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Automated Disease Detection in Silkworms Using Machine Learning Techniques

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Abstract. Silkworm diseases pose a major threat to the sericulture industry, with early detection remaining a challenge due to limited infrastructure. This study focuses on detecting Grasserie disease, which can rapidly spread in silkworm rearing units, leading to significant economic losses. A novel dataset of 668 healthy and 574 Grasserie-affected silkworm images forms the basis of this research. The study applies machine learning techniques, using the Histogram Oriented Gradient (HOG) feature descriptor combined with Kernel Principal Component Analysis (KPCA) and supervised classifiers. The integration of Support Vector Machines (SVM) with HOG and KPCA achieved high accuracy (93.16%), recall (93.38%), and precision (91.94%), offering a faster, more accurate alternative to manual detection methods. This approach holds great potential for developing real-time, IoT-based diagnostic tools that enable farmers to quickly identify infected silkworms, reducing disease spread and economic losses, and can be extended to other agricultural applications requiring early disease detection.

Keywords: Automated Detection, Computer Vision, Disease Classification, Image Processing, Sericulture, Grasserie, Machine learning.

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1. Introduction

Sericulture, the art and science of silk production, has a rich history that dates back thousands of years. Among the various species of silk-producing insects, Bombyx mori, commonly known as the silkworm, has been the primary focus of sericulture due to its exceptional ability to produce high-quality silk [1, 2]. The process of rearing silkworms and cultivating silk, known as sericulture, has played a significant role in the socio-economic development of numerous regions worldwide. One such region renowned for its long-standing tradition of sericulture is South India, where the climate and conducive environment have fostered the thriving growth of the Bombyx mori species. The life cycle of silkworms is a fascinating and intricate process that comprises several distinct stages, each crucial to the production of silk [3]. Understanding this lifecycle is essential for successful sericulture. The typical life cycle of a silkworm can be divided into four main stages: egg, larva (caterpillar), pupa (cocoon), and adult moth [4, 5]. While sericulture has been a source of livelihood and cultural heritage in South India, it has faced challenges over the years, with one of the most detrimental being the outbreak of grasserie disease in silkworms. In recent times, the advent of machine learning methods has opened up new avenues for the early detection and control of grasserie disease, revolutionizing the sericulture industry [5-7].

Among the various challenges faced in sericulture, one of the most detrimental diseases affecting silkworms is grasserie disease [8]. Grasserie, caused by Bombyx mori nuclear polyhedrosis virus (Bm NPV), a baculovirus, is a highly contagious and devastating infection that poses a significant threat to the silkworm population [8-10]. When infected with Bm NPV, silkworm larvae experience severe pathology, leading to symptoms such as lethargy, loss of appetite, sluggish movement, and a failure to spin proper cocoons [11]. The disease's symptoms do not become evident until several days have passed. Initial indications start to manifest approximately 5 to 7 days after infection. During the early stages of infection, the silkworm's skin takes on a shiny and fragile appearance, and the larvae experience difficulties in the moulting process. As the infection progresses, the intersegmental areas swell, causing the larvae to move around restlessly on their rearing tray or rack. Additionally, the haemolymph (the insect's blood) becomes cloudy and milky white, containing a substantial number of hexagonal polyhedra, while the silkworm's outer covering becomes susceptible to easy ruptures [12-14]. The virus can spread rapidly within the silkworm rearing units and can cause significant economic losses in the sericulture industry. Additionally, infected silkworms may also exhibit abnormal spinning behavior, resulting in the production of weak and low-quality cocoons. The rapid spread of grasserie disease within silkworm rearing units can decimate entire populations, leading to considerable financial repercussions for sericulturists and impacting the silk industry on a larger scale. As the prevention and early detection of grasserie disease remain vital for sustaining the sericulture industry, novel approaches utilizing machine learning methods hold promise in combating this formidable threat and safeguarding the silk production process.

As of the current state of the sericulture industry, the detection of Grasserie disease in silkworms primarily relies on conventional methods that involve manual inspection and visual assessment by experienced sericulturists [15, 16]. These methods are time-consuming, labor-intensive, and subjective, which can lead to inconsistent results and delayed diagnosis. Sericulturists closely monitor the behavior and appearance of silkworms during their growth stages, looking for telltale signs of infection such as reduced appetite, abnormal spinning, and lethargy [17]. Furthermore, microscopic examination of infected silkworm tissues, including gut and excreta, can provide insight into the presence of nuclear polyhedrosis virus, confirming the occurrence of the disease [18]. However, these traditional diagnostic approaches may not always be reliable, especially when dealing with early-stage infections or subtle manifestations of the disease. As the sericulture industry faces the ongoing threat of Grasserie disease and its detrimental impact on silk production, researchers are exploring advanced approaches, including molecular diagnostics and machine learning-based systems, to develop more efficient and reliable detection methods for timely intervention and effective disease management.

Despite the critical importance of early detection and control of Grasserie disease in sustaining the sericulture industry, current methods rely heavily on manual inspection and visual assessments, which are time-consuming, subjective, and often insufficient for identifying early-stage infections. There is a clear need for more reliable, efficient, and scalable diagnostic techniques that can overcome these limitations. This study addresses this gap by applying, the HOG feature descriptor integrated with KPCA and SVM to detect Grasserie disease in silkworms using camera images. The novel use of these machine learning techniques demonstrates a significant advancement over traditional methods, offering a more accurate, rapid, and objective approach to disease detection, and paving the way for developing practical IoT-based tools for real-time monitoring in sericulture.

2. Materials and Methods

The process for detecting Grasserie disease in Bombyx mori silkworms through image analysis begins with the collection of samples. These samples are photographed using a mobile camera, and the resulting images are saved on a computer for subsequent steps. The acquired images undergo preprocessing to eliminate any noise or unwanted elements. Following this preprocessing step, relevant features are extracted from the silkworm images. To simplify and streamline the data, dimensionality reduction techniques are applied. Finally, the reduced feature matrix is inputted into machine-learning algorithms to identify and detect the presence of the disease. In our work, we present a robust framework designed for the identification of Grasserie diseases in silkworms. Emphasizing the significance of deep and high-dimensional features, these attributes play a crucial role in the accurate detection and characterization of diseases in silkworm populations.

2.1. Sample Collection and Image acquisition

This study utilized a double hybrid variety of silkworm known as FC1 x FC2 double hybrid silkworm. In the southern region of India, CSR (Central Sericultural Research) hybrids FC1 (CSR6 x CSR26) and FC2 (CSR2 x CSR27) are commonly employed to create these double hybrids, which are known for their resilience, higher productivity, and ability to thrive in various climatic conditions. The research collected samples from farmers located in Namakkal district within the Tamil Nadu state of India. These samples were specifically obtained from silkworm rearers authorized by the sericulture department. In total, 1242 samples were gathered for this study, consisting of 668 healthy silkworms and 574 silkworms affected by Grasserie disease. Initially, the differentiation between diseased and healthy silkworms was carried out in collaboration with experienced farmers.

Starting from the fifth day following infection, an expert meticulously inspected each infected silkworm individually, identifying and selecting them as diseased samples. The process of capturing images took place within a single day, and the photographs of the silkworms were taken using a Samsung Galaxy S20 FE smartphone equipped with a 12-megapixel camera. The smartphone was positioned at a height of 30 cm above the silkworms, with a tripod ensuring that the camera lens pointed downward and that the silkworms maintained their natural posture. To maintain the silkworms' original body shape after resizing the images, the aspect ratio of the capture device's screen was set to 1:1. The silkworms were placed on a black background. Figure 1a and 1b shows the images of a diseased and healthy silkworm respectively.

Figure 1. (a) Diseased silkworm (b) Healthy silkworm

Preprocessing is a critical step in preparing the collected images for analysis. Initially the original images were cropped to focus on the region of interest, eliminating any irrelevant background areas that could interfere with feature extraction. The cropped images were then resized to a standard resolution of 640 × 480 pixels, ensuring uniformity across the dataset while preserving the aspect ratio to maintain the silkworms' natural proportions. A binary segmentation process was then employed to distinguish the silkworm from the background. This involved converting the images to a binary format where the silkworm was represented in white pixels and the background in black. This step was crucial to remove any extraneous noise, such as shadows or reflections, and to create a clean input for feature extraction. Each image was converted to grayscale to simplify the data and focus on essential structural features, which are more informative for detecting disease-related patterns than color information. Grayscale images reduce computational complexity by decreasing the number of channels from three (RGB) to one, making subsequent processing steps faster and less resource-intensive.

To ensure consistency in feature extraction, the pixel values were normalized to a standard scale (typically between 0 and 1). Normalization helps in enhancing the convergence rate during training by eliminating variations in lighting conditions and ensuring that all images contribute equally to the training process. Finally, to address the potential issue of limited data and to improve the generalization capability of the model, data augmentation techniques such as rotation, flipping, and scaling were applied to artificially expand the dataset. This step helps prevent overfitting by ensuring the model is exposed to a variety of scenarios, making it more robust to real-world variations.

2.2. Feature Extraction

Feature extraction is the process by which relevant information is distilled from the silkworm images to create a set of distinctive attributes that characterize the visual aspects of the silkworms. These features can include details such as texture, color, shape, and various other visual characteristics. Extracting these informative features is fundamental to our approach as it enables us to transform complex image data into a format that machine learning algorithms can readily analyze [19]. The efficacy of our disease detection model greatly depends on the selection and quality of these extracted features, allowing us to accurately differentiate between healthy and diseased silkworms, contributing to the advancement of silkworm health management in sericulture practices. We have used the feature extraction method Histogram Oriented Gradient (HOG).

Histogram Oriented Gradient (HOG) stands as a pivotal feature extraction technique employed for addressing object identification challenges within the realm of computer vision. Initially introduced by Robert K. McConnell, this concept gained significant prominence when researchers Navneet Dalal and Bill Triggs demonstrated its high-accuracy capabilities for human detection [12]. HOG's advantage in object identification is rooted in its utilization of gradient magnitude and orientation to characterize objects. The HOG feature extraction process comprises several key steps.

To begin, the original image, as seen in figures 2.a and 3.a, with dimensions 640 × 480, istransformed into grayscale and resized to 128x64, as depicted in figures 2.b and 3.b, to enhance the quality of results. Subsequently, the gradients of this resized image are calculated using equations 1 and2 given below.

$$G_x(r,c) = I(r,c+1) - I(r,c-1) \qquad (1)$$

$$G_y(r,c) = I(r-1,c) - I(r+1,c) \qquad (2)$$

Where $G_x$is the gradient in x direction and G_y is the gradient in the y direction, r and c refer to the rows and columns respectively, I is the intensity value of a pixel.

Once G_x and G_y have been determined, magnitude and orientation are computed using equations 3 and 4. Figures 2.c, 3.c, 2.d, and 3.d represent the magnitude and orientation of these gradients.

$$Magnitude(\mu) = \sqrt{G_x^2 + G_y^2} \qquad (3)$$

$$Angle\ (\theta) = |tan^{-1}(\frac{G_y}{G_x})| \qquad (4)$$

The next step involves dividing the magnitude and angle arrays into 8x8 blocks. The gradient angle is partitioned into nine bins, each with a step size (Δθ) of 20 degrees. Bin boundaries [Δθ.j, Δθ.(j+1)] are established for each bin, with its center, denoted as c_j, given by equation 5. For each angle value (θ), magnitude values are assigned to the corresponding bins using equations 6, 7, and 8.

$$c_j = \Delta\theta.(j + 0.5) \qquad (5)$$

$$j = \lfloor \frac{\theta}{\Delta\theta} - \frac{1}{2} \rfloor \qquad (6)$$

$$V_{j+1} = \mu.[\frac{\theta}{\Delta\theta} - \frac{1}{2}] \qquad (7)$$

$$V_{j+1} = \mu.[\frac{\theta - c_j}{\Delta\theta}] \qquad (8)$$

The Histogram of the HOG feature descriptor is computed for 8x8 patches of the image. Each cell within the patch contains 9x1 values. Subsequently, four 9x1 blocks are combined to create new 2x2 blocks, each comprising 36 features. The values in these feature blocks are then normalized using the L2 norm, as specified in equation 9, with the inclusion of a small value (ε) to prevent zero division error.

$$f_b = \frac{f_b}{\sqrt{||f_b||^2 + s}} \qquad (9)$$

In the end, the final feature vector for an image consists of 7x15x36, resulting in a total of 3780 features. The conclusive visualization of the HOG feature is presented in Figures 2e and 2e.

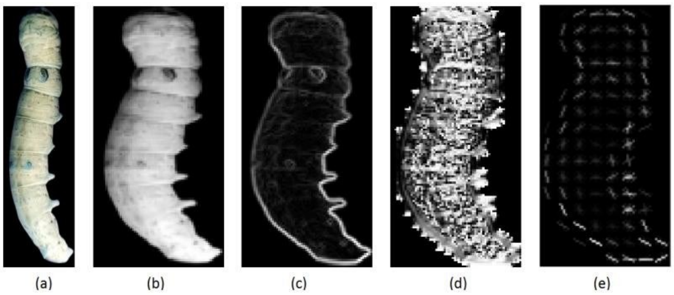

Figure 2. HOG feature descriptor of infected silkworm a) Original Image b) resized image c) magnitude visualization d) orientation visualization e) HOG feature descriptor

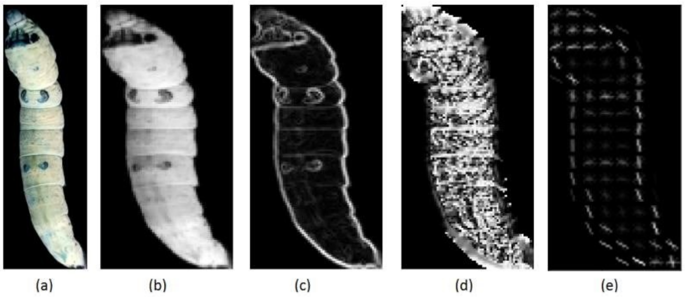

Figure 3. HOG feature descriptor of healthy silkworm a) Original Image b) resized image c) magnitude visualization d) orientation visualization e) HOG feature descriptor

2.3. Dimensionality reduction

Following the HOG feature extraction phase, the subsequent critical step is dimensionality reduction. In this context, dimensionality reduction techniques play a pivotal role in optimizing the effectiveness and efficiency of our machine learning model. The feature vectors derived from the HOG descriptors are typically high-dimensional, containing a multitude of components. However, this abundance of features can lead to increased computational complexity and may even introduce noise into the analysis.

Dimensionality reduction methods are employed to address these challenges by selecting a subset of the most informative features while reducing the overall dimensionality of the data. This not only streamlines the model's training process but also helps prevent overfitting, ultimately enhancing the model's ability to discern between healthy and diseased silkworms with improved accuracy and reliability. In this work, kernel principal component analysis (KPCA), is used.

KPCA is an extension of principal component analysis (PCA) that addresses non-linear data relationships. It employs a kernel trick, which transforms the data into a higher-dimensional space, where a linear PCA can then be applied. KPCA allows for the capture of complex, non-linear relationships among data points [19]. KPCA starts by selecting an appropriate kernel function (e.g., polynomial, radial basis function) to map the data into a higher-dimensional space. In this space, linear PCA is applied to reduce dimensionality. The resulting principal components are then projected back into the original space. KPCA is used in various fields, such as image processing, food quality analysis, and medical diagnosis, where non-linear patterns need to be extracted from high-dimensional data.

2.4. Classification

The classification algorithm, support vector machine (SVM) is used in this work.

SVM is a supervised classification method used for both linearly separable and non-separable datasets. Its primary aim is to identify the optimal hyperplane that effectively distinguishes between different classes. To achieve this, SVM seeks to maximize the margin, which is the distance between the support vectors (the data points closest to the hyperplane) and the hyperplane itself [20]. The overarching objective in finding this optimal hyperplane is to enhance the separation between classes by maximizing the minimum distance. The distance from a data point (x_0 ,y_0) to the hyperplane is obtained by

$$d_H(\Phi(x_0)) = \frac{|w^T(\Phi(x_0))+b|}{\|w\|_2} \qquad (10)$$

Where $\Phi(x_0)$ represents the point vector, w stands for the weight vector, b is the bias term, and $\|w\|_2$ represents the Euclidean norm. The objective at hand is to optimize the hyperplane's minimum distance, specifically by maximizing the distance to the support vector from the hyperplane.

$$w* = \underset{w}{argmax}[min_n\, d_H(\Phi(x_n))] \qquad (11)$$

Where $w*$ weight vector for the optimum hyperplane, $\Phi(x_n)$ is the minimum distance data point.

The decision is based on the hyperplane, and when dealing with non-linear data, a kernel function is employed to project the data points into a higher-dimensional space.

$$K(X,Z) =< \phi(X), \phi(Z) > \qquad (12)$$

In this context, the kernel function, denoted as K, takes inputs X and Z in an n-dimensional space, while ϕ is a function responsible for mapping data from n dimensions to m dimensions. The kernel function essentially takes data from the initial feature space and transforms it into the target feature space. Many research studies have commonly utilized the RBF (Radial Basis Function) kernel because it offers computational efficiency, particularly in high-dimensional spaces [18-20].

2.5. Validation

To ensure the reliability and generalizability of the proposed machine learning model for detecting Grasserie disease in silkworms, a robust validation strategy was employed. The dataset was randomly partitioned into training and testing subsets using an 80/20 split, where 80% of the data was used for training the model and 20% for testing. Cross-validation, specifically 10-fold cross-validation, was performed to further evaluate the model's performance.

Potential biases in this study could arise from several sources, including the sample collection process, the imaging technique, and the choice of features. For instance, since the silkworm samples were collected from a specific geographical region (Namakkal district in Tamil Nadu, India), the model might not fully capture the variability present in silkworm populations from other regions or countries, potentially limiting its generalizability. Additionally, the use of a single camera type and fixed image acquisition settings could introduce biases related to lighting conditions, camera angle, and background, affecting the model's robustness in different real-world scenarios. To address these potential biases, the study utilized a diverse dataset representing various silkworm images and ensured consistent imaging conditions. However, future work could benefit from expanding the dataset to include samples from different regions, silkworm breeds, and varying environmental conditions. Moreover, incorporating a broader range of imaging devices and settings could enhance the model's adaptability and performance in diverse practical applications.

3. Results and Discussion

3.1. Performance Evaluation Metrics

To assess the effectiveness of our trained machine learning model, we employ a range of metrics. When it comes to predicting new data or images, we rely on a confusion matrix as a visual tool to gauge the model's performance. This confusion matrix comprises four key components: True Positive (TP), True Negative (TN), False Positive (FP), and False Negative (FN). TP and TN denote instances where the model's predictions align correctly with reality. FP signifies erroneous positive predictions, and FN indicates incorrect negative predictions. We derive more distinct metrics from this confusion matrix to thoroughly evaluate our model's performance. These precise metrics include Accuracy, Precision, Recall (or Sensitivity), Specificity, and the F1 score, each calculated using specific formulas.

$$\text{Accuracy} = \frac{\text{TP}+\text{TN}}{\text{TP}+\text{FP}+\text{TN}+\text{FN}} \quad (13)$$

$$\text{Precision} = \frac{\text{TP}}{\text{TP}+\text{FP}} \quad (14)$$

$$\text{Recall or Sensitivity} = \frac{\text{TP}}{\text{TP}+\text{FN}} \quad (15)$$

$$\text{Specificity} = \frac{\text{TN}}{\text{TN}+\text{FP}} \quad (16)$$

$$\text{f1 score} = \frac{2\times\text{Recall}\times\text{Precision}}{\text{Recall}+\text{Precision}} \quad (17)$$

For further evaluation, we utilize the Receiver Operating Characteristics (ROC) curve. By assessing the value of the ROC, we can estimate the area under the ROC curve (AUC). The ROC curve provides a straightforward way to gauge a model's or classifier's performance in distinguishing between classes. A higher AUC indicates a more effective predictive ability of the classifier or model.

3.2. Disease detection using SVM

In this work we have used cross validation method of evaluation. K-fold cross-validation is a common technique in machine learning for assessing the performance of a model. It involves dividing the dataset into K subsets, using K-1 subsets for training and the remaining subset for testing, and repeating this process K times to ensure comprehensive evaluation and mitigate potential overfitting issues. In this study we have performed 10-fold cross validation for classification.

The classification evaluation of our proposed SVM classifier, employing HOG feature descriptors and three dimensionality reduction techniques, is detailed in Table 1. Among these variations, the HOG-KPCA-SVM classifier stands out, demonstrating superior classification results compared to HOG-MDS-SVM and HOG-Isomap-SVM. This is evident in its high sensitivity at 93.38% and an accuracy of 93.16%. Additionally, it showcases commendable precision, F1 score, and specificity at 91.94%, 92.65%, and 92.96%, respectively. In Figure 5, we present an ROC curve, which provides a comprehensive view of the classification performance of the HOG-KPCA-SVM model by examining the relationship between the true positive rate (TPR) and the false positive rate (FPR). Notably, the mean

AUC score, as depicted in Figure 5, is calculated at 0.94, underscoring the model's strong classification capabilities.

Table 1. Classification results of SVM

Model	**Hog-Kpca-Svm**
Accuracy (%)	93.16
Recall (%)	93.38
Specificity (%)	92.96
Precision (%)	91.94
F1 Score (%)	92.65

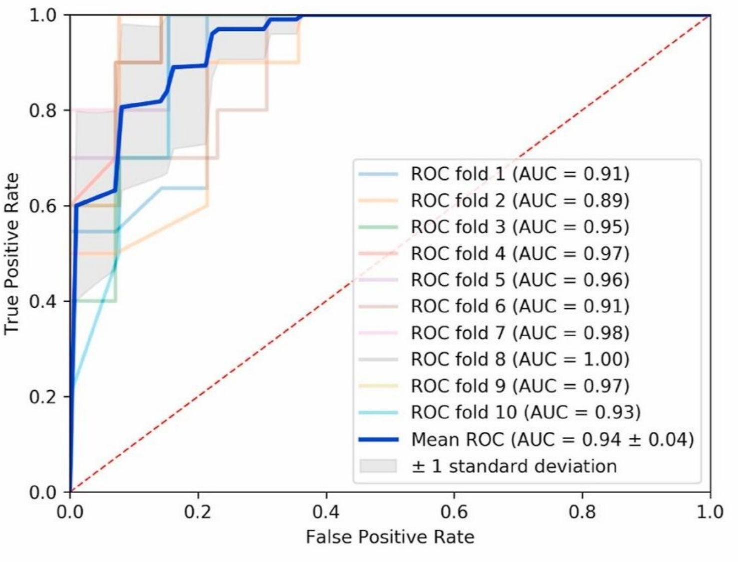

Figure 5. ROC curve for HOG-KPCA-SVM

The proposed HOG-KPCA-SVM classifier demonstrates a significant advancement over traditional methods, such as manual inspection and microscopic examination, for detecting Grasserie disease in silkworms. Manual inspection is labor-intensive, subjective, and often prone to inconsistencies due to human error or variability in expertise. Microscopic examination, while more accurate, is still time-consuming, requires specialized equipment, and may not detect early-stage infections effectively. In contrast, our method offers a systematic, automated approach that relies on robust feature extraction and machine learning, achieving a high classification accuracy of 93.16%. This automated approach minimizes human error, reduces the need for specialized training or equipment, and enables scalable deployment across various sericulture farms. However, potential limitations of our approach include the need for sufficient computational resources for training and the dependency on image quality for accurate detection.

In their study, Nagashetti et al. achieved an impressive accuracy of 97% in differentiating between 670 healthy silkworms and 527 silkworms affected by Grasserie disease, utilizing deep learning techniques [21]. Zhen et al. utilized 600 silkworm images of nuclear polyhedrosis virus and white Muscardine disease to evaluate the performance of the Attention-Concatenation Dense Convolutional Neural Network (AC-DenseNet). They achieved a remarkable maximum accuracy of 85.6%, demonstrating the effectiveness of AC-DenseNet for distinguishing between the two diseases in silkworms [6]. Xia et al. developed an application for Silkworm Disease Recognition using the Local

Binary Pattern (LBP) feature extraction technique and an SVM-based classification method, achieving an accuracy of 73.8% [22]. The system employs client/server network architecture, allowing users to capture silkworm disease images in real-time using a mobile app and seamlessly upload them to a cloud server platform. In comparison to existing methods, our study demonstrates a competitive performance with a 93.16% accuracy in distinguishing between healthy and Grasserie-infected silkworms, utilizing a combination of HOG feature extraction, KPCA for dimensionality reduction, and SVM for classification.

4. Conclusions

In this research, we have introduced a significant machine learning-based classification model designed to identify infected silkworms. Our primary objective is to classify silkworms into two distinct categories, affected by Grasserie and healthy. We have rigorously evaluated our model using various metrics and have presented the classification outcomes with visual representations of these results. In addition to developing our classifier, we have applied cutting-edge image processing techniques to make input images more adaptable for our classification model. This research represents a substantial step towards the creation of an advanced automated silkworm disease detection system. Our approach leverages not only modern image processing techniques but also integrates in-demand supervised learning methods. Notably, our developed classifier outperforms other systems in terms of accuracy, particularly when applied to our real-world, novel dataset. Looking ahead, our future efforts will center on the practical implementation of an IoT device using the proposed system. This endeavor aims to provide a specific solution for sericulture farmers, enabling them to promptly identify infected silkworms and take necessary measures to avert unexpected losses in their farming activities. Additionally, we intend to expand the usability of our system in various sectors of sericulture by working with different silkworm datasets. Our research not only advances the field of silkworm disease detection but also paves the way for practical, real-world solutions with the potential to revolutionize sericulture practices and enhance the economic security of farmers in the industry. Future research will focus on implementing an IoT-based device using the developed model to enable rapid detection of infected silkworms, reducing losses for sericulture farmers. Additionally, the model's applicability will be expanded by testing it with diverse silkworm datasets under various rearing conditions to enhance its generalizability and robustness.

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