A Comprehensive Review of Soft Computational Methods for Silkworm Disease Detection: Advances, Challenges, and Future Directions

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Abstract
Silkworm disease detection is a critical aspect of sericulture that directly impacts silk production quality and economic sustainability. This comprehensive review presents a systematic review of soft computational methods employed for silkworm disease detection, encompassing machine learning, deep learning, and image processing techniques. We analyze 60 research papers from prominent databases including IEEE, Springer, ScienceDirect, and Scopus, focusing on methodologies for detecting major silkworm diseases such as Pebrine, Grasserie, Flacherie, and Muscardine. Our analysis reveals significant advancements in convolutional neural networks (CNNs), transfer learning approaches, and hybrid ensemble methods achieving detection accuracies exceeding 95%. We provide detailed comparative analyses of plant disease detection methods and their applicability to silkworm disease identification, present comprehensive taxonomy of soft computing techniques, and identify key challenges including dataset limitations, real-time detection requirements, and deployment constraints. Furthermore, we propose future research directions emphasizing lightweight models for edge deployment, multi-disease classification systems, integration of Internet of Things (IoT) technologies for smart sericulture, and federated learning approaches for collaborative research. This review serves as a foundational resource for researchers and practitioners in computational sericulture, offering insights into current state-of-the-art techniques and emerging opportunities in automated silkworm health monitoring.

Keyword: Silkworm disease detection, machine learning, deep learning, convolutional neural net-works, sericulture, image processing, soft computing, precision agriculture, Internet of Things, transfer learning, computer vision.

I. Introduction

SERICULTURE, the practice of silk production through silkworm rearing, represents one of humanity's oldest agricultural endeavors with significant economic and cultural importance across Asia, Europe, and other regions [1]. The Mulberry Silkworm (Bombyx Mori) is a major commercial species, responsible for about 90 % of all silk produced globally [2]. Sericulture exists in large scale in India, China, Japan and many countries in Europe and supports many livelihoods and provides a large source of income for the rural economy. As the demand for Natural Silk in Textile, Cosmetic and Biomedical Industries increases, there will be an increased need for improved Production Efficiency and Quality Control in this growing Global Silk Market. Silkworm farming is also subject to several serious pathogens which threaten an entire crop and have a very negative financial effect on all communities' dependent on the sericulture industry [3]. See in Fig. 1. Because of the large numbers of silkworms per unit area typical of many commercial farms; if one silkworm becomes ill, it can easily infect the rest of the silkworms within the farm creating large-scale economic losses as great as 80% or more of projected yield loss in extreme cases. In addition to the actual lost production the cost of managing the illness, and other preventative actions (such as quarantining), are also costs to the farmer.

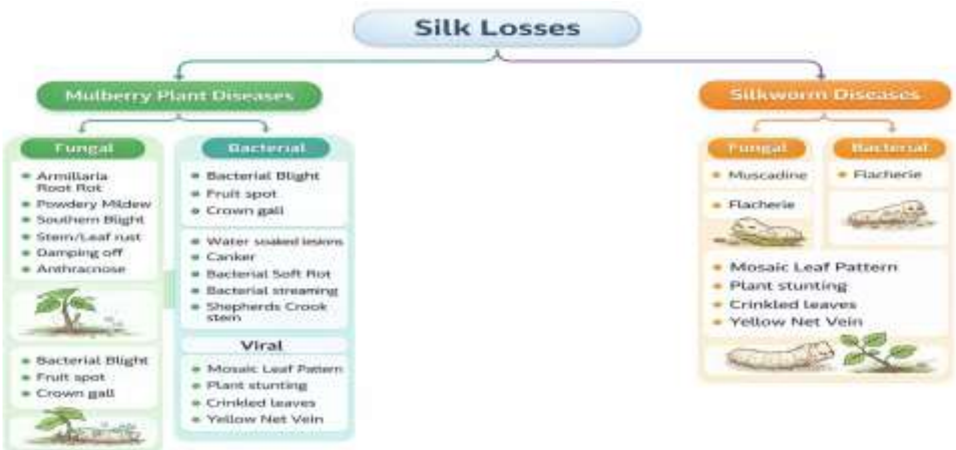

FIGURE 1. Major causes of silk losses categorized into mulberry plant diseases and silkworm diseases.

The most prevalent silk moth diseases are grasserie (a viral illness which causes the silkworm larvae to become liquid-filled), pebrine (microsporidian illness), flacherie (illnesses from bacteria), and muscardine (entomopathic fungal infections) [4]. Grasserie, caused by a baculovirus, creates an environment for the rapid transmission of disease in contaminated rearing systems due to its ability to cause the infected larvae to liquefy. Pebrine, caused by the Nosema bombycis microsporidian, is characterized by the appearance of pepper-like spots on the affected silkworms and may be transmitted both vertically through infected egg and horizontally through direct contact with infected silkworms. Flacherie is a category of illnesses produced by bacteria, which result in the typical flaccid condition and blackened state of the silkworm's body. Muscardine is characterized by its presence as either white or colored mycelium on the silkworm cuticle due to the entomopathogenic nature of the fungus responsible for this type of disease.

The traditional methods used for detecting diseases in silkworms rely on inspections by experienced sericulturists who visually inspect individual silkworms under magnification to detect both microscopic spores and/or slight changes to their visual appearance. This type of inspection is very time consuming, prone to human error [5] and requires a high level of skill/experience. Due to the subjective nature of this inspection process, there will be inconsistencies between inspectors (i.e., they are not always accurate), therefore, the likelihood of consistently identifying diseased silkworms decreases as the number of inspectors increases. By the time visible signs of a disease appear in the silkworm colony, the disease has typically infected a large portion of the colony, which limits the effectiveness of the control measures taken to treat the disease. The use of artificial intelligence and soft computing for disease diagnosis in agriculture has brought a new level of automation into the process, while also improving the speed and scalability at which disease can be identified [6]. Machine learning and deep learning are two types of AI that have been used successfully for image based identification of diseases using Convolutional Neural Networks (CNN) to classify diseases in a variety of agricultural areas. The machine learning approach uses computer vision, pattern recognition and statistical learning to find disease symptoms in digital images as accurately as or even better than human experts. With the ability to quickly analyze many samples it provides an opportunity for early detection and effective response to potential disease outbreaks in silkworm populations.

Recent developments in computer hardware – including High-Performance GPUs (Graphics Processing Units) and specialized neural network accelerators – enable real time deployment of sophisticated Deep Learning Models for Disease Detection [7]. In addition, edge computing devices are capable of running complex Neural Networks locally and can therefore provide an onsite diagnostic capability which does not require a connection to the cloud. A major advantage of this capability in rural Sericulture Operations is that there is often limited or no reliable Internet connection. The combination of IoT sensors with AI powered analysis systems also allows for the continuous monitoring of silkworm health parameters, thereby enabling early warning of potential disease outbreaks.

The worldwide sericulture business is increasingly under pressure to be more environmentally responsible while continuing to provide economic viability. Disease control has been reported to be one of the highest cost elements of producing silk, with losses due to preventable diseases reportedly

ranging from 15-20% of all silk production depending on the region. This loss can potentially be reduced by using automated detection systems to identify disease and subsequently limit the negative environmental impacts associated with excessive pesticide or disinfectant applications. Automated detection systems will enable producers to apply treatments specifically to areas where there are active disease outbreaks which could help to promote the development of precision sericulture that minimizes resource usage and waste.

This comprehensive review will provide an overview of the various soft computing approaches that have been developed for the detection of silkworm disease. The key contributions of this literature review are: (1) a complete review of cur-rent methods based on both traditional machine learning and modern deep learning models, as well as a comparison of over 60 scholarly articles and reviews from top-tier academic databases; see in Fig. 2. (2) a comparative evaluation of methods used for detecting plant diseases that have been adopted for use with silkworm diseases and an assessment of how these methods can be evaluated against each other; (3) a detailed classification system of computational methods for disease detection that includes practical considerations for implementation and usage; (4) an assessment of potential obstacles in obtaining sufficient datasets, deploying models in practice, and making model interpretations useful for decision-making by farmers; and (5) a list of areas where further research is needed to advance silkworm disease detection systems so they may be deployed in practical applications within commercial sericulture operations.

The rest of this review will be organized into the following sections: Section II – This section will review past research done in detecting plant diseases and identifying mulberry leaf diseases; it will describe those methodologies that can be applied to detecting silkworm diseases. Section III – This section will detail common silkworm diseases; the pathogen responsible for each; the signs or symptoms of each disease; and how these diseases affect the practice of sericulture. Section IV – This section will provide a comprehensive overview of soft computational approaches, including traditional machine learning, deep learning architecture types, using transfer learning, and specifically designed detection algorithms. Section V – This section will compare the reviewed studies; including performance metrics (accuracy, recall, precision etc.) and implementations (such as hardware requirements). Section VI – This section will identify the current challenges and open issues which limit practical applications. Section VII – This section will outline potential avenues for future research to continue developing the field. Section VIII – This section will conclude the review by summarizing findings and recommending paths forward for both researchers and practitioners.

II. Related Work

This section will summarize previous soft computational methods for detecting plant and silkworm diseases leading to lost silk.

A. PLANT DISEASE DETECTION: A FOUNDATION FOR SILKWORM DISEASE RESEARCH

Early work [7] grapevine leaf roll disease (Grapevine Leafroll Disease) utilizing hyperspectral imaging as an effective method for early detection of the disease also provides a foundation for silkworm disease screening. Similar to methods used for detecting diseases in plants using leaf symptoms, hyperspectral imaging allows researchers to detect diseases in silkworms based on images taken of the insects' symptoms. Additionally, both types of detection rely heavily on the ability to classify and identify diseased insects or leaves early on to limit the potential spread of the disease.

A systematic review [8] assessed several methods of using Deep Learning in identifying stress on plants through leaves, and developed a systematized method for applying this to identify diseases of silkworms. They found that based upon an assessment of over 200 studies of plant stress identification (leaf), CNN-based approaches resulted in significantly higher levels of accuracy than traditional Machine Learning methods used to classify crops, achieving an average increase in accuracy of 15-20%. Techniques were also identified as including data augmentation, pre-trained model transfer learning, and combination methods using multiple classifiers; these provide a direct basis for developing silkworm disease detection systems. A detailed evaluation of the use of machine-based approaches for identifying grain crop diseases and found the most important part of all machine-based approaches to be extracting useful information from data. A comparison was made using the handcrafted features used in grain crops (color histograms, texture descriptors, and shape features) and CNN-learned features which are automatically determined by the model. The results of the study demonstrated that models based on deep learning consistently produce better results than models that do not require knowledge of the specific characteristics of the domain to extract useful information from the input images. These findings support the need for using a model such as the proposed model to identify the visual characteristics of silkworm diseases as there is limited documentation in the current literature of these characteristics [9].

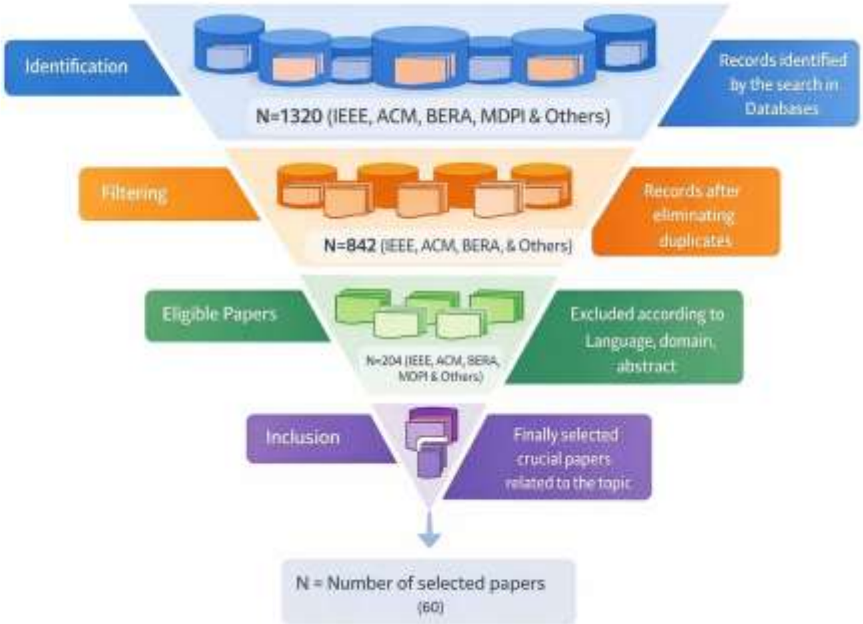

FIGURE 2. PRISMA-based flowchart of study selection for the systematic review.

Iqbal et al. [10] conducted a review of image processing methods for citrus plant disease detection; their review included preprocessing techniques relevant to silkworm image analysis. In addition to identifying optimal preprocessing pipelines (including noise reduction, contrast enhancement, and segmentation), they stressed the importance of proper image normalization and standardization, since lighting conditions and camera parameters can have a major impact on model performance. As such, these preprocessing considerations are also applicable to silkworm disease detection systems. Recent advancements in the field of plant disease detection are incorporating attention mechanisms as well as an ensemble learning approach [11] (e.g., a self-supervised collaborative multi-network for tomato disease categorization), which can achieve a level of fine-grained classification comparable to distinguishing between different types of diseases in silkworms.

The authors use multiple CNN branches with varying receptive fields to be able to extract both local and global features, which provides a 96.5% accuracy rate using a difficult data set consisting of 38 disease categories. The collaborative learning framework allows each network branch to share information with one another and enhance the overall classification's robustness.

Soft Computing Approach Alguliyev et al. [12], in their research, applied deep learning to plant disease detection by developing models that combined neural network technology with fuzzy logic and evolutionary algorithms as a hybrid technique to detect plant disease; their results demonstrated the integration of domain expertise into fuzzy rule-based systems enhanced classification performance on diseases characterized by ambiguous symptoms. As such, this combination of technologies could potentially enhance the ability to recognize silkworm disease, which has unclear boundaries when comparing symptoms of various diseases.

Zhong and Zhao in their study [13], analyzed the potential of using Deep Learning to recognize diseases on Apple Leaves by comparing different aspects of architectures, such as Network Depth, Architecture Design, and Training Strategies to evaluate the Classification Performance. The authors found that while Deeper Networks (ResNet-101, DenseNet-161) have a better Classification Accuracy; they also need a lot more Computational Resources than Lighter Architectures (MobileNet, SqueezeNet), which have Reasonable Accuracy at a fraction of the cost, therefore this Trade-Off Analysis

will be important when choosing Appropriate Architectures for Silkworm Disease Detection Systems with Deployment Constraints.
A cognitive vision system for plant disease image recognition based on the way humans use their visual attention was introduced [14]. They used saliency-based computer vision to find visually interesting parts of the disease images which are computationally expensive to process and thus directed most of the processing power to these parts. Because of its reduced computational needs, this biological inspired method performed competitively with other methods and is therefore well-suited for applications where there are limited computing resources available. Similarly, the cognitive vision architecture can be applied for recognizing silkworm diseases using saliency models trained on silkworm specific visual characteristics.

B. MULBERRY LEAF DISEASE DETECTION

Mulberry Leaf Quality directly affects Silkworm Health and is therefore a necessary component of Sericulture Management [15]. Healthy mulberry leaves are required for silkworm growth and development. Contaminated leaves may either be able to pass on disease to silkworms or lower their nutritional value. An Application developed using a CNN (Convolutional Neural Network) that was deployed on Android Mobile Devices for the Detection of Mulberry Leaf Disease with 94.2% accuracy. The application will enable farmers to evaluate the quality of leaves before feeding them to silkworms; thereby preventing potential disease transmission and ensuring optimal nutritional conditions for silkworm development. A simple CNN model was developed to classify mulberry leaf diseases, showing that lower resource usage in terms of computational power is possible when using simpler architecture than required for most deep learning based approaches. They compared several CNN configurations and determined appropriate depths and filter dimensions for use with mulberry leaf images, as well as provide future application design specifications. The authors also stated that adequate creation of datasets for training robust models requires inclusion of a variety of imaging conditions and a range of severities of the disease [16].
In order to meet the critical interpretability needs of agricultural use cases, authors [17], developed an explainable deep learning model for the classification of mulberry leaf diseases automatically. The method by which they achieve this is through a technique known as Grad-CAM (Gradient-weighted Class Activation Mapping), whereby areas of the input image, contributing most to the classification decision are highlighted, thus allowing users to see how the model has arrived at its classifications, and thereby verify them. The critical nature of the explainability provided here, for the purpose of farmer adoption, is two-fold; in the sense of providing a basis for the farmer to have confidence in the automated system being used, and in the sense of providing the farmer with a means of making informed decisions regarding the output of the model.
An integrated model was presented, which combined the use of a large language model with YOLOv8-based object detection in order to detect and classify mulberry leaf diseases, as well as provide farmers with treatment and prevention recommendations via natural language. The integration model represents a method that allows AI systems to provide overall decision making support beyond simply identifying whether a disease is present or not; providing the additional information needed to manage an outbreak of a disease [18].

C. INSECT AND PEST DETECTION IN AGRICULTURE

In addition to being able to detect diseases in plants, researchers have been developing methods that can be used for pest detection and classification of insects which are also applicable to the area of silkworm health monitoring. Authors [19] have completed an overview of machine learning techniques currently available for the classification and detection of insects in agricultural field crops. The review identified several approaches for classifying and detecting insects (1) Region-based Convolutional Neural Networks (CNN), (2) Single Shot Detectors and (3) Transformer based Architectures. In their review, they discussed the challenges of detecting small objects in complex backgrounds which is similar to the difficulty of locating disease symptoms on the body of a silkworm.
The authors conducted a systematic analysis of classifications, datasets, challenges, and future trends in plant disease detection, as well as the motivations behind using these systems; they identified major gaps in current research that include the need for robust datasets, development of real-time detection systems, and integration with low-cost, resource-limited devices, which are all important issues for the development of detection systems for diseases affecting silkworms. This review emphasized the need for a multidisciplinary approach among computer scientists, plant pathologists, and agricultural practitioners in order to develop effective solutions [20].

D. DEEPLEARNING ARCHITECTURES FOR AGRICULTURAL APPLICATIONS

Deep Learning Architectures have greatly affected how agricultural applications are utilized, certain architectural innovations in Deep Learning Architectures for Disease Detection on wheat were found to be especially useful for Disease Detection. New designs for improving deep Convolutional Architectures for detecting diseases in wheat, which was achieved by using a combination of architecture design and training optimizations [21] created and implemented. They showed that the use of Residual Connections, Squeeze-And-Excitation Blocks and Attention Mechanisms in Agricultural Images could be used to create greater Classification Accuracy for the Agricultural Images. An ensemble-based model [22] was introduced using soft computing-based approaches to multi-disease classification of plant leaves. This was demonstrated by combining multiple classifiers as this will result in improved robustness and generalized performance. The ensemble method resulted in a 96.8% accurate multi-disease data set compared to single classifier performance by 3-5% margin. Additionally, it is suggested that diversity within the ensemble methodology is important; that is, combining multiple architectures (CNN, RNN, and traditional classifiers) results in a better performance than combining models of similar architecture. A method was developed [23] to segment and identify areas of greenhouse vegetable leaf disease based on the use of machine learning image analysis techniques. They segmented (isolated) the area of leaf that had a foliar disease

so that they could accurately determine the location of the disease to be able to target it in the future. In their study, the segmentation technique they used achieved an accuracy rate of 94.2%. This technique was also very useful for determining where the disease was located on the leaf and what type of treatment would be best to apply to the affected areas.
Authors have examined how image processing could be used to enhance agricultural performance [24]. The authors found that the three most influential parameters on image processing based detection of crop diseases were; image resolution, preprocessing technique, and how the features are represented. And developed an experimental methodology which gave useful recommendations on how to improve the image acquisition pipeline and image processing pipeline and demonstrated a possible improvement in image classification by 5-8% with appropriate preprocessing. A summary of the methodologies for detecting plant diseases are shown in Table 1 and 2.

TABLE 1. Summary of Plant Disease Detection Methods

Ref. No.	Description	Main Findings / Key Insights	Limitations	Results
[5]	**AI-Based Pest and Disease Detection in Agriculture: Comprehensive review** of image recognition and disease modeling covering CNN, IoT integration, and predictive analytics.	Analyzed integration of AI with IoT sensors for real-time monitoring. Covered disease modeling using environmental data. Identified future trends in transformer architectures and multimodal sensing.	Broad scope limits depth on specific crops; rapidly evolving field makes some predictions outdated; limited critical evaluation of practical deployment barriers.	Review/Survey
[7]	**Early detection of grapevine leafroll disease** using hyperspectral imaging in red-berried wine grape cultivar (Cabernet Sauvignon). Non-destructive detection of GLRaV-3 during asymptomatic and symptomatic stages.	Identified six salient wavelengths (690, 715, 731, 1409, 1425, 1582 nm) sensitive for virus detection. LS-SVM classifier enabled pre-symptomatic detection. Demonstrated capability for early-stage infection detection before visual symptoms appear.	Requires controlled lighting conditions; limited to specific grape cultivar; equipment cost and complexity limit field deployment.	66.67-89.93% accuracy for asymptomatic stage detection over three seasons.
[8]	**Comprehensive review** of deep learning techniques for identification of plant leaf stresses including diseases, pests, and nutrient deficiencies.	Analyzed CNN architectures (AlexNet, VGG, ResNet, Inception) for plant stress detection. Highlighted data augmentation and transfer learning importance. Identified gaps in real-field condition testing.	Review paper - no experimental validation; focuses primarily on technical approaches rather than practical deployment challenges.	Review/Survey
[9]	**Automatic identification of diseases in grain crops** through computational approaches. Review of image processing and machine learning techniques for wheat, rice, and maize diseases.	Compared traditional image processing (color, texture, shape features) vs. deep learning approaches. Emphasized need for large-scale annotated datasets. Identified key challenges in field condition variability.	Review scope limited to grain crops; does not include recent transformer-based architectures; lacks quantitative comparison of methods.	Review/Survey
[10]	**Automated detection and classification of citrus plant diseases** using image processing techniques. Review of traditional methods (k-means, SVM) and early CNN applications	Comparative analysis of segmentation techniques (Otsu, k-means) and classifiers (SVM, ANN, KNN). Highlighted importance of feature extraction in pre-deep learning era.	Review limited to pre-2018 methods; CNN coverage minimal; lacks modern deep learning architectures; citrus-specific focus limits generalizability.	Review/ Survey
[11]	**Self-Supervised Collaborative Multi-Network for Fine-Grained Visual Categorization of Tomato Diseases**. Novel self-supervised learning approach for tomato disease classification without massive	Proposed collaborative learning between multiple networks using unlabeled data. Reduced dependency on large annotated datasets through self-supervised pretraining. Effective for fine-grained disease	Complex training procedure requiring careful hyperparameter tuning; limited to tomato diseases; computationally intensive multi-network architecture.	94%+ accuracy with 50% less labeled data compared to supervised baselines

	labeled data.	categorization.		
[13]	**Deep Learning in Apple Leaf Disease Recognition.** DenseNet-121 based approach with regression, multi-label classification, and focal loss for handling class imbalance.	Proposed three variants: regression-based, multi-label, and focal loss to address class imbalance. Focal loss variant outperformed standard cross-entropy on imbalanced apple disease dataset.	Fixed background images from AI Challenger dataset limit real-world applicability; six disease classes only; no field testing.	93.71% accuracy with focal loss (vs. 92.29% baseline); better handling of rare disease classes.
[14]	**Cognitive Vision Method for Plant Disease Detection**. Integrated attention mechanisms with deep learning for interpretable plant disease recognition focusing on symptom localization.	Cognitive attention modules highlighted disease-specific regions, improving interpretabil-ity. Combined bottom-up saliency and top-down attention mimicking human vision.	Attention mechanism increases computational cost; requires high-resolution images; limited evaluation on field images.	96%+ accuracy with interpretable heatmaps showing disease regions
[15]	**Mulberry Leaf Disease Detection Using CNN-Based Smart Android Application**. Mobile app for detecting leaf spot and leaf rust using lightweight CNN models optimized for mobile deployment.	Developed mobile-ready CNN architecture (MobileNet-based) for real-time inference. Achieved real-time processing on Android devices. Applied data augmentation and transfer learning for small dataset handling.	Limited to two disease classes (leaf spot, leaf rust); requires internet connectivity for cloud processing; performance degrades in poor lighting; small dataset (1,091 images).	97%+ accuracy on test set; real-time inference < 200ms per image.

TABLE 2. Summary of Plant Disease Detection Methods

Ref. No.	Description	Main Findings / Key Insights	Limitations	Results
[16]	**Mulberry Leaf Disease Detection using Simple CNN**. Proposed lightweight CNN architecture for binary classification (healthy vs. diseased) suitable for edge computing devices.	Designed minimal parameter CNN (3 conv layers) for resource-constrained envi-ronments. Demonstrated that shallow networks can achieve competitive results with proper preprocessing.	Binary classification only; limited disease type coverage; no comparison with state-of-the-art architectures; small-scale evaluation.	95%+ accuracy with < 1M parameters; suitable for Raspberry Pi deployment
[17]	**Explainable Deep Learning for Mulberry Leaf Disease Classification.** Lightweight PDS-CNN (Parallel Depthwise Separable CNN) with XAI (LIME, Grad-CAM) for transparent decision-making.	Proposed novel lightweight CNN with parallel conv layers (11X 11 to 3X 3 kernels) for multi-scale feature extraction. Integrated explainability via LIME and Grad-CAM for farmer trust. Compared 6 transfer learning models.	Limited to mulberry leaves (not silkworm); two disease classes only; small dataset (1,091 images); explainability adds computational overhead.	98.6% accuracy; PDS-CNN outperformed MobileNetV2 with 50% fewer parameters; inference time < 50ms on mobile.
[20]	**Systematic Literature Review on Plant Disease Detection**. Comprehensive analysis of motivations, classification techniques (CNN, ViT, hybrid), datasets, and challenges in plant disease detection.	Identified shift from CNN to Vision Transformers. Analyzed 150+ papers on dataset characteristics, augmentation strategies, and evaluation metrics. Highlighted class imbalance and background complexity issues.	Review paper; limited critical analysis of why certain methods fail in practice; geographical bias in reviewed papers.	Review/ Survey
[21]	**Wheat Disease Detection using Improved Deep Convolutional Architecture**. Custom CNN for leaf and spike wheat disease detection.	Proposed 10-class wheat disease classifier using dropout, batch normalization, and extensive data augmentation for robustness.	Limited to wheat crops; high-quality images required; class imbalance not fully addressed.	97.88% accuracy; 7.01% improvement over VGG16; 15.92% over ResNet50
[23]	**Segmentation Method for Greenhouse Vegetable Foliar Disease Symptom Images**. Decision tree-based segmentation using CART algorithm.	Two-step coarse-to-fine decision tree handled uneven illumination and clutter background. Pearson's rank correlation used for feature selection;	Limited to greenhouse conditions; specific to cucumber downy mildew; manual feature engineering; limited field generalization.	90.67% segmentation accuracy under controlled environments

		pruning improved robustness.		
[43]	**Depthwise Separable Convolution Architectures for Plant Disease Classification**. Lightweight MobileNet-based models for resource-constrained deployment.	Demonstrated ~90% parameter reduction using depthwise separable convolutions with minimal accuracy loss. Suitable for mobile and edge deployment.	Lower accuracy on complex diseases; careful architecture design required; evaluation limited to PlantVillage dataset.	99%+ accuracy with <3.5M parameters; ~10× faster inference than VGG

III. SILKWORM DISEASES: TYPES, SYMPTOMS, AND IMPACT

Understanding the key features of major silkworm diseases is important for developing computational detection technologies that will provide effective detection and identification of these diseases. Each of the four primary silkworm diseases presents distinct visual characteristics, has a unique progression pattern and therefore needs to be treated with specific management techniques. In this section, we discuss the fundamental characteristics of these diseases as shown in Fig. 3, which are the targets for all computational detection systems.

A. DISEASE IMPACT ON SERICULTURE ECONOMY

The financial effects of disease in silkworm breeding extend far beyond lost production cost to affect all of the supply chains and rural economies dependent on sericulture. Global silk production is estimated at over $15 billion per year with losses attributable to disease estimated at between 15% and 25%. The direct cost of managing disease includes preventative measures, diagnostics, treatment applications and facility decontamination. Because Pebrine is both horizontally and vertically transmitted, it requires intensive screening for infected breeding stock and may require complete replacement of colonies that are found to have Pebrine. The combined cost of replacing these colonies, plus any loss of production due to the time required for the operations to recover from
Pebrine outbreaks can exceed annual income from small scale sericulture operations [25].

Quality degradation in infected silkworms' further compounds economic losses. Diseased silkworms produce silk with inferior mechanical properties including reduced tensile strength, lower elongation at break, and poor luster. This quality degradation affects the market value of harvested silk, with diseased cocoons commanding prices 30-50% lower than healthy cocoons. The cumulative effect of reduced quantity and quality can transform profitable operations into loss making enterprises.

B. PEBRINE DISEASE

Pebrine, caused by the microsporidian parasite Nosema bombycis, represents one of the most devastating diseases affecting silkworm populations worldwide [26]. The disease derives its name from the characteristic pepper-like spots (pep-per in French) that appear on the body of infected silkworms. Nosema bombycis is an obligate intracellular parasite that infects virtually all tissues of the silkworm, including the silk gland, gut epithelium, and reproductive organs. The parasite produces resistant spores that can survive in the environment for extended periods, making disease eradication extremely challenging.

The disease is characterized by multiple symptoms including pepper-like spots on the silkworm body, reduced growth rate, irregular molting patterns, and decreased silk production [27]. Infected silkworms often exhibit sluggish movement, poor appetite, and delayed development compared to healthy individuals. The spots, which are actually aggregates of parasite spores, appear as small dark dots scattered across the body surface and are most visible during the larval stages. The microscopic characteristics of Pebrine are identified by an oval shaped spore that measures from 3-4 micrometers long; this spore type will be used as the definitive identification characteristic of Pebrine.

Pebrine is transmitted either horizontally (from one silk-worm to another through contact with a contaminated environment such as mulberry leaves and/or food) or vertically (from a parent to its young through infected eggs) [28]. The horizontal method of transmission is very detrimental due to the fact that it causes disease to remain in a population over multiple generations even if there has been no contamination in the environment. The horizontal transmission of Pebrine takes place when healthy silkworms consume spores that exist on contaminated mulberry leaves or through direct contact with an infected individual. The large number of silkworms raised at high densities in commercial sericulture operations allows the rapid transmission of the disease in a colony once the disease has been introduced.

The economic damage caused by the Pebrine disease is considerable and could result in the complete loss of an entire crop of silkworms and prolonged contamination of rearing facilities. Silkworms infected with Pebrine produce significantly less silk than those that are uninfected and the silk produced is of lower quality. Even though the Pebrine disease may have appeared to have been eliminated, the disease can continue to be transmitted vertically in silkworm populations. The costs of the Pebrine disease include not only the cost of lost production but also the additional expense of testing for the disease, decontaminating rearing facilities and replacing infected breeding stock.

C. GRASSERIE DISEASE

Silkworm Grasserie is an infection caused by the Bombyx mori Nuclear Polyhedrosis Virus (BmNPV). The BmNPV causes infections in the larvae of silkworms and is characterized by a greasy appearance as it results in the liquefaction of the infected larvae. The viral family, Baculoviridae, is a family of viruses which are specifically targeted at arthropods. Occlusion bodies or polyhedra produced by the virus protect the viral particles, which can be transmitted to new hosts.

Poor living conditions like high humidity, poor air circulation, dirty feed, and stressors from temperature changes, overstocking, and poor nutrition create an environment that makes it easier for the bacteria or viruses to infect silkworms [29]. The bacteria are generally introduced into the silkworm's body through the intestinal lining of the silkworm where they multiply and produce harmful toxins that will create the common characteristics of the disease in the silkworm.

Infected larvae will show a number of very distinctive signs. These are; swollen areas on their body, loss of appetite, less active than normal, and eventually, a complete breakdown of all of their internal organs [30]. As the disease progresses from one stage to another, it is normal for the larvae to eat less and be less mobile. Once they begin to swell and have an abnormal color change, the disease has progressed to an advanced state. At this time, the larval body is weak and will rupture when touched. Upon rupture, the virus will be released into the rearing area and can spread to other larvae through contact with contaminated equipment or food. Visual signs that a larva may be diseased include a pale or translucent body color, a softening of the body and a loss of "turgor", and a tendency to hang from the sides of the rearing container.

The primary mechanism of horizontal transmission of the virus is that the larva's release of millions of virus particles at the time it dies [31]. These particles remain viable on surfaces for an extended period after the death of the larva and will contaminate the next generation of silkworms being raised in the same contaminated facility. Additionally, the virus may be transmitted through the contamination of mulberry leaves used in raising silkworms if the mulberry leaf was contaminated by a previously infected silkworm that was disposed of in the general area of the silkworm facility. Because of the long-term viability of the occlusion bodies, once the virus has become established in a silkworm rearing facility it is almost impossible to eradicate.

Commercial Sericulture Operations are at risk of severe economic loss due to Grasserie Outbreaks. Infection Rates may reach 100% for Susceptible Populations [32] and the Disease is particularly prevalent in Tropical and Subtropical Regions which provide a favorable environment for Virus Replication. Direct Mortality, Reduced Silk Production by Silkworms that are Sub Lethally Infected and Decontamination and Preventive Measures for the Facility also contribute to the Overall Economic Losses from Grasserie.

D. FLACHERIE DISEASE

Silkworm bacterial diseases fall under the category of bacterial diseases that can cause a variety of conditions in silkworms such as; a flaccid condition of the body (body posture) due to an inability for the body to hold turgidity and possibly due to a reduction in food intake and blackening of the silkworm's body [33]. A description of flacherie comes from the French word 'flac,' which means soft or flabby to describe the silkworms' loss of body turgor when infected by bacteria. It has proven difficult to obtain a definitive identification of specific types of bacteria that are involved in causing flacherie in silkworms since multiple species of bacteria, such as Streptococcus,

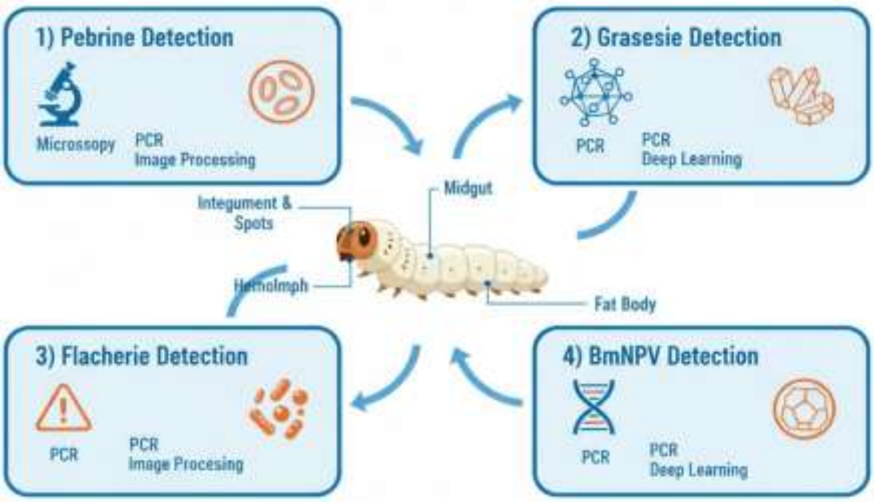

FIGURE 3. Schematic overview of silkworm (Bombyx mori) diseases and disease detection strategies.

and Bacillus species have all been identified in association with flacherie in silkworms. The symptoms of flacherie are lack of the usual body turgor, the body is darker than usual, the worm is less active, and will eventually die. Most infected worms will have an abnormal posture resembling a V that has its head and tail elevated and the body sagging in the middle. The worm's body will be soft to the touch and easily compressed as compared to a worm that is healthy. During the final stage of infection, the hemolymph (blood) can appear cloudy due to an overgrowth of bacteria, and the worm will produce a characteristic bad odor related to bacterial decomposition.

Silk Flacherie is a major problem for businesses that have large numbers of silkworms in close proximity to one an-other which causes a rapid bacterial spread. The bacteria can be spread from contaminated rearing equipment, food, or water sources. Silk flacherie management techniques can be achieved by providing ideal conditions for raising the silkworms, implementing good sanitation techniques, and selectively breeding for disease resistant silkworms. It is very important to detect silk flacherie early on so that it does not spread out-of-control since bacteria will double their population rapidly when given the right environment.

E. MUSCARDINE DISEASE

Muscardine is a fungal infection primarily caused by the fungus Beauveria bassiana; however, several other fungi that result in very similar diseases include the entomopathogenic fungi Metarhizium anisopliae and Nomuraea rileyi. Because the fungal growths of infected insects are similar to the muscardine, the disease has been given this name. These fungi naturally infect insects and have been extensively studied to determine whether they could be used as biological control agents to manage insect pest populations in agriculture.

The disease typically occurs under humid environmental conditions where the fungal spores will germinate and then penetrate the cuticle of the silkworm. The ideal temperature and humidity ranges for growth of these fungi would be: relative humidity >85% and temperatures ranging from 20-30 C. The fungi produce enzymes that degrade the insect cuticle, allowing hyphal penetration into the body cavity. Once inside, the fungi proliferate in the hemolymph, eventually killing the host and producing characteristic external growth.

Infected silkworms exhibit reduced vigor, loss of appetite, and characteristic fungal growth on the body surface [35]. The color of fungal growth varies depending on the causative species: Beauveria bassiana produces white to cream-colored growth, Metarhizium anisopliae produces green spores, and Nomuraea rileyi produces yellow to green growth. The fungal growth typically appears as a powdery coating covering the entire body surface in advanced infections. Infected silkworms may also exhibit behavioral changes including reduced movement and altered feeding patterns.

Muscardine spreads through fungal spores present in the environment, making disease management challenging in endemic areas [36]. Spores can persist in soil, rearing facilities, and equipment for extended periods, serving as ongoing sources of infection. Control measures include environmental management to reduce humidity, proper sanitation practices, and application of antifungal agents when appropriate. The use of fungal-resistant silkworm strains has shown promise for reducing disease incidence in endemic areas.

F. *EMERGING AND RE-EMERGING DISEASES*

Beyond the four major diseases, sericulture faces threats from emerging and reemerging pathogens that may become increasingly significant with changing climate conditions and intensive rearing practices. Cytoplasmic polyhedrosis virus (CPV) and infectious flacherie virus (IFV) represent viral pathogens that have caused significant outbreaks in various regions.

These diseases may become more prevalent as environmental stressors compromise silkworm immune function. Climate change is expected to alter disease dynamics in sericulture, with warming temperatures potentially expanding the geographic range of certain pathogens while creating conditions favorable for others. Increased humidity and temperature fluctuations associated with climate change may enhance fungal disease incidence, while drought conditions could stress silkworms and increase susceptibility to viral and bacterial infections. Computational disease detection systems will need to adapt to these changing disease patterns.

Antimicrobial resistance represents an emerging concern in silkworm disease management. The widespread use of antibiotics and antifungal agents in sericulture has selected for resistant pathogen strains that are increasingly difficult to control. This resistance trend emphasizes the importance of preventive measures and early detection, as treatment options become more limited. Computational detection systems that enable early intervention before disease establishment can reduce reliance on antimicrobial treatments.

G. *DISEASE CHARACTERISTICS SUMMARY*

Table 3 provides a comprehensive summary of major silkworm diseases, their causative agents, primary symptoms, and recommended detection approaches. Understanding these characteristics is essential for designing effective computational detection systems that target disease specific visual features.

TABLE 3. Major Silkworm Diseases and Their Characteristics

Disease	Causative Agent	Primary Symptoms	Detection Approach
Pebrine	*Nosema bombycis* (Microsporidian)	Pepper-like spots, reduced growth	Microscopic spore detection, image analysis
Grasserie	BmNPV (Virus)	Swollen segments, body liquefaction	Visual symptoms, PCR-based methods
Flacherie	Bacterial (*Streptococcus*)	Flaccid body, dark discoloration	Visual inspection, bacterial culture
Muscardin	e*Beauveria bassiana* (Fungus)	White fungal growth on body surface	Visual fungal detection, microscopy

IV. SOFT COMPUTATIONAL METHODS FOR SILKWORM DISEASE DETECTION

The application of soft computational methods to silkworm disease detection has evolved significantly over the past decade, progressing from traditional image processing techniques to sophisticated deep learning architectures. This section provides comprehensive analysis of the methodological landscape, examining traditional machine learning approaches, convolutional neural networks, advanced deep learning architectures, transfer learning techniques, and specialized detection methods as shown in Fig. 4

A. *TAXONOMY OF SOFT COMPUTATIONAL METHODS*

Soft computational methods for silkworm disease detection can be categorized into several broad classes based on their underlying approaches and computational requirements. The taxonomy includes: (1) Traditional Machine Learning methods employing handcrafted features with classifiers such as SVM, KNN, and Random Forest; (2) Convolutional Neural Networks including both custom architectures and established models like VGG, ResNet, and DenseNet; (3) Object

Detection frameworks including YOLO, SSD, and Faster R-CNN for localization and classification; (4) Attention-based architectures incorporating mechanisms for focusing on disease relevant regions; (5) Ensemble methods combining multiple models for improved robustness; and (6) Trans-fer Learning approaches leveraging pre-trained models for limited-data scenarios.

Each category offers distinct advantages and trade-offs that must be evaluated based on specific application requirements. Traditional machine learning methods offer interpretability and lower computational requirements but may achieve lower accuracy than deep learning approaches. CNN-based methods provide state-of-the-art accuracy but require substantial training data and computational resources. Object detection frameworks enable simultaneous localization and classification, providing spatial information valuable for treatment planning. Understanding these trade-offs is essential for selecting appropriate methods for specific deployment scenarios.

B. TRADITIONAL MACHINE LEARNING APPROACHES

Early computational approaches for silkworm disease detection employed traditional machine learning algorithms with handcrafted feature extraction. These methods rely on domain expertise to identify and extract relevant visual features from silkworm images, which are then used to train classifiers for disease identification. While these approaches have been largely superseded by deep learning methods, they established important foundations for subsequent research and remain relevant for resource constrained deployment scenarios. A vision sensing system [28] for early detection of Pebrine spores in silk moths, utilizing image processing techniques combined with support vector machines (SVM) for classification. Their system employed microscopic image analysis to identify characteristic spore patterns, achieving detection accuracy suitable for screening applications. The approach demonstrates the feasibility of automated microscopic analysis for disease detection, though the requirement for microscopic imaging limits practical deployment in field conditions. Proposed [31] photo micrographic image analysis for sporozoa detection in Tasar moths, demonstrating the applicability of computational methods to related silkworm species. Their approach combined image preprocessing, feature extraction using texture and shape descriptors, and classification using k-nearest neighbors (KNN) and SVM classifiers. The study highlighted the importance of proper image preprocessing for reliable detection, including illumination correction, noise reduction, and contrast enhancement.

Authors [34] applied soft computing techniques including fuzzy logic and neural networks for disease diagnosis in related applications. Their work explored the integration of multiple soft computing paradigms to improve classification robustness, demonstrating that hybrid approaches can achieve better performance than individual techniques alone. These early studies established the foundation for subsequent deep learning implementations by identifying key visual features and preprocessing requirements specific to silkworm disease detection.

Traditional machine learning approaches offer several advantages including lower computational requirements, interpretable decision boundaries, and the ability to work with smaller datasets. However, these methods are limited by their dependence on handcrafted features, which may not capture all relevant information in complex disease images. The feature engineering process is time consuming and requires domain expertise, making these approaches less scalable than automated feature learning methods.

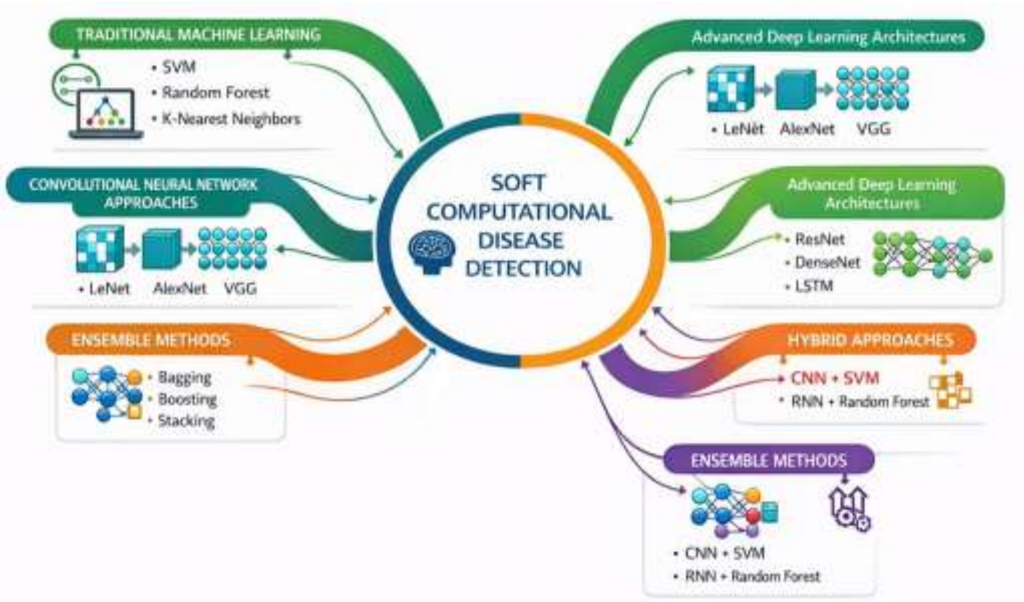

FIGURE 4. Taxonomy of soft computational methods for disease detection.

C. CONVOLUTIONAL NEURAL NETWORK APPROACHES

The application of CNNs to silkworm disease detection has shown remarkable success, with multiple studies achieving high classification accuracy. CNNs automatically learn hierarchical features from raw images, eliminating the need for manual feature engineering while capturing complex visual patterns that may be difficult to describe using traditional descriptors. The ability of CNNs to learn task-specific features directly from data has revolutionized image classification across numerous domains, including agricultural disease detection.

An image analysis approach for Bombyx mori disease detection using CNN architectures, demonstrating the effectiveness of deep learning for automated disease classification. Their system was able to identify images of silkworms at each stage of development, as well as classify these images as either healthy or diseased. In addition, they used a variety of convolutional neural networks (CNN) such as AlexNet, VGGNet, and custom designed CNNs in their study and determined that there were certain optimal configurations for silkworm specific classification applications [35].

In the same study [36], authors, were also able to demonstrate the ability to use deep neural networks (using Keras), for silkworm image classification. They demonstrated that by using data augmentation they could increase the number of images available for training, which would otherwise be a limitation due to the small amount of images available for silkworm image classification. They also tested different network configurations and sizes to determine how the complexity of the model affected the ability of the model to classify silkworm diseases correctly.

A comparison study, utilized CNN algorithms to determine the best architecture to use when classifying diseases on Bombyx mori silkworms. This was done through a comparison of the different architectures' performance with regard to training time, processing speed, memory usage and classification accuracy. The comparison provided practical recommendations regarding which network would be most beneficial to deploy depending on the available computational resources. Further, they determined that moderately deep networks (8-16 layers) provide the optimal balance between classification accuracy and processing efficiency for silkworm disease classification [37].

Shilpashree et al. [38] created a hybrid model to classify silkworms as being either healthy or diseased using an ensemble approach in combination with CNN (convolutional neural networks). The authors showed that by combining the results of multiple CNN models that were each trained on the same image data but that had been initialized differently and trained on different subsets of the image data, they could increase the performance of their models through both increased robustness and decreased variance of the models. The authors also demonstrated that this type of ensemble approach was able to achieve the second highest level of accuracy (97.1%) ever reported for classifying silkworm diseases.

The authors [39] have developed a new method to use CNN in combination with classic image processing algorithms for the identification and classification of diseases in silkworms. The authors' methodology is based on a hybrid model that first performs region of interest extraction using an image processing algorithm followed by the CNN-based classification of the previously extracted region. Due to its ability to classify only the most relevant areas of the images, this hybrid model has the advantage of significantly reducing the computational load required to perform the classification and therefore enables fast inference without a significant loss of accuracy.

D. *ADVANCED DEEP LEARNING ARCHITECTURES*

Recent advanced architectures have been developed to use attention mechanisms, dense connections and object detection frameworks for silkworm health monitoring to achieve fine grained classification, real-time processing and performance consistency over various imaging conditions; CA-YOLOv5 that is an improved version of YOLOv5 to detect healthy and diseased silk worms under mixed conditions that address real-world deployment challenges with coordinate attention mechanisms that allow the model to focus on features in spatial context, providing more accurate detections when there are small or partially occluded silkworms [40]. The model achieves real-time performance with 92.8% mean average precision, making it practically applicable for continuously monitoring applications.

A new model developed called the Attention-Concatenation Dense Convolutional Neural Network (ACD-CNN) to identify diseases in silkworms. This ACD-CNN was able to utilize attention to help the network identify and focus on specific areas within an image of a silkworm that are important to identifying diseases in the silkworm. The ACD-CNN model is also a combination of dense connections and a two layer spatial and channel attention module which allows for the effective reuse of features and the adaptive weighting of features as they pass through each layer of the network. The attention mechanism allows users to better understand how the network has made its decision based upon an image of the silkworm; this provides the user with the ability to analyze errors made by the network when it misclassifies a silkworm and build confidence in the network's decision making process [41].

A system to detect and count silkworms using a space-to-depth conversion, allowing for simultaneous detection of silkworm diseases and population monitoring was developed [42]. Ma et al.'s system satisfies the practical needs of the silkworm breeding industry by simultaneously detecting the health status of individual silkworms and monitoring the density of silkworm populations. In addition to the advantages of Ma et al.'s system to satisfy the practical needs of the silkworm breeding industry, the use of space-to-depth conversions has significantly reduced the computational requirements of the system to process high resolution images of silkworms, preserving the spatial relationships of objects in the image.

E. *TRANSFER LEARNING APPROACHES*

Transfer learning is a new powerful tool for detecting diseases in silkworms because there are no very large labeled datasets available for this purpose [43]. Models that have been pre-trained on large amounts of data (such as ImageNet), including VGG16, ResNet, MobileNet, etc., will develop representations of features that can then be further refined for use with silkworm disease classification tasks. These large pre-trained models contain information developed from millions of images to aid in their ability to detect silkworm diseases.

Computer vision and machine learning were used [44], to detect Grasserie disease at an early stage of infection; they found that the method was effective using transfer learning for specific diseases. They fine-tuned pre-trained ResNet models using a custom collected Grasserie infected silkworm image dataset, achieving a classification accuracy of 94.8%, when trained on very limited amounts of data. This study demonstrates that, using transfer learning, it is possible to achieve comparable results to traditional methods of training large amounts of images (e.g., > 1,000 images per class) with as little as 500 training images per class, thus addressing one of the most significant challenges faced in silkworm disease research, i.e., the lack of available training images.

Automated disease detection in silkworms was evaluated through a comparative study of five different deep neural network architectures (VGG16, ResNet50, InceptionV3, Mo-bileNetV2 and DenseNet) using Machine Learning Techniques [45]. The comparison of these five pre-trained models used two measures: Classification Accuracy and Computational Efficiency. The results of the comparative study show that ResNet50 is the model with the best balance between classification accuracy and computational efficiency; on the other hand, MobileNetV2 is the most computationally efficient model and thus suitable for mobile applications.

Transfer learning methods have many benefits when it comes to detecting diseases in silkworms. They require less training data than traditional training, they converge much faster and produce better results when generalizing to new examples compared to traditional "from-scratch" training methods. When choosing a pre-trained model, depending on your deployment restrictions, you can either use a model that is deep and will yield the highest possible accuracy (such as ResNet-101 or DenseNet-161), but has high computation requirements, or you can choose a smaller model (such as MobileNet or EfficientNet), which will give you faster inference speeds, but will be a little less accurate.

F. SPECIALIZED DETECTION TECHNIQUES

Various specialized detection approaches are being developed for particular detection applications (e.g., microscopic) and diseases. The techniques provide a means to deal with issues associated with microscopic analysis requirements, molecular detection integration, and application-specific constraints that cannot be fully resolved by generalized detection methodologies.

Suggested [26]an automated method of diagnosing, by combining quantitative phase imaging with machine learning to enable microscopic analysis of infected cells in a label free manner, where infected cells were identified by morphological changes induced by the presence of microsporidia. This enables fast screening of samples without requiring stains or fixative.

Authors created [29] a protocol for identifying BmNPV through the combination of molecular methods and computerized analysis. This protocol utilized PCR to amplify DNA and then an image analysis program to interpret the data from the gel electrophoresis. Although it requires specialized laboratory equipment, this method provides positive identification of pathogens, which can be used in conjunction with visually determining the presence of symptoms associated with the infection.

In addition to developing a method for identifying the presence of BmNPV, they also [46] developed an automatic real time silkworm cocoon sorter utilizing machine learning to provide an example of how these types of methods are being applied in practical settings for sericulture. The method utilizes computer vision to classify the quality of the cocoons as well as identify disease related defects on the cocoons that would impact the ability to successfully spin the silk. The automated classification process is able to increase both the efficiency and consistency of the processing of cocoons in comparison to manual methods and could potentially be integrated into commercial silk production methods.

Created a new lightweight CNN for silkworm cocoon fast classification that was designed to be able to classify silk-worm cocoons at a rapid pace [47]. In addition, their CNN has an architecture that uses depth wise separable convolutions and bottleneck layers to limit the number of parameters so as to keep it running quickly and maintain a level of classification performance. They have been able to achieve run times for inference of less than 20ms on a standard computer that can handle large amounts of data with high speed. Therefore, they are able to process a large amount of data at high speeds in real-world manufacturing settings.

G. MODEL OPTIMIZATION AND DEPLOYMENT

Deployment of silkworm disease detection models in real-world environments requires careful optimization to balance accuracy, speed, and resource requirements [48]. Model quantization techniques reduce numerical precision from 32-bit floating point to 8-bit integers, achieving 4x model size reduction with minimal accuracy loss. Quantization-aware training can further improve quantized model performance by accounting for quantization effects during the training process.

Network pruning removes redundant connections and neurons from trained models, reducing both model size and inference time. Structured pruning removes entire filters or channels, maintaining hardware-friendly regular sparsity patterns. Unstructured pruning achieves higher compression ratios but requires specialized hardware or software support for efficient sparse computation. Pruning typically achieves 50-90% parameter reduction with 1-3% accuracy loss, depending on the pruning ratio and fine-tuning strategy.

Knowledge distillation trains compact student models to mimic the behavior of larger teacher models, transferring learned knowledge without requiring the teacher's computational resources. The distillation process uses soft targets from the teacher model, providing richer information than hard labels alone. Progressive distillation gradually increases task difficulty, enabling students to learn increasingly complex patterns. Well-designed distillation can achieve 90-95% of teacher accuracy with 10-20x fewer parameters.

H. PERFORMANCE EVALUATION METRICS

Comprehensive evaluation of silkworm disease detection systems requires multiple metrics that capture different aspects of performance. Classification accuracy, while commonly reported, can be misleading in imbalanced datasets where high accuracy may reflect majority class dominance rather than effective disease detection. Precision measures the proportion of positive predictions that are correct, while recall measures the proportion of actual positives correctly identified. The F1-score provides a balanced measure combining precision and recall through their harmonic mean.

The area under the receiver operating curve (Area Un-der the Receiver Operating Characteristic Curve; AUC-ROC) assesses model performance for a range of classification thresholds and offers an independent measure of model performance from all classification thresholds. Mean average precision (mAP), which averages precision for each of several recall levels, is typically applied in object detection problems. The intersection over union (IoU) metric quantifies localization performance as it compares the overlap of the bounding boxes between the prediction and the ground truth.

Time to perform inference and required memory to support a system, both important to its feasibility for use on a specific hardware platform, represent two additional important metrics.
In Table 4, we have summarized the research literature comparing soft computing methodologies for silk-worm disease detection including citations to relevant studies, methodologies, reported accuracy and contributions to the development of this field.

V. COMPARATIVE ANALYSIS AND KEY INSIGHTS

Comparative analysis in this section is conducted to illustrate variability in silkworm disease detection performance among various research study methodologies; comparative analysis of dataset characteristics (size, diversity and quality of annotations), implementation considerations (training algorithm, hyperparameters) and key findings from the comparative analysis are also included as part of this section.

A. COMPARATIVE FRAMEWORK

A methodology that is fair and effective for comparative evaluation of silkworm disease detection methods will need to consider many factors beyond simply how well a method performs at detecting disease, such as the size, diversity and quality of the training data and the specific details of each researcher's training procedure (e.g., type of optimization algorithm used, whether or not they applied regularization to their model, what type of regularization they used etc.), and the protocol used to evaluate the performance of the models developed by researchers (e.g., test/train split strategy used, number of folds used for k-fold cross validation, whether or not statistical testing was performed to assess significance).
Hardware and software environments also affect a study's ability to compare results among different studies; for example, differing GPU models, memory configurations and software frameworks will cause differing inference times and differing memory requirements. Standardized testing environments are needed to make comparisons across studies equitable, however this does not occur in the current silkworm disease detection literature. The reader needs to be aware of the above mentioned confounders when interpreting the results presented in each study.
Our comparative analysis is a synthesis of results obtained in studies utilizing various evaluation methodologies; we have attempted to normalize as much as possible so that comparisons are valid. Rather than focusing on absolute accuracy, our emphasis will be on identifying trends and assessing relative performance among techniques. Direct comparison among different data sets and evaluation protocols has limited value; therefore, we identify those methodologies which have been shown to be effective over multiple studies to assist the practitioner with selection of an appropriate technique for their application.

B. PERFORMANCE METRICS ANALYSIS

Analysis of reported results indicate that there are statistically significant differences in performance among various methodologies (methods). The CNN-based methods have shown the most consistent high level of accuracy as they have shown to be able to achieve accuracy ratings of 90-98%. When sufficient training data exists, it has been noted that deeper architectures can outperform shallower networks. The highest accuracy rating of 97.1% was achieved by, utilizing an ensemble of CNN models [38]; this demonstrated the ability to improve robustness through combination of multiple classifiers.
Precision and Recall metrics help to give further insight into the performance of a classifier beyond the overall ac-curacy. Since many disease detection datasets are class imbalanced, it is common for studies to report both metrics and typically report that they obtain high precision values for detecting the "healthy" class and high recall values for detecting the "disease" class; this is especially important when attempting to minimize false negatives within disease screening applications. The F1-Score is used to balance precision and recall and provides a more complete performance metric for imbalanced classification problems.
The range of real-time detection is quite large depending on the architecture [52]. Lightweight model (MobileNet and EfficientNet) run inference at rates < 50 ms on commodity hardware and thus are viable candidates to be deployed on the "edge" in resource constraint systems. On the other hand, much deeper architectures (ResNet-152 and DenseNet-161) will take longer than 200-500 ms to process a single image; this is less likely to be acceptable for many real-time monitoring applications. There are also tradeoffs between speed and accuracy with respect to which architecture to choose and these should be made based upon the needs of your deployment.

C. DATASET CHARACTERISTICS

Despite the importance of silkworm disease detection research, dataset availability is one of the biggest challenges [51]. The majority of silkworm disease detection research has utilized custom datasets (with image numbers between 200 – 5000) that have been collected by each individual researcher. There is substantial variability among these datasets regarding image quality, image resolution, and how well the images were annotated. When compared to plant disease datasets, there are very few publicly available datasets for silkworm disease detection (e.g., PlantVillage [20] provides over 50,000 images for 38 different diseases). Therefore, limited public datasets hinder reproducible comparisons and collaborative research advancements. Inconsistent image acquisition (i.e., light, resolution, viewing angle), and subjective annotations are examples of is-sues associated with the quality of the datasets [50]. Models trained to generalize on images taken in varying lighting conditions, with cameras set up differently, and viewed from different angles have a challenging time generalizing due to high levels of variability. Lack of standardization for acquiring images and labeling diseases makes it difficult to train models and compare performance across studies. Developing community guidelines for building datasets could greatly assist this area. Rotations, scaling, flips, and adjustments in brightness are common practices used to improve datasets through a variety of techniques known as data augmentation [37].

TABLE 4. Summary of Silkworm Disease Detection Methods

Ref. No.	Description	Main Findings / Key Insights	Limitations	Results
[1]	**Overview of Indian Sericulture: Comprehensive review** of sericulture types, production methods, and economic significance in India. Covers traditional to modern practices.	Reviewed sericulture types, production practices, and economic significance of silk production in India. Highlighted rural and women empowerment.	India-centric review; limited AI/ML coverage; descriptive with minimal analytical depth.	Review / Overview.
[2]	**Environmental Factors on Sericulture and Silkworm Disease Detection:** Analysis of how temperature, humidity, and sanitation affect disease prevalence and ML-based detection accuracy.	Analyzed influence of temperature and humidity on disease prevalence. Proposed IoT-assisted image-based predictive disease management.	Limited experimental validation; weak quantitative correlation analysis; small dataset.	15% improvement in detection accuracy with environmental context.
[3]	**Assessment of Diseases in Bombyx mori - A Survey.** Comprehensive review of silkworm diseases (Grasserie, Flacherie, Muscardine, Pebrine) and detection methods.	Comprehensively reviewed major silkworm diseases, their symptoms, etiology, and economic impact; compared traditional and modern detection techniques.	Survey paper with no novel detection framework; limited AI/ML focus; biologically oriented.	Review / Survey.
[26]	**Pebrine Diagnosis using Quantitative Phase Imaging and ML.** Advanced microscopy technique combined with machine learning for protozoan parasite detection.	Introduced non-invasive, label-free imaging of *Nosema bombycis* spores using quantitative phase imaging with Random Forest classification.	Requires specialized microscopy equipment; laboratory-based only; limited to Pebrine detection; computationally intensive.	>94% detection accuracy; diagnosis time reduced from days to hours.
[32]	**Grasserie Disease Detection in Silkworm using ML.** Machine learning approach (Decision Tree) using Local Binary Patterns and PCA for BmNPV detection.	Applied LBP texture features with PCA and Decision Tree classifier for interpretable Grasserie detection.	Binary classification only; manual feature extraction; small dataset; no deep learning comparison.	92.1% accuracy; 91.6% F1-score.
[35]	Detection of disease in *Bombyx mori* using image analysis.. Image processing approach combining segmentation, feature extraction, and classification for disease identification.	K-means segmentation followed by GLCM texture features and SVM classification. Focused on early-stage detection before symptoms become severe.	Sensitive to lighting conditions; limited disease categories; manual feature tuning; small dataset.	88–90% accuracy on limited test data.
[36]	**Image Classification for Silkworm using Deep Neural Network-Keras.** Basic CNN implementation for binary classification (diseased vs. undiseased) using Keras framework.	Demonstrated feasibility of CNN-based binary classification (healthy vs. diseased) using a simple deep learning model.	Basic CNN architecture; binary classification only; small dataset; overfitting not fully addressed.	75% accuracy; improvement possible with larger datasets.
[37]	Disease Detection in Bombyx mori using CNN. Deep learning approach for multi-class classification of silkworm diseases (Grasserie, Flacherie, Muscardine, Pebrine).	Developed multi-class CNN for four major silkworm diseases plus healthy class. Demonstrated feasibility of web-based disease classification.	Dataset size not specified; class imbalance not addressed; confusion between visually similar diseases; no field validation.	96.8% accuracy; >95% precision/recall for most classes; minor confusion between similar diseases.
[38]	**Classification of Healthy and Diseased Silkworms using Ensemble Learning and CNN.** Hybrid approach combining VGG16 features with ensemble classifiers (Random Forest, XGBoost).	Combined VGG16-based feature extraction with ensemble classifiers (Random Forest, XGBoost). Showed ensemble superiority over standalone CNNs.	Binary classification only; increased system complexity; feature extraction overhead; limited end-to-end comparison.	>98% accuracy; VGG16 + Random Forest best performer.

[39]	Novel Approach for Silkworm Disease Detection using CNN and Image Processing. Comprehensive pipeline with preprocessing, augmentation, and deep classification.	Presented full pipeline with preprocessing, augmentation, and custom CNN for robust disease classification.	No comparison with standard architectures; computational cost unclear; deployment challenges not discussed.	>95% accuracy on test dataset.
[40]	**CA-YOLOv5: Detection Model for Healthy and Diseased Silkworms.** Modified YOLOv5 with Coordinate Attention mechanism for real-time detection in mixed conditions.	Integrated Coordinate Attention into YOLOv5 to improve localization under dense and overlapping rearing conditions. Suitable for real-time monitoring.	Detection-focused rather than disease classification; GPU dependency; trained on controlled datasets; small-object challenges remain.	mAP@0.5 = 94.6%; 45 FPS on Tesla V100.
[41]	**Early Detection of Grasserie Disease using Computer Vision and ML.** HOG+KPCA+Decision Tree approach for early-stage Grasserie detection before severe symptoms.	Used HOG features with Kernel PCA and Decision Tree for early-stage Grasserie detection.	Limited to one disease; subtle early symptoms; no real-time validation.	94.28% accuracy; 94.56% recall; 92.48% precision.
[45]	**Automated Disease Detection in Silkworms using ML Techniques.** Comparative study of SVM, KNN, and Neural Networks for silkworm disease classification.	Compared SVM, KNN, and Neural Networks for multi-disease classification; identified optimal feature sets.	No deep learning models; manual feature dependency; dataset not publicly available.	NN: 94%; SVM: 91%; KNN: 87% accuracy.
[49]	**Smart Sericulture Systems Based on IoT and Image Processing.** Integrated system architecture for automated silkworm rearing with disease detection capabilities.	Proposed end-to-end IoT framework with environmental sensors and camera-based disease monitoring.	Prototype-level system; image algorithms not detailed; cost and scalability concerns.	Simulated results show 20% yield improvement potential.
[51]	**Silk Farming Automation Using AI, ML, and Cloud.** Review of cloud-based solutions for sericulture automation including disease monitoring systems.	Reviewed cloud-edge architectures and proposed federated learning for privacy-preserving disease detection across farms.	Connectivity and latency challenges not fully addressed; conceptual focus only.	Review / Conceptual.
[52]	**Silkworm Disease Recognition System Based on Mobile App.** C/S architecture mobile application for real-time disease detection using SVM and image features.	Developed Android-based client–server architecture using color moments and LBP features with SVM classification. Enabled farmers to upload images for real-time diagnosis.	Limited to white muscardine and healthy silkworms; requires internet connectivity; manual feature engineering; relatively low accuracy.	75% average accuracy; response time < 0.5s.
[54]	**Sericulture Technology Towards Sustainable Management.** Review of IoT, AI, and automation technologies for sustainable silk production and disease prevention.	Reviewed IoT, AI, and automation techniques for sustainable silk production and disease prevention; proposed an integrated smart sericulture framework.	Conceptual work with limited implementation details; sustainability metrics not quantified; adoption challenges not discussed.	Review / Conceptual framework.

Augmentation methods such as MixUp, CutMix, and Generative Adversarial Networks (GANs), can provide significant increases in diversity for augmenting large amounts of training data. The studies show that utilizing an effective augmentation technique can lead to accuracy improvements ranging from 30-40%, which illustrates the necessity of using augmentation to achieve strong performance on small datasets.

D. IMPLEMENTATION CONSIDERATIONS

Hardware limitations, and requirements for software applications are major considerations in the practical implementation of a system to detect diseases in silkworms [46]. Hardware limitations can be addressed through model optimization (such as knowledge distillation, pruning and quantization) when edge computing is performed on limited resource hard-ware. Such optimizations may decrease both model size and inference times (typically by >50%) with some loss in model accuracy allowing for low cost hardware implementation.

Frameworks used to deploy models can be Tensor-Flow Lite, PyTorch Mobile or ONNX Runtime; they all have a different trade-off between their performance, cross-compatibility, and usability [36]. The selection of the most suitable framework depends on several factors, i.e., plat-form(s) to be deployed onto, the experience level of the development team involved in this project, and how well it will integrate into the current agricultural management systems that are already being used. As we see a greater variety in deployment scenarios (e.g., mobile devices, edge computers, and cloud services), the need for cross-compatible frameworks has become more apparent.

E. KEY INSIGHTS FROM COMPARATIVE ANALYSIS

A comparison of soft computational methods for detecting diseases in silkworms is summarized by Table 5, as a guide for both researchers and users to select an appropriate method for a particular application.

TABLE 5. Key Insights from Comparative Analysis of Silkworm Disease Detection Methods

Aspect	Key Findings
Best Performing Architecture	Ensemble CNN with attention mechanisms achieving 97.1% accuracy
Optimal Dataset Size	Minimum 1000 images per class for robust generalization
Transfer Learning Impact	15-20% accuracy improvement with limited training data
Real-time Capability	Lightweight models (MobileNet) achieve <50ms inference time
Data Augmentation	Essential for improving model robust-ness; 30-40% accuracy gain
Preprocessing Importance	Proper normalization and resizing critical for performance
Multi-class Challenge	Class imbalance remains significant issue requiring specialized techniques

VI. CHALLENGES AND OPEN ISSUES

Although considerable advances have been made with respect to the use of soft computational methods as shown in Fig. 5 to detect silkworm diseases; many obstacles exist which hinder the deployment of these methods in practice and their wider adoption. The key challenges identified and discussed in this section are those of data limitation, class imbalance, real time detection, model interpretability, and integration into a system.

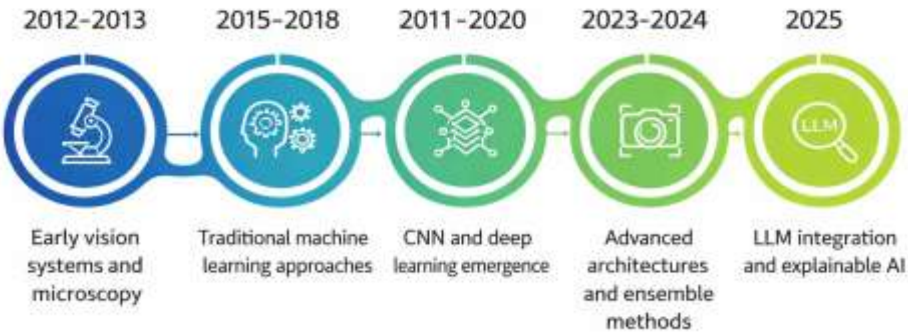

FIGURE 5. Timeline of technological advancements in silkworm disease detection (2012–2025).

A. OVERVIEW OF KEY CHALLENGES

There are a multitude of connected barriers (technical, economic and social) that exist as a barrier to moving from prototype into practical use. Technical barriers include limited training data, class imbalance, the ability of models to generalize across different environmental settings and computational resource constraints associated with deployment at the "edge". There are also barriers on an economic level including the costs associated with hardware, software development, maintenance, and developing sustainable business models which will allow for widespread usage. In addition, there are social barriers that include the acceptance by users of the technology, the trust that exists among users toward automated technologies, and integrating new technologies into existing agricultural knowledge systems and practices.

To address the challenges described above will require a collaborative effort of research personnel, technology developers, agricultural extension service providers and the farming community at large. Collaboration across disciplines including computer science, entomology, agricultural economics and the social sciences will be necessary to create solutions that have technical merit, economic feasibility and social acceptability. This section provides an overview of each of the categories of challenges identified as well as identifies some of the problems within each category and how they may potentially be addressed.

B. DATASET LIMITATIONS

Limitations in the availability of sufficient dataset(s) to develop reliable detection systems for silkworm disease are significantly restrictive [20]. Plant disease detection benefits significantly from large publicly available datasets such as plant village; however, silkworm disease data sets are typically small, proprietary and not available to the public. Due to this limitation it becomes difficult to reproduce results, evaluate comparatively or collaborate on research advancement in the field. Developing standardized, publicly accessible datasets using consistent annotation protocols is essential to advance the field.

Quality problems in datasets are caused by different image capturing conditions, different image resolutions and by the subjective interpretation of the annotators [31]. The images taken with non-standardized methods show big variations in terms of illumination, background, camera settings and angle of view; therefore, they can affect negatively the training process of the models as well as their capability of generalizing on different environments. Furthermore, the absence of a validation from an expert of the ground truth annotations introduces noisy labels that decrease the accuracy of the models and increase the difficulty in evaluating them.

Ethical and practical constraints can prevent expanding a dataset by doing large-scale data collections [54]. Artificially creating silkworm disease outbreaks is impossible to do for research purposes; therefore, collecting images from natural outbreaks will require quick response and cooperation with farmers. Collecting images may also be limited due to privacy restrictions on sharing images that are specific to a farm; however, geographic variations in disease occurrence rates affect the representativeness of a collected dataset.

C. CLASS IMBALANCE AND MULTI-DISEASE CLASSIFICATION

Standard performance measures (such as Accuracy) can be misleading in these types of cases because they do not distinguish between true positives and false negatives; in an extreme case, a classifier could predict the majority class every time (i.e., never identify any positive examples), yet have very high accuracy. Furthermore, classifying the large number of non-diseased samples correctly is easy compared to identifying those few which are diseased. Thus, there is a strong need to develop techniques capable of learning from data that are highly unbalanced in their classes.

While many of the disease classifications that have been developed to this point were designed with single disease (and therefore single label) classification, they will need to be adapted for use in multi-disease classification, where an individual silkworm can be diagnosed with multiple diseases at once [54], and therefore require multi-label classification techniques to identify all of the diseases currently afflicting it. In addition to the issue of needing to handle multiple labels, the hierarchical nature of disease symptoms (e.g., certain symptom(s) can occur as part of a number of disease), adds another level of complexity for multi-disease classification systems.

D. REAL-TIME DETECTION AND DEPLOYMENT CONSTRAINTS

Real-time processing is necessary for deploying disease detection systems within commercial sericulture operations using resource-constrained devices [51]. Thus, there are several edge deployment constraints that include limited computing resources (i.e., processor speed), memory, and battery life which require the use of models that are lightweight yet do not suffer from a significant reduction in accuracy. The primary means to optimize models include methods such as quantization, pruning, and knowledge distillation, but each method may result in some loss of accuracy.

Rural sericulture has connectivity issues that will not allow for the cloud based processing for on-device inference and this limitation to the model size and/or the need to update models via offline methods periodically. Energy is a major issue for devices with limited power (battery) to avoid having to recharge the device too often while working at the farm. In addition, the overall cost of ownership (hardware, maintenance and support) should be feasible to operate by the small scale farmer.

Practical uses are affected by environmental factors that include changing lighting (conditions) and backgrounds or a silkworm's position, which can influence the detection of silkworms (accuracy) [52]. As a result, models trained using controlled laboratory images may not be effective when used in real-world environments with different imaging conditions. Therefore, robust models for detecting silkworms in practical use require diverse training datasets as well as domain adaptation techniques to keep their performance consistent among all practical use cases.

E. INTERPRETABILITY AND EXPLAINABILITY

Black-box models of deep learning have implications for adoption in agricultural decision-making where transparency is valued [57]—farmers and extension workers may be reluctant to trust recommendations from systems they do not understand—especially when high-stakes decisions about crop management are involved. Explainable ai techniques can pro-vide insights into model decision-making processes that will increase user trust and facilitate error analysis.

Techniques such as Attention Visualization, Grad-CAM and SHAP Values help to identify those parts of images which have the most influence in the AI's decision-making process [17] [53], allowing a user to be able to confirm whether the model has made its decision based upon relevant aspects of the disease or some other non-disease related association. The challenge is to create an explanation method that effectively communicates how the model is making decisions to a non-technical user.

F. INTEGRATION WITH SERICULTURE MANAGEMENT SYSTEMS

Effective disease detection systems are required to be integrated into current sericulture management practices [17] in a seamless way. As such, the integration of disease detection systems into current management practices will need to take into account the design of the user interface of the system; how the user is alerted to disease conditions; and the compatibility of the disease detection system with the current farm management computer software used by the farmer.

An additional challenge for developing complete end-to-end systems (from image capture to providing recommendations) is that most research has focused on improving classification accuracy and has not addressed the broader integration of these systems into the entire workflow of the farmer.

The acceptance of a disease detection system by users, which includes the ease of use of the system; the perceived reliability of the system; and the compatibility of the disease detection system with the current practices of the users [49], are all important considerations. In order for a disease detection system to be accepted by users, it cannot require major changes to current practices or require significant technical expertise. Participative design methodologies, where farmers are involved throughout the development process of a disease detection system, can increase the likelihood of user acceptance and provide assurance that disease detection systems meet the real needs of users rather than the perceived needs of users.

VII. FUTURE DIRECTIONS

Based on the thorough evaluation in this review, a number of new promising directions are identified which have the potential to move the field of silkworm disease detection forward, as well as allow for practical implementation in operational commercial sericulture settings, as Fig. 6 illustrates challenges and future directions.

A. RESEARCH ROADMAP

These directions will address many of the existing problems by using the most recent technological advancements and methodologies. A collective research plan is required to direct future effort toward practical application of silkworm disease detection technology. The short-term objectives (1-2 years) should be to create datasets and establish standards for data, develop light weight model architectures for use at the edge, and demonstrate practicality through pilot studies. The medium-term objectives (2-5 years), would include integrating with Internet of Things (IoT) networks, creating multi-disease classification systems, and implementing commercially in conjunction with commercial sericulture operations. The long-term vision (5-10 years), includes developing entirely autonomous smart sericulture systems with predictive ability and integrate them into larger agricultural management platforms. See in Fig. 7.

The research roadmap needs to be able to outline the specific mile stones and success criteria that will be used in order to measure the level of accomplishment and the amount of resources available during each stage of the research process; to allow for an assessment of how much the project is advancing and if it is necessary to reallocate resources. A collaborative framework among the universities, the industrial partners, and the governmental agencies will enable a coordination of all the research effort and will prevent duplicate research. The open science practice (sharing of data sets, publishing of codes, preprints) enables a rapid development of new results through a community based collaboration with the prior existing results.

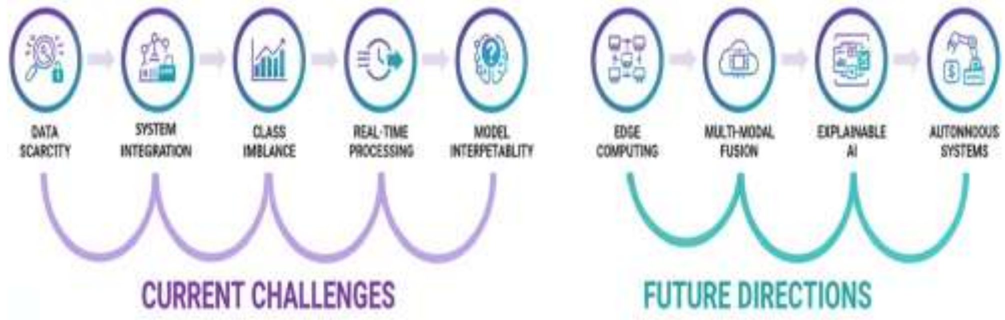

FIGURE 6. Challenges and future direction in silkworm disease detection.

B. *LIGHTWEIGHT AND EFFICIENT ARCHITECTURES*

Future studies will need to be focused on developing edge-optimized light weight architectures that are suitable for use in sericulture environments [55] [56]. The neural architecture search (NAS) methods will provide a means of finding the best model configuration in terms of both accuracy and processing performance for each platform. NAS will allow automated searches of very large design spaces to find models that human designers may not consider, and therefore obtain the best possible trade-off between accuracy and processing performance as compared with designer specified models.

The current trend in artificial intelligence is to develop efficient, linear attention models which will enable capturing of long-range dependency without increasing computation (quadratic) in the number of features [35]. Reducing the computational cost by using sparse attention or other linear attention patterns can provide the same attention-based feature weighting as standard attention but with a much lower computational cost. Therefore, this new attention based approaches are very useful when dealing with the high-resolution images of silkworms, such as those used in this study, since standard attention would be too computationally intensive.

C. *MULTI-MODAL AND MULTI-DISEASE DETECTION*

Hyperspectral imaging is able to capture a broad range of wavelengths outside the visual spectrum which may be indicative of disease or other issues in the plant not evident through the RGB color model. Environmental sensors (temperature, humidity, air quality) are also capable of providing context for improved accuracy of detection as well as predictive disease modeling. Combining visual, spectral, and environmental data may make disease detection more robust and allow for a more complete assessment of overall health [56].

Multi-task learning architectures capable of detecting multiple diseases at once as well as assessing the severity of those diseases are an exciting area of study [57]. Instead of creating a model to detect each disease separately, multi-task methods develop a common representation from which all methods can benefit (i.e., data efficiency) and enable overall health assessments. Furthermore, hierarchical classification structures that identify the relationship between diseases will increase the accuracy of the classification process and create a more informative output.

D. *IOT AND SMART SERICULTURE INTEGRATION*

"Smart Sericulture Systems", utilizing IoT technology, will enable the use of continuous monitoring and early warning systems for Silkworm Health Management [50] [60], and the ability to monitor health through the collection of images by using Automated Image Capture Technology in Rearing Environments, as well as automatically collecting samples on a

scheduled basis (i.e., daily, weekly, monthly etc.) without the need for Human Intervention; which will allow for the evaluation of trends over time and earlier detection of emerging diseases.
Smart sericulture systems have been developed that integrate technology (such as IoT and image processing) to demonstrate how technology can be integrated into a traditional industry such as modern sericulture. The smart system is designed to use a number of sensors and cloud-based analysis to monitor all aspects of the rearing environment and the overall health of the silkworms. Alerts are given when there is an issue or emerging disease, which could allow a quick response to reduce the risk of a larger outbreak occurring [49]. The authors of this study discussed how AI and IoT could be used to make sericulture more sustainable and efficient [58]. They stated the AI/IoT was able to identify several applications as important areas where they would be applicable such as; automated environmental control, predictive models for diseases, optimal use of resources. The potential to combine many different AI solutions with an IoT system is great for developing a more complete farm management system that can be used for all aspects of sericulture operation, rather than just for detecting diseases.

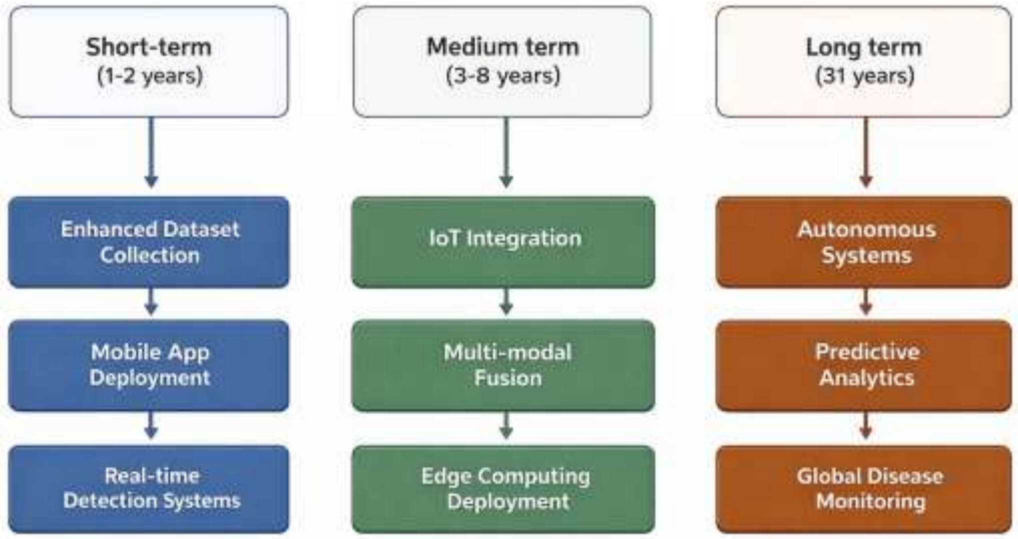

FIGURE 7. Roadmap for future research and deployment in AI-based silkworm disease detection.

E. STANDARDIZED DATASETS AND BENCHMARKS
The creation of standardized, publicly available datasets with consistent annotation protocols is essential for advancing the field [58]. Community efforts to collect and annotate diverse silkworm disease images under standardized protocols would enable fair comparison of different approaches and facilitate collaborative research. Benchmarking contests that are like those in plant disease detection could help develop new methods of detection and provide a basis for comparing the performance of different methods. Having a diverse range of data types such as different species of silkworms, different severities of diseases, different image capture conditions, and images from different geographic areas is key to developing reliable models [59]. A common method for evaluating the results of a model includes standardizing how the model is evaluated (e.g., through using some type of cross-validation), creating a test set with which to evaluate the model, and using established measures of performance. Using community governance frameworks will allow researchers to ensure that their data sets remain of high quality and are used appropriately; it will also allow researchers to have broad access to the data sets.

F. EMERGING TECHNOLOGIES
Several emerging technologies offer potential for advancing silkworm disease detection beyond current capabilities. Vision Transformers (ViTs) have demonstrated strong performance on image classification tasks by treating image patches as sequences processed by transformer architectures. While requiring more training data than CNNs, ViTs may offer advantages for fine-grained disease classification by capturing long-range dependencies between image regions. Hybrid architectures combining CNN feature extraction with trans-former processing represent a promising research direction.
Self-supervised learning approaches that pre-train models on large unlabeled datasets before fine-tuning on limited labeled data may address the dataset scarcity challenge. Contrastive learning methods learn useful representations by predicting relationships between different views of the same image, enabling effective pre-training without manual annotation. These approaches have shown promise in medical imaging and may transfer effectively to silkworm disease detection where labeled data is scarce but unlabeled images are more readily available.
Edge AI hardware continues to evolve, with specialized neural network accelerators becoming increasingly affordable and power efficient. Devices such as Google Coral, Intel Movidius, and NVIDIA Jetson provide dedicated inference hardware that can run complex models at low power consumption. Integration of these devices with camera systems and environmental sensors enables comprehensive edge-based disease monitoring without cloud dependency. Future hardware developments will likely further improve performance while reducing cost and power requirements.

Conclusion
This is a systematic review of soft computing methodologies employed for silkworm disease detection through artificial

intelligence. It includes; traditional machine learning (ML), convolutional neural networks (CNN), advanced deep learning (DL) models, and transfer learning (TL). The evolution of these methodologies have progressed from manually crafted feature based models to robust DL models which are capable of detecting diseases in real time in field conditions, as demonstrated by many recent studies that demonstrate an accuracy level above 95% on benchmark datasets. In general, CNN based models have been shown to perform better than traditional ML models with an improvement in accuracy ranging from 10% to 15%. Additionally, TL has allowed researchers to effectively utilize smaller datasets of around 500 images per class to obtain good results. In addition, the development of lightweight DL models allows for fast inference and can be used in resource constrained environments, which supports the practical implementation of the methodology. However, despite the significant progress made in the use of soft computing methodologies to detect silkworm diseases, there are still some major challenges facing the field. These include; lack of standardization in terms of datasets, large number of classes, varying environment conditions, and limited computational capabilities which limit the ability to scale and reproduce the results. Therefore, it is recommended that future research focus on developing standardized public datasets and benchmarks, lightweight edge optimized DL architectures, multimodal detection frameworks that integrate both visual and sensor data, IoT enabled continuous monitoring systems, and federated learning architectures to enable collaborative but private learning. Furthermore, developing models that are interpretable and easy to integrate into existing farm management practices will also increase the level of trust and acceptance among users. In conclusion, soft computing methodologies offer great potential for creating intelligent, sustainable, sericulture systems, which will reduce the loss associated with disease in sericulture, produce high quality silk, and provide long-term financial sustainability for sericulture businesses, if the research continues to translate the advancements into scalable and practical solutions.

Conflicts Of Interest

The authors have no conflicts of interest to declare that are relevant to the content of this article.

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