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Grasserie Disease Identification in Bombyx mori Silkworm using Ensemble Learning Approach

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***Abstract* — Sericulture is an agricultural activity that involves rearing of silkworms for the production of cocoons which is in turn used to produce raw silk. In countries like India where agriculture is pre-dominant, sericulture is considered to be one of the most important economic activities. India ranks second among the silk producing countries in the world, accounting for over 17 percent of the world's production. The major activities of sericulture comprise of food-plant cultivation to feed the silkworms, spin silk cocoons and reel them for unwinding the silk filament for processing and weaving to produce valuable silk products. Though technology has been a boon to the agricultural sector, there is not much implementation of technological methods in disease detection in silkworms. But diseases in silkworms pose a major threat and causes a huge economic loss to farmers which in turn necessitates early identification of diseases and this is quite an arduous process. Identification and detection of diseases at an earlier stage would be helpful for a farmer to take essential precautionary measures to avoid spreading of diseases. With the advancement in technology, a variety of methods have been developed to address this issue. In this paper, different machine learning algorithms are compared for their accuracy and the best ensemble learning algorithm is adopted which can be further implemented on a hardware model for real-time applications. The developed algorithm aids the machine in decision making and hence identifies grasserie disease in Bombyx mori silkworm.**

Keywords— Bombyx mori silkworm, deep neural networks, image classification, sericulture, silkworm diseases, TensorFlow.

I. INTRODUCTION

Silk is the most elegant textile in the world and is known as the "Queen of Textiles". Rearing of silkworms to produce silk is known as sericulture which stands for development of a largely agrarian economy like India. It provides a livelihood for millions of people and most importantly contributes to women empowerment by creating a large number of opportunities for them to work. The fact that it is low capital intensive makes it one of the most important economic activities in the country. India has the unique distinction of being the only country producing all the five known commercial silks, namely: Mulberry, Tropical Tasar, Oak Tasar, Eri and Muga. Sericulture is a labor-intensive economic activity that employs over 7.9 million people in India. Most of the rural households practice sericulture, which improves their economic condition as well as elevates the employment opportunities in the country. There is a great potential for massive growth in the demand of silk in the years to come which is evident from the current growth rate of silk demand accounting for about 5% increase annually. This necessitates the production of high quality of silk which in turn requires adoption of measures to ensure good health of silkworms. Silkworms being very sensitive organisms need to be reared under highly cautious conditions. As depicted in [1], silkworms are prone to a variety of fungal, viral and bacterial ailments due to unfavorable environmental conditions, unhealthy rearing conditions, negligence of farmers and feeding on diseased mulberry leaves. Once the worms are infected, it damages around 30-40% of the yield which pushes farmers into crisis. Hence detection of diseases is the prominent process to lower loss in the yield. This is a major challenge in the sericulture industry as explained in [2] and causes serious economic losses to farmers. Farmers need to take utmost care in maintaining the optimum environmental parameters for healthy rearing of silkworms. At present, not many methods involving Artificial Intelligence techniques and Internet of Things (IoT) have been implemented for recognition and classification of diseases in silkworms. Currently, traditional methods involving sophisticated clinical methods are widely being adopted for identifying different classes of diseases in silkworms which often require highly accomplished professionals and scientists in order to conduct clinical research and experiments which is not possible by farmers in rural households. Moreover, these methods are time consuming which is not reliable in cases where disease recognition is to be performed spontaneously and efficiently.

This paper adopts a method that uses machine learning ensemble algorithms to identify grasserie disease in Bombyx mori silkworm. Initially, six different machine learning classification algorithms are trained by feeding the silkworm image dataset consisting of images of both healthy and diseased worms. The accuracies of all the models are evaluated and the best model is selected based on careful analysis of evaluation metrics. This method will reduce complexity in disease identification and the time required to identify them. It also eliminates the requirement of skilled people for carrying out such processes. By using signal processing methods, detecting the disease in earlier stages helps farmers to avoid loss in their yield by taking necessary actions to prevent spreading of diseases.

II. RELATED WORK

The growing demand of silk and its associated products has entailed the sericulture industry to adopt efficient mechanisms and methods for rearing silkworms in order to ensure production of high quality of silk. However, the worms get infected due to a variety of other factors pertaining to external conditions and human negligence. As described in [3], diseases in silkworms usually arise due to contaminated rearing house and rearing bed, feeding on contaminated mulberry leaves or direct ingestion of bacteria into the silkworm haemocoel and this will ultimately lead to the breaking of cuticle. The article [4], mentions about diseases in silkworm eggs and has adopted blob analysis to identify diseases in these eggs. In the literature [5], a brief survey on various diseases that occur in silkworm, techniques to identify these diseases are presented. The authors of [6], have presented a clinical approach for detection of flacherie virus in Bombyx mori using RT-PCR and nested PCR. The experimentation involved in this method is quite intensive which requires highly skilled people to carry out complex mechanisms in order to identify diseases in silkworms. As elucidated in [7], IoT is leading the way in automating agricultural processes. Here, the authors have implemented an IoT system involving an inter-connection of sensors for disease recognition in silkworms along with an image processing unit. The IoT system consists of an ARM processor integrated with a number of sensors and actuators. The images are captured using a digital camera and are processed using a variety of algorithms such as image denoising, feature extraction, Ostu’s image identification algorithm and application of Gabor filters. The processor is interfaced with humidity, temperature and color sensors. In [8], the authors have presented an automated embedded system that can directly be used for real time monitoring of external environmental conditions suitable for healthy rearing of silkworms. It also explains the application of digital image processing techniques such as edge detection, correlation, histogram analysis of images and image transformation techniques to the images captured by the camera integrated with the embedded system. The authors of [9] have adopted an attention-based deep learning method to solve the problem of suppressed characteristics of diseased portions in images of silkworms. This attention-based model is coupled with a dense convolutional neural network for effective disease recognition. The proposed model has achieved an average disease recognition rate of 85.65 for 600 silkworm disease images. This algorithm has outperformed most of the traditional deep learning algorithms. In the literatures [10-12], various models of CNNs have been proposed for disease recognition in leaves, apples and cucumbers respectively. This forms the basis for further research in developing highly efficient deep learning models. The article [13] has proposed an approach to identify mildew disease in pearl plant millet in which the results were 95% accurate. This method is based on transfer learning with feature extraction. In the paper [14], a method for classification and identification of pathological diseases in plant species using web applications is proposed. A technique to identify diseases in corn plant, based on convolutional neural network is defined in [15]. In the literature [16], a method based on image processing and deep neural network is discussed for the identification of different varieties of flowers using Tensor flow framework. The above cited literatures and articles have proposed various methods to identify, recognize and classify diseases in different varieties of plants, leaves, fruits and flowers. This paper deals with the identification and classification of grasserie disease in Bombyx mori silkworm using machine learning classification algorithms. In [17], an image analysis approach has been described for the purpose of disease identification in silkworms that involves a Convolutional Neural Network (CNN) trained on healthy and diseased images of Bombyx mori silkworms. In [18-23], different deep neural networks have been described for the purpose of disease identification not only in silkworms but also in plants and crops. Such methods based on deep neural networks have shown superior performance when compared to traditional image processing methods.

III. METHODOLOGY

Grasserie is a common viral disease of silkworms caused by baculovirus. Some of the major factors contributing to this disease are high temperature, high humidity and poor quality of host plant leaves. At present, detection of this disease is done by tracing the initial inoculum in the body of the silkworm. Most of the existing techniques are clinical methods that use microscopes making them cost ineffective and they involve high complexity which is not affordable by farmers. This necessitates the adoption of deep learning and machine learning techniques in order to efficiently identify diseased worms which is less complex in nature and easy to implement with hardware for real-time monitoring of the silkworm rearing chamber. The following block diagram representation depicts the machine learning method adopted in this paper to effectively identify diseases in Bombyx mori silkworm.

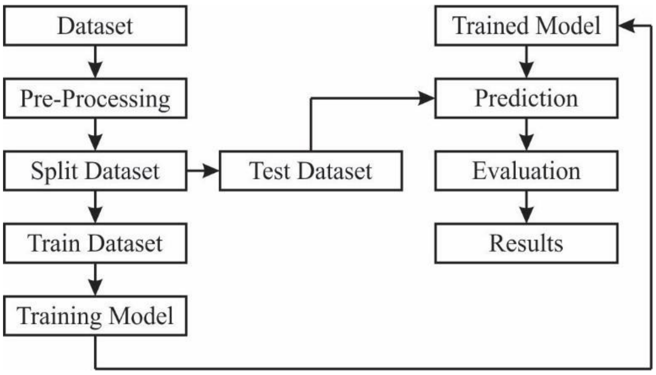


Fig. 1. Proposed Methodology

Figure 1 represents the methodology adopted for the purpose of disease identification in silkworms. In this method, the initial step involves collection of silkworm images and preparation of image dataset. This includes images of both healthy as well as diseased silkworms. The initial dataset consists of 243 images of healthy silkworms and 361 images of diseased silkworms. Following this, image lists are created with appropriate labels namely, “Healthy” and “Grasserie”. These lists are then iteratively converted into arrays and the images are resized with dimensions (150*150*3). The conversion of image lists into arrays ensures faster computation of machine learning algorithms. The next step involves splitting of the image dataset into train and test samples. Nearly 20% of the images are taken for testing purposes and is not trained. The train dataset is then given as input to various machine learning classification algorithms which learns features at various levels from the image samples. These algorithms are called supervised machine learning algorithms as dataset is labelled and the final desired result is known to the classifier. In this paper, six different algorithms are trained with the silkworm image dataset and the performance of the models are compared in order to obtain the best classification algorithm. Table 1 shown below briefly provides an overview of the classification algorithms that were trained using the silkworm image dataset along with their test set accuracies. It can be inferred that AdaBoost classifier results in maximum test accuracy of 81.818% followed by k Nearest Neighbors (kNN) classifier. The AdaBoost classifier works on the basis of a boosting algorithm that combines the accuracy of several base classifiers to produce a final output with an overall increase in accuracy. Hence for the purpose of identifying Grasserie disease in Bombyx mori silkworm, the AdaBoost classifier is adopted in this paper.

TABLE 1: COMPARISON OF DIFFERENT CLASSIFICATION ALGORITHMS ALONG WITH TEST ACCURACIES

Name of the Algorithm	Test Accuracy (in %)
AdaBoost Classifier	81.818
K Nearest Neighbors Classifier	79.338
Random Forest Classifier	77.686
Support Vector Machine Classifier	77.685
Gradient Boost Classifier	76.859
Meta-Bagging Generator	76.033

IV. ENSEMBLE TECHNIQUES

Ensemble Techniques are machine learning methods which produce an optimal predictive output by combining several base learning models. Ensembles are much more accurate in most of the cases than the individual classifiers which form them. An ensemble algorithm contains numerous hypotheses or learner models that are a subset of training data and they are finally combined to obtain the results. The function of ensemble methods is that they adopt an algorithm that boosts the performance of weak learners. The learning algorithms which output only a single hypothesis tend to suffer from statistical, computational and representation problems which can be overcome by implementing ensemble methods. Most of the traditional learning algorithms fail in obtaining higher accuracy due to higher variance, higher bias or due to higher computational variance which are a result of the above stated problems. The ensemble methods to a large extent maintain both bias and variance of traditional learning algorithms at the optimal level. The various ensemble techniques that exist are bagging, boosting and stacking. Bagging is also known as Bootstrap Aggregation which is an effective yet simple ensemble method. Bootstrap is a method of data sampling with replacement and it uses multiple versions of the training set. In this paper, two different bagging methods are tested for their accuracies namely: Meta-Bagging Generator and Random Forest Classifier which showed accuracies of 76.033% and 77.686% respectively. Boosting algorithms can be seen as model averaging methods. These algorithms are widely used ensemble methods and most powerful in terms of learning hypothesis. Typical boosting algorithms combine three weak learners to generate a strong learner. In this paper, two boosting algorithms are compared for their accuracies namely: AdaBoost and Gradient Boost Classifier. These models have obtained accuracies of 81.818% and 76.859% respectively. Stacking is a method in which multiple classifiers are combined and predictions are generated by using different learning algorithms on a single dataset. This technique consists of two parts, where a set of learner-level classifiers are first generated and then a meta-level classifier is learned. The meta-level classifier combines the outputs of the learner-level classifiers to give the final predictive result. For this problem, the AdaBoost classifier algorithm has shown the highest accuracy of 81.818%.

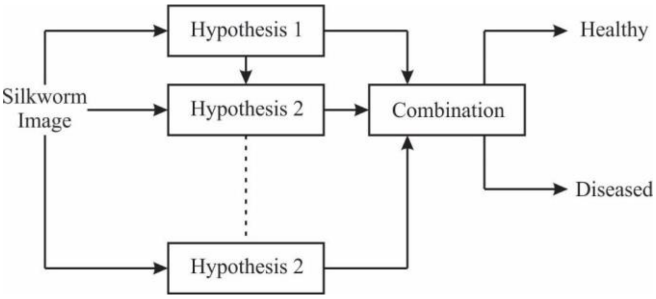


Fig. 2. Ensemble Learning Method

Figure 2 represents a block diagram of the Ensemble Learning method used in disease identification of silkworms. The input block consists of the silkworm images which consists of both healthy and diseased worms. This is fed to a series of hypothesis also known as learner models. This network learns different low-level features like and high-level features and the learned parameters are combined to obtain the final weights of the model which is used to distinguish between healthy and diseased silkworms. The following section describes the working of the AdaBoost classifier and presents a mathematical intuition of the algorithm.

V. ADABOOST CLASSIFIER

AdaBoost which is also known as Adaptive Boosting is an ensemble-boosting classifier. It combines multiple weak classifiers to increase overall accuracy of the result. The prime function of AdaBoost is to set the weights of the base classifiers and train the data samples in each iteration which thus ensures accurate predictions of unseen data. The basic working principle behind AdaBoost is that the boosting classifier should be trained iteratively on various weighed training samples and in each iteration, the training error should be reduced to maximum extent which is possible by providing an appropriate fit to the training samples. The AdaBoost classifier works on the following mathematical model. Initially, training subset $(x_1, y_1)....(x_m, y_m)$ is chosen at random where each xi belongs to the sample space of the training subset and each y_i represents a class label. Assuming that N represents the total number of input samples, the classifier calls a weak hypothesis repeatedly in $t = 1, 2, 3, ..., T$ rounds. The algorithm maintains a set of weights over the training sample i and these set of weights is denoted by $D_t(i)$. At the beginning of the first iteration, the weights are set equally for each sample which is represented as $D_i(i) = \frac{1}{N}, \quad 1 = 1, 2, ..., N$ where D_t represents the distribution of the given data. The weights of the incorrectly classified samples are increased in each round so that the weak hypothesis focuses on the incorrectly predicted samples. For T rounds, a sample D_t is obtained by sampling D with replacement by taking into consideration the weights of the data points. A weak hypothesis is then obtained as

$h_t : X \rightarrow \{1, -1\}$ by training a weak learner using D_t . The weak hypothesis is iteratively updated to obtain the most optimized loss or the error function. The weighted error function is given by: $\sum_{i=1}^{N} D_t(i)\{h_t(x_1 \neq y_i)\}$ (1)

The weak hypothesis or the learner algorithm is updated after each round from 1 to T and the updated data points are given by:

$$D_{t+1}(i) = \frac{D_t(i) e^{-y_i \alpha_t h_t(x_i)}}{\sum_{i=1}^{N} D_t(i) e^{-y_i \alpha_t h_t(x_i)}} \quad (2)$$

Finally, at the end of the T^{th} round, the output weighted resultant hypothesis is obtained as

$$H(x) = sign\left(\sum_{t=1}^{T} \alpha_t h_t(x)\right) \quad (3)$$

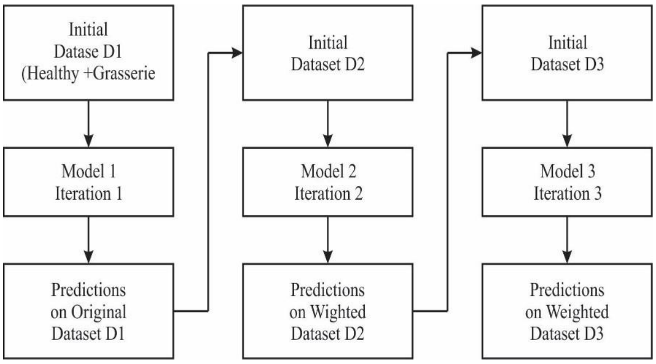


Fig. 3. AdaBoost Classifier

From figure 3, it can be inferred that initially the dataset D1 is fed to the ensemble classifier that consists of images of both Healthy and Grasserie silkworms. D1 is a sampled version of the original dataset. The model learns features at various levels and predictions are made on this sampled dataset. This weighted model is the first hypothesis or the learner algorithm. These predictions are fed to the next sampled dataset D2 and the second hypothesis is made to learn from this dataset. This process continues and finally at the last level, the weighted hypothesis from every level is combined to give the overall prediction of the classifier model.

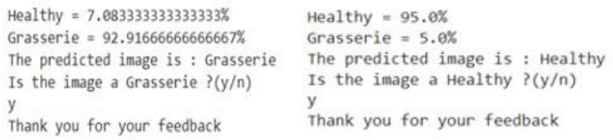
VI. RESULTS AND DISCUSSION

The proposed methodology has been tested under several conditions considering two classes of silkworm images namely: “Healthy” and “Diseased”. The image dataset is trained on Google colab platform with GPU hardware accelerator. Once the dataset has been pre-processed and split into train and test set, various classification machine learning algorithms are trained to identify and classify Grasserie disease in silkworms. AdaBoost Ensemble Technique showed the highest accuracy of 81.81%. Once the appropriate algorithm is chosen, a hardware model has to be designed so that the proposed system can be employed in real time. For real time applications, Raspberry Pi can be used which works on Raspbian OS. An alternative to Raspberry Pi is a Jetson Nano by NVIDIA that works on Ubuntu.

Fig. 4. Diseased Worm

Fig. 5. Healthy Worm

Figure 4 and Figure 5 represent the input fed to the AdaBoost classifier belonging to two classes namely Grasserie affected silkworms and Healthy silkworms respectively. On passing these images to the classifier algorithm, the silkworms are rightly classified as healthy or diseased. A GUI is developed for increasing the accessibility of the model to farmers. The GUI is would enable farmers to capture and upload images of silkworms in order to determine its health. The trained model is saved in pickle file format for easy usability. Figure 6 depicts the GUI interface provided to farmers for viewing and analyzing the health of silkworms.



```
Healthy = 7.083333333333333%
Grasserie = 92.91666666666667%
The predicted image is : Grasserie
Is the image a Grasserie ?(y/n)
y
Thank you for your feedback
```

```
Healthy = 95.0%
Grasserie = 5.0%
The predicted image is : Healthy
Is the image a Healthy ?(y/n)
y
Thank you for your feedback
```

Fig. 6. GUI Interface

Figure 7 represents a 2x2 confusion matrix which gives an overview of the overall performance of the model. The vertical axis of the matrix represents the true classes of the dataset and the horizontal axis represents the predicted values on the test data. Taken in clockwise order, the blocks of the confusion matrix represent the following values: True Positives, False Negatives, False Positives and True Negatives. Here, index 0 represents the healthy class and index 1 represents grasserie class. The initial dataset obtained after pre-processing consists of 604 images of silkworms which includes both healthy as well as diseased worms. After the dataset is split, 20% of the data is untrained and taken for testing purposes i.e., 121 images which further consists of 49 healthy samples and 72 grasserie image samples. The confusion matrix also depicts the percentages of correctly and falsely predicted classes of images. Out of 49 healthy samples, 37 images (30.58% of 121) are correctly predicted whereas 12 (9.92% of 121) are false. Out of 72 grasserie samples, 62 (51.24% of 121) are rightly predicted whereas 10 samples (8.26% of 121) are falsely predicted.

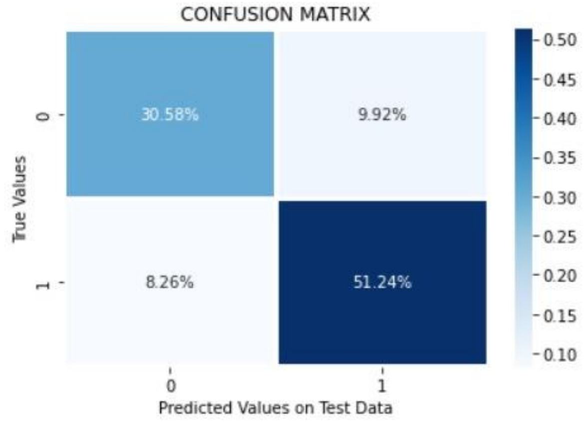


Fig. 7. Confusion Matrix

VII. LIMITATIONS AND CHALLENGES FACED

The machine learning ensemble algorithms are comparatively more accurate than traditional image processing methods. They are computationally faster, less complex and hardware compatible. Even though these algorithms are efficient, there are several challenges faced in this process. The main challenges were in the procurement of the image dataset and in the orientation of the silkworm. The disease can be detected more accurately if the silkworms are in correct orientation. If orientation of the silkworms while procurement of images is improper, it would lead to incorrect results. The size of the dataset used for training the model greatly defines its accuracy. Hence a large sized dataset is always desirable for higher accuracy. In order to obtain larger dataset, image augmentation can be employed.

VIII. CONCLUSION

Silkworms need to be reared with utmost care and due to a plethora of reasons and circumstances, these worms are affected with dreadful diseases that might cause a huge loss in the sericulture industry. This necessitates the introduction of technological interventions to reduce human interference and ensure high efficiency. This paper provides an efficient ensemble learning algorithm to recognize diseases in silkworms with an accuracy of 81.81% on test data and is also hardware compatible for real time applications. The proposed model is saved in pickle file format which makes it reusable and accessible. This method does not involve computationally expensive neural networks and thus involves minimal complexity but ensuring that the accuracy is not compromised. The results obtained are faster and reliable which will alert farmers in the initial stages of the disease so that precautionary methods can be adopted to avoid further spread of the disease. The model would be employed on hardware such as Raspberry Pi or NVIDIA Jetson Nano for efficient real time monitoring of the rearing chamber. This system can be further developed into an end-to-end IoT system for monitoring other essential parameters such as temperature, moisture and humidity along with disease classification and identification of silkworms. The current model is restricted to identify only Grasserie disease which can be further extended to identify other diseases as well.

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