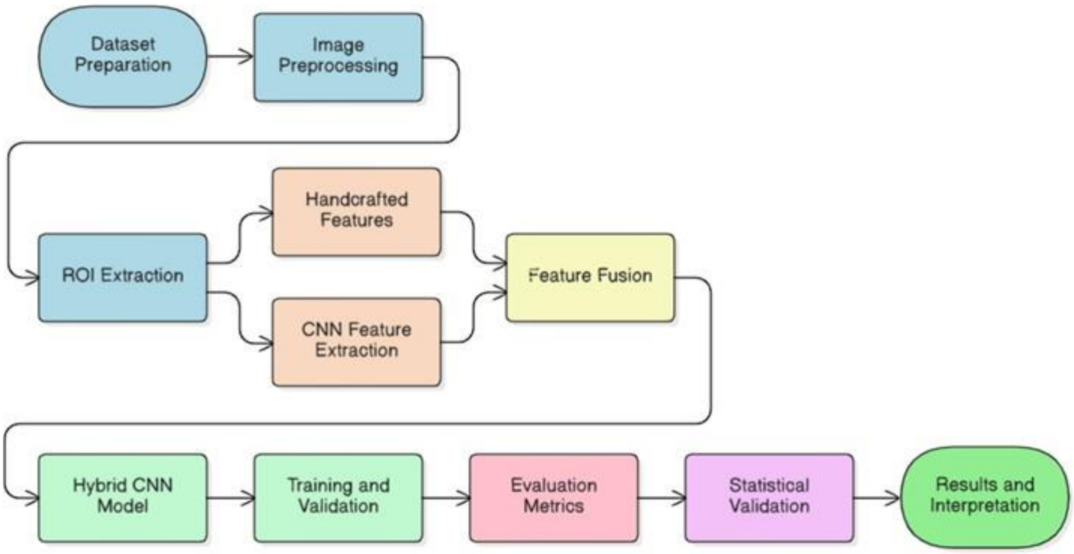

Figure 2. Various steps in the methodology

where I_{norm} is the normalized pixel intensity and I_{pixel} is the original pixel value.

C. Region-of-Interest (ROI) Extraction

An ROI was created to include the eighth, ninth and 10th body segments of the pupae, where distinguishing features were noticeable. Female pupae exhibit a vertical line in one of these segments, whereas male pupae show a dot. The extraction was performed using Equation:

$$ROI = I[start_y : end_y, :] \tag{2}$$

where $start_y = height - (segment\ height \times 3)$ and $end_y = height$. The segment height is defined as:

$$segment\ height = \frac{height}{10} \tag{3}$$

The bottom 30% of the normalized ventral image corresponds to the posterior abdominal region containing the 8th–10th abdominal segments.

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D. Feature Extraction

Two types of features were extracted from the ROI: handcrafted features and CNN-based features.

Handcrafted Features The handcrafted feature extraction stage was developed based on the characteristic ventral morphological markers of Bombyx mori pupae. Hu Moments were used to quantify the dot-like morphological feature, while the Vertical Line Feature was computed using the mean absolute variation of grayscale pixel intensities. These handcrafted descriptors were integrated with CNN-derived deep features to improve the discriminative capability of the proposed hybrid framework.

$$Hu\_Moments = cv2.HuMoments(cv2.moments(gray\_roi)).flatten()[0] \tag{4}$$

where $gray\_roi$ is the grayscale version of the ROI.

$$Vertical\_Line\_Feature = \frac{1}{n}\sum_{i=1}^{n}\sum_{j=1}^{m-1} |I_{gray}[i,j] - I_{gray}[i,j+1]| \tag{5}$$

I_{gray} is the ROI in grayscale, i, j are the pixel indices, n is the number of row pixels.

Feature Extraction Using CNN: Feature maps were developed using a CNN with convolution, grouping, and fully connected layers. The output of each convolutional layer $O^{(l)}$ was calculated as:

$$O^{(l)} = \sigma(W^{(l)} * I^{(l-1)} + b^{(l)}) \tag{6}$$

$W^{(l)}$ is the weight matrix, $I^{(l-1)}$ the input to the l^{th} layer, $b^{(l)}$ is bias and the convolution operation $*$, and σ is the ReLU activation:

$$\sigma(x) = \max(0, x) \tag{7}$$

The pooling was performed as follows:

$$P^{(l)} = \max(O^{(l)}[i : i+2, j : j+2]) \tag{8}$$

E. Model Development

The proposed hybrid framework combines biologically meaningful handcrafted morphological descriptors with CNN-derived deep features. Handcrafted features capture expert-defined anatomical characteristics, while CNN features learn hierarchical image representations. Their integration provides a more comprehensive feature representation for gender classification. Hybrid CNN model: A hybrid model was designed in which individual features and features of the CNN model were integrated. The features of the CNN deep architecture and the handcrafted features were done in the following manner.

$$Combined\_Features = Concatenate(x, y) \tag{9}$$

$$P(y|F) = \frac{1}{1 + \exp(-W^T F + b)} \tag{10}$$

Where F is the concatenated vector of features.

F. Model Training and Evaluation

The proposed hybrid CNN model was implemented using TensorFlow/Keras. The input images were resized to 128 × 128 pixels. The dataset was divided into training and testing sets using an 80:20 train–test split with random state = 42. The model was trained for 20 epochs with a batch size of 32 using the Adam optimizer and binary cross-entropy as the loss function. Model performance was evaluated using accuracy, precision, recall, F1-score, ROC–AUC, confusion matrix, ROC curve, and Precision–Recall curve.

$$L = -\frac{1}{N}\sum_{i=1}^{N}\left(y_i \log(p_i) + (1 - y_i)\log(1 - p_i)\right) \tag{11}$$

p_i is hypothetical probability, y_i is the reference target, and N is the number of instances. The metrics included accuracy, Precision, Recall, F1, ROC-AUC:

$$Accuracy = \frac{TP + TN}{TP + TN + FP + FN} \tag{12}$$

$$Precision = \frac{TP}{TP + FP} \tag{13}$$

$$Recall = \frac{TP}{TP + FN} \tag{14}$$

$$F1 = \frac{2 \times (Precision \times Recall)}{Precision + Recall} \tag{15}$$

$$AUC = \int_0^1 TPR(FPR)\, dFPR \tag{16}$$

where (TPR) true positive rate and (FPR) false positive rate.

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G. Statistical Validation and Robustness Testing

To ensure reliability and rule out chance-level classification, multiple statistical tests were employed.
Binomial Test: Significantly exceeded the chance level (p = 0.5):

$$p = \sum_{k=x}^{n} \binom{n}{k} (0.5)^k (0.5)^{(n-k)} \tag{17}$$

where x is the number of correct predictions from n trials.
Wilson CI for Accuracy: The 95% confidence interval for classification accuracy was calculated using the Wilson score method:

$$CI = \frac{\hat{p} + \frac{z^2}{2n} \pm z\sqrt{\frac{\hat{p}(1-\hat{p})}{n} + \frac{z^2}{4n^2}}}{1 + \frac{z^2}{n}} \tag{18}$$

$\hat{p}$ observed precision, n sample size, and z critical value.
McNemar's Test: Used to check disagreement between predicted and actual labels:

$$\chi^2 = \frac{(|b-c|-1)^2}{b+c} \tag{19}$$

b number of instances misclassified as positive instead of negative, and c vise versa.
Matthews Correlation Coefficient (MCC):

$$MCC = \frac{TP \times TN - FP \times FN}{\sqrt{(TP+FP)(TP+FN)(TN+FP)(TN+FN)}} \tag{20}$$

Cohen's Kappa:

$$\kappa = \frac{p_o - p_e}{1 - p_e} \tag{21}$$

p_o observed agreement and p_e expected agreement by chance.
Youden's J:

$$J = Sensitivity + Specificity - 1 \tag{22}$$

Brier Score: The calibration of the predicted probabilities was assessed using the Brier score.

$$Brier = \frac{1}{N}\sum_{i=1}^{N}(f_i - o_i)^2 \tag{23}$$

f_i predicted probability and $o_i \in \{0, 1\}$ true result.
Cross-Validation Accuracy:

$$Acc_{cv} = \frac{1}{k}\sum_{i=1}^{k} Acc_i \tag{24}$$

Statistical analysis was performed to complement the evaluation of the proposed framework. Standard performance metrics, including Accuracy, Precision, Recall, F1-score, ROC-AUC, MCC, Cohen's Kappa, Specificity, Youden's Index, and Brier Score, were used together with confidence intervals. McNemar's test is described as a comparative test for classifier performance and interpreted within its appropriate scope.

H. Hardware and Software

A system featuring a 12th genIntel® Core™ i5-12450H processor, 16 GB RAM, and 64-bit Windows OS. Python 3.12.4 was used for the implementation, and a standard digital camera was used for image capture.

IV. Results

A hybrid CNN model was investigated to determine the gender of silkworm pupae from a data set of 996 images of the ventral-side. Half of the images were labeled male and the other half female, with 498 samples each. The performance of the model was evaluated using several approaches.

A. Model Performance Evaluation

(Table 2) There is an absolute male and female pupae classification reached accuracy of 100 in precision, recall, F1 which means that there is no wrong classification. The ROC-AUC score of 1.00 also helps to support the usefulness of the model.
Confusion Matrix: The confusion matrix (Table 3, Fig. 3) confirms that all male and female pupae were correctly classified. This indicates zero misclassification errors.
Figure 4, Visualization of the classification results, which shows a clear separation between male and female pupa.

Table 2. Performance Metrics

Metrics	Value
Accuracy	100%
Precision	1.00
Recall	1.00
F1-Score	1.00
ROC-AUC Score	1.00

Table 3. Confusion Matrix

	Predicted Male	Predicted Female
Actual Male	99	0
Actual Female	0	100

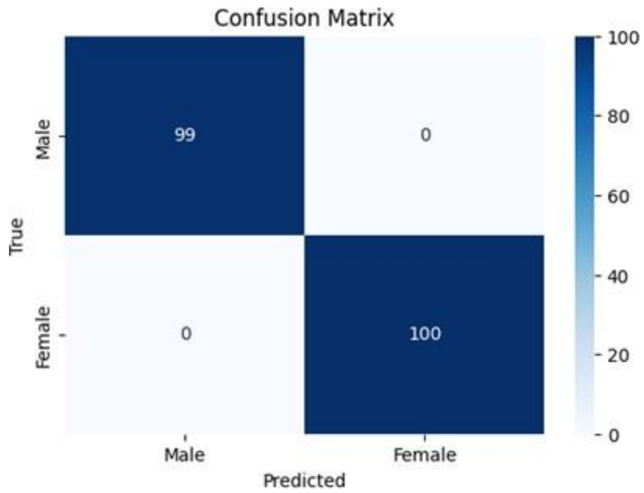

Figure 3. Confusion Matrix

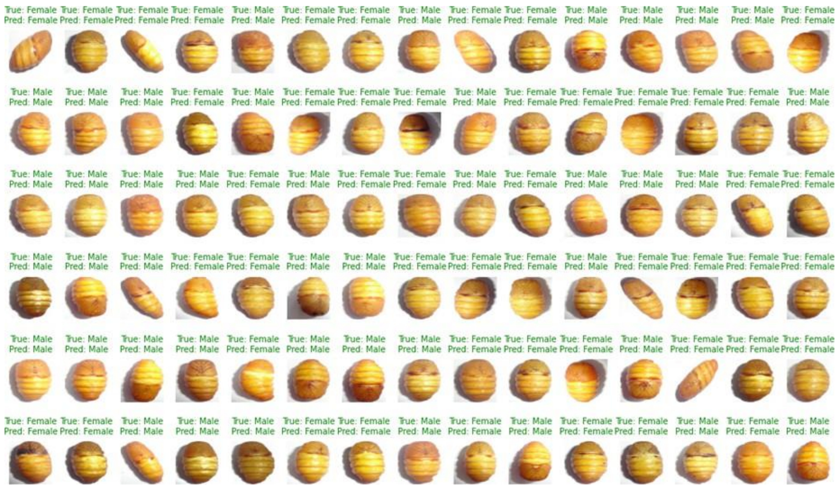

Figure 4. Silkworm Pupae Gender Classification Results

B. ROC Curve

The ROC curve (Fig. 5) confirms that the model achieved an AUC of 1.0, indicating perfect discrimination.

C. Precision–Recall Curve

Fig. 6 shows that the model maintained consistently high precision and recall values across thresholds.

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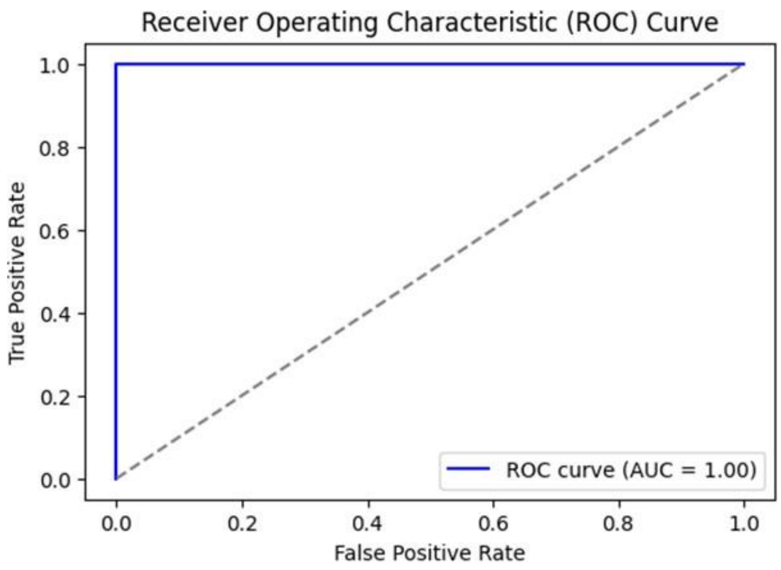

Figure 5. ROC Curve with AUC of 1.0 for the hybrid CNN model

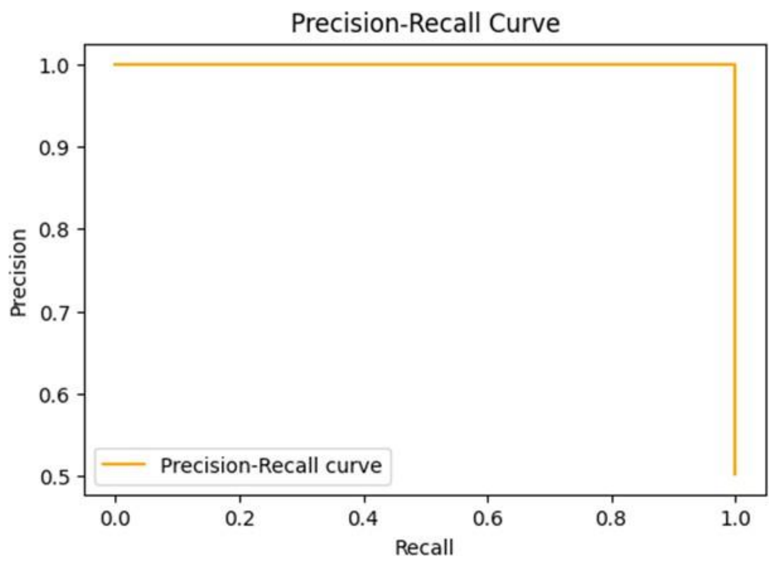

Figure 6. Precision–Recall Curve with perfect values for the hybrid CNN model

D. K-Fold Cross Validation

To validate robustness, the model consistently achieved 100% accuracy in all folds (Table 4, Fig. 7).

E. Training and Validation Curves

Figure 8 shows that the model achieved maximum accuracy with minimal loss within 20 epochs, confirming the optimal fitting. The description of the training curves has been revised to improve the interpretation of the reported accuracy and loss during model training.

F. Histogram of Predicted Probabilities

Figure 9, The model demonstrated high confidence, with clear separation between male and female predictions.

G. Residual Analysis

The residual plots (Fig. 10) show the differences between the actual and predicted probabilities. The residuals were negligible, confirming strong reliability.

H. Calibration Analysis

(Fig. 11)The predicted probabilities represent the confidence of the proposed model for the dataset used in this study, which was collected under ordinary natural daylight conditions. Therefore, the probability plots should be interpreted only within the scope of the present dataset and should not be considered a complete evaluation of probability calibration.

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Table 4. Five-Fold Cross-Validation Accuracy

Fold	Accuracy (%)
1	100.00
2	100.00
3	100.00
4	100.00
5	100.00

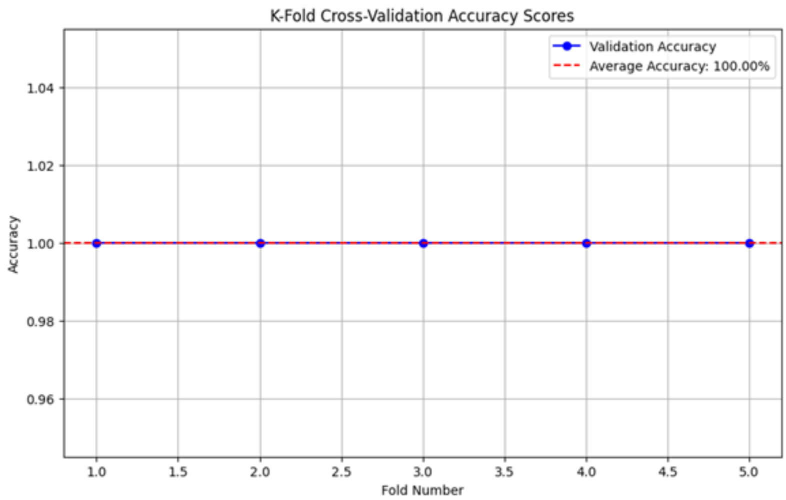

Figure 7. Fold-wise accuracy representation

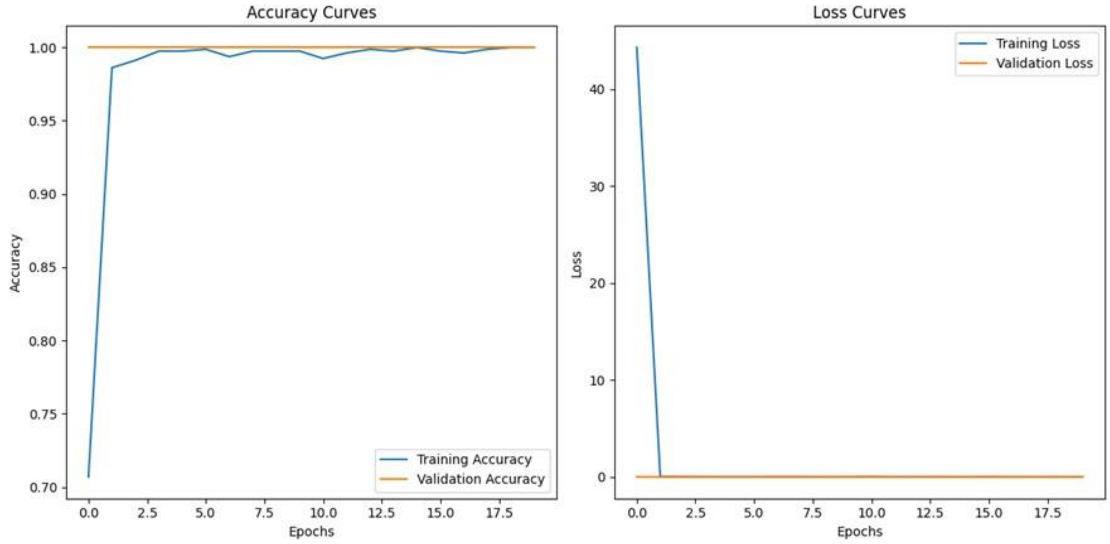

Figure 8. Training and validation accuracy and loss curves

I. Statistical Significance and Robustness Analysis

The statistical evaluation supports the consistency of the proposed framework. However, statistical tests such as McNemar's test become less informative when classification performance approaches perfect agreement. Therefore, the primary conclusions are based on standard performance metrics and cross-validation results.

- The binomial test vs. random guessing confirmed the significance with $p < 0.000001$ (199/199 correct predictions).
- Wilson score 95% CI for accuracy = [0.981, 1.000].
- Bootstrapped 95% CI for AUC = [1.000, 1.000].
- McNemar's test yielded $p \approx 5.96 \times 10^{-8}$, which confirmed that there is no disagreement between the predictions and the truth of the ground.
- Reliability indices: MCC = 1.000, Cohen's Kappa = 1.000, Specificity = 1.000, NPV = 1.000, Youden's J = 1.000.
- Calibration analysis: Brier score = 0.0000.

These results confirm that the performance of the model is not an artifact of overfitting or random chance, but reflects the genuine discriminative power of morphological features in the abdominal segments of the silkworm pupae.

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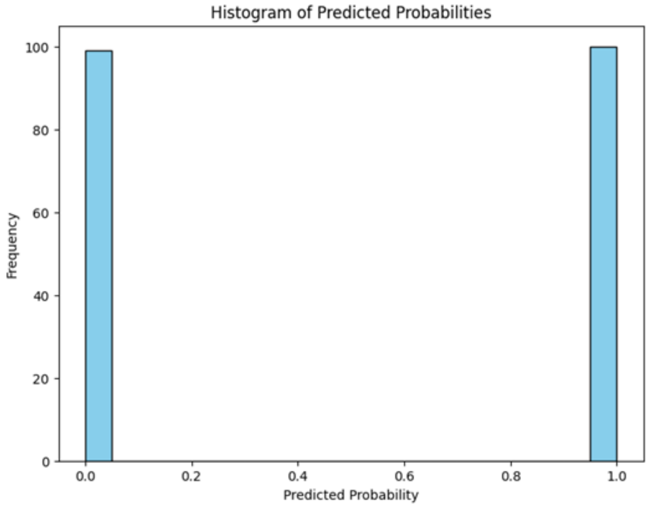

Figure 9. Histogram of predicted probabilities for male and female classification

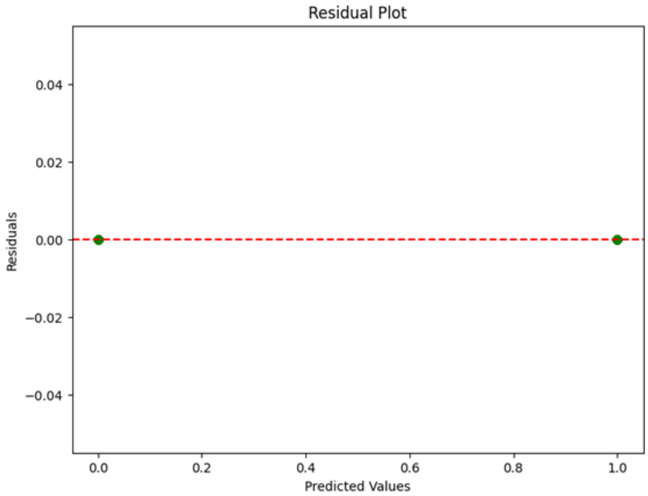

Figure 10. Residual plot with insignificant probability residuals

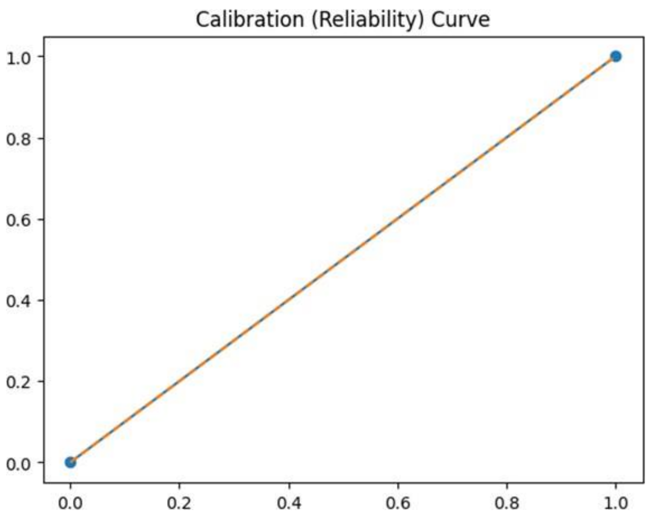

Figure 11. Calibration curve demonstrating reliability of predicted probabilities

V. Discussion

Different methods have been used for the classification of silkworm pupae and cocoons, each with unique strengths and limitations. Magnetic resonance imaging (MRI) and T2-weighted imaging, although highly accurate, are expensive and

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suitable primarily for laboratory-based sex determination. Optical penetration and Near-IR techniques are faster, but are prone to scattering and noise, making them better suited for rapid classification tasks. Normalized Cross-Correlation (NCC) pattern matching offers reasonable speed but relatively low accuracy, whereas spectral imaging provides high precision under controlled conditions, but is constrained by wavelength limitations. X-ray imaging, when coupled with PCA or AdaBoost, allows non-invasive classification inside cocoons but requires costly equipment. Methods such as Zernike moments with SVM offer shape-based classification but involve complex feature extraction. The proposed hybrid deep learning model overcomes several of these limitations by integrating CNN-derived deep features with handcrafted morphological descriptors (Hu Moments and the Vertical Line Feature) extracted from the ventral tail segments (8th–10th). Statistical validation established the robustness of the model: the binomial test indicated significance ($p < 0.000001$), Wilson 95% CI for accuracy was [0.981, 1.000], and the bootstrapped CI for AUC was [1.000, 1.000]. Reliability indices such as MCC (1.000), Cohen's Kappa (1.000), specificity (1.000), NPV (1.000), Youden's J (1.000) and the Brier score (0.0000) further confirmed unbiased calibration and reliability. The Five-fold stratified cross-validation yielded consistent performance (mean accuracy = 1.000 ± 0.000), confirming generalizability and eliminating concerns of overfitting. These findings demonstrate that the model is non-invasive, reliable, and inexpensive, making it practical for sericulture where sex determination is critical for breeding ratios and seed quality. Although this study focuses on *Bombyx mori* pupae under standard lighting conditions, limitations include sensitivity to pose, orientation, and environmental variability. Despite this, the strong reliability of the baseline provides a foundation for future work, including adaptation to diverse environmental conditions, incorporation of transfer learning for other architectures, and application to other economically important insect species. This work highlights that hybridizing deep learning with biologically meaningful handcrafted features, combined with thorough statistical validation, results in a practical silkworm pupae sex classification framework of direct relevance to sericulture.

VI. Future Scope and Challenges

The proposed framework was evaluated under normal daylight conditions using a single-centre dataset. Validation on datasets collected from different centres, silkworm races, and imaging conditions will be considered in future work. Future research directions can focus on several key areas to achieve further improvement and better applicability of the proposed model. To begin with, generalization could be improved by applying transfer learning methods using architectures such as VGG16, ResNet, and Dense Net. Second, the creation of such a model for silk seed producers, which features an automated classification for real-time action, would simplify the classification and increase its relevance in the practical aspect of the model. This could include a graphic application for the users where they can take photographs as well as send photographs for classification by the breeders and get results instantly. Third, the ability of the model could be expanded to include the classification of economically important insect pupa of different species. Finally, the attention of researchers to the study of new other morphological features such as body size and color patterns might result in increased reliability in classification. All strategies would aim to improve automated sex determination in sericulture and related industries. All images were captured in standard daylight conditions; therefore, the reliability of the model under variable lighting or orientation remains to be validated. Addressing these factors in future work will be essential for real-world deployment at the industrial scale.Future work will focus on validating the proposed framework using multi-centre datasets collected under diverse environmental conditions.Future studies will include comparisons with CNN and handcrafted-feature approaches to further evaluate the contribution of each component.The limitations of applying certain statistical tests under near-perfect classification performance have been acknowledged to provide a balanced interpretation of the reported results.A more detailed evaluation of probability calibration requires testing on larger datasets collected under different lighting and environmental conditions. This remains an area for future investigation.Future work will focus on developing benchmark datasets and additional implementation resources to facilitate independent validation and comparative evaluation.Future studies will include a comprehensive comparison of the proposed framework with recent deep learning architectures, including ResNet50, DenseNet, EfficientNet, MobileNetV3, and Vision Transformer (ViT).Future work will focus on improving computational efficiency, validating the framework under diverse imaging conditions, and evaluating its deployment in practical sericulture applications.

VII. Conclusion

This study designed a hybrid deep learning architecture that integrates CNN-based feature extraction with handcrafted morphological descriptors for non-invasive sex classification of silkworm pupae. This work achieved 100% accuracy,recall,precision, F1-score, and ROC-AUC. Statistical significance was confirmed through the binomial test ($p < 0.000001$), Wilson 95% CI for precision ([0.981, 1.000]) and bootstrapped CI for AUC ([1.000, 1.000]). Additional validation through MCC (1.000), Cohen's Kappa (1.000), specificity (1.000), NPV (1.000), Youden's J (1.000) and a Brier score of 0.0000 confirmed its reliability and robustness. The Five-fold cross-validation (mean accuracy = 1.000 ± 0.000) provided additional evidence of consistency.The proposed framework is statistically reliable, non-destructive, and cost-effective, making it highly suitable for use in silk seed production. If validated further under field conditions, this approach can significantly improve sex classification, breeding efficiency, and seed quality in sericulture. Furthermore, the methodology paves the way for extending hybrid deep learning approaches to other insect classification problems and applications in agriculture.

VIII. Declarations

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Conflicts of Interest: There are no conflicts of interest.
Consent for Publication: Both authors have given their consent for this publication . All necessary ethical approvals have been obtained for the use of the materials involved in this study.
Data availability: The data set used in this is not publicly available. The datasets generated during the current study are available from the corresponding author upon reasonable request.
Materials Availability: The research materials used in this study were obtained from the Silk Seed Production Center,

Palampur, Kangra District, Himachal Pradesh, India.

Authors Contributions: Jyoti Sharma: conceptualization, methodology, software, data curation, investigation, validation, formal analysis, visualization, resources, original draft writing, review and editing. **Pradeep Chouksey:** conceptualization, methodology, data curation, investigation, validation, formal analysis, supervision, visualization, project administration, resources.

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