

# A Machine Learning Based Framework for a Stage-Wise Classification of Date Palm White Scale Disease

Abdelaaziz Hessane, Ahmed El Youssefi, Yousef Farhaoui\*, Badraddine Aghoutane, and Fatima Amounas

**Abstract:** Date palm production is critical to oasis agriculture, owing to its economic importance and nutritional advantages. Numerous diseases endanger this precious tree, putting a strain on the economy and environment. White scale *Parlatoria blanchardi* is a damaging bug that degrades the quality of dates. When an infestation reaches a specific degree, it might result in the tree's death. To counter this threat, precise detection of infected leaves and its infestation degree is important to decide if chemical treatment is necessary. This decision is crucial for farmers who wish to minimize yield losses while preserving production quality. For this purpose, we propose a feature extraction and machine learning (ML) technique based framework for classifying the stages of infestation by white scale disease (WSD) in date palm trees by investigating their leaflets images. 80 gray level co-occurrence matrix (GLCM) texture features and 9 hue, saturation, and value (HSV) color moments features are extracted from both grayscale and color images of the used dataset. To classify the WSD into its four classes (healthy, low infestation degree, medium infestation degree, and high infestation degree), two types of ML algorithms were tested; classical machine learning methods, namely, support vector machine (SVM) and  $k$ -nearest neighbors (KNN), and ensemble learning methods such as random forest (RF) and light gradient boosting machine (LightGBM). The ML models were trained and evaluated using two datasets: the first is composed of the extracted GLCM features only, and the second combines GLCM and HSV descriptors. The results indicate that SVM classifier outperformed on combined GLCM and HSV features with an accuracy of 98.29%. The proposed framework could be beneficial to the oasis agricultural community in terms of early detection of date palm white scale disease (DPWSD) and assisting in the adoption of preventive measures to protect both date palm trees and crop yield.

**Key words:** precision agriculture; machine learning; ensemble learning; feature extraction; date palm; diseases

## 1 Introduction

The date palm is a crop with significant socioeconomic and ecological importance in Morocco<sup>[1]</sup>. The latter has been prioritized by Morocco's Green Plan (MGP)

through promoting and helping farmers in growing these trees, which account for around 60% of agricultural revenue in oasis and employ over two million people<sup>[2]</sup>. Plant disease detection and classification

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is a key factor of precision farming<sup>[3]</sup>. Identifying the diseases that affect date palms and determining the degree of infestation is one of the challenges facing the farmer, especially when the symptoms are very similar, which makes choosing the appropriate practice and treatment difficult and, in many cases, wrong. Palm date scale is sap-sucking pests that feed and form colonies on palm leaflets. The palm date scale is considered a minor pest of low agricultural significance<sup>[4]</sup>. Still, in very high infestation levels, the palm date scale (see Fig. 1) can cause tissue necrosis which can cause harmful damages from negatively affecting the quality of produced fruits to the death of the tree<sup>[5]</sup>. The choice to use chemical treatment or not is determined by the degree of the infestation. This is considered a time and labor expensive task as visual control needs to be done regularly by farmers or experts.

The aim of this study is to evaluate the effectiveness of machine learning methods in identifying and staging of the white scale disease (WSD) within the date palms. For that reason, feature extraction techniques were performed on a multiclass image dataset to produce two types of descriptors, namely gray level co-occurrence matrix (GLCM) and hue, saturation, and value (HSV) color moments. The retrieved characteristics were then used to train various classical and ensemble-based machine learning (ML) models which are multiclass support vector machine (SVM), *k*-nearest neighbors (KNN), random forest (RF), and light gradient boosting machine (LightGBM). To measure the performance of the different models, Accuracy, Precision, Recall, and F1-score were calculated. This suggested solution would assist date palm growers and owners in protecting their crops and increasing productivity by utilizing machine learning techniques for accurate classification and identification of WSD infestation degrees.

The main contributions of this work are as follow.

- To examine the potential for WSD detection and

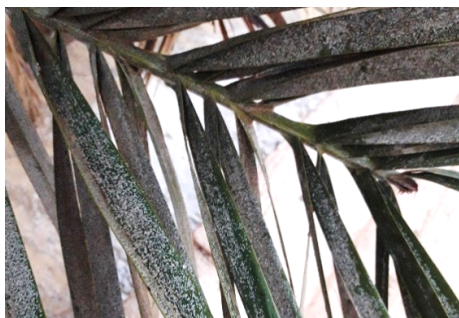


Fig. 1 Example of a palm tree infected by white scale.

infestation degree classification using classical and ensemble-based machine learning methods.

- To explore two features (GLCM-based features and HSV Color Moments) to find the most effective for WSD stage-wise classification.
- To conduct a set of experiments to analyze the effect of using only texture feature versus the use of combined color and texture patterns in recognizing and classifying WSD.
- To measure the classification performance of each model using various stage-wise metrics.

This paper is structured as follows. In Section 2, we present a brief literature review of studies conducted to identify and diagnose plant diseases using feature extraction and machine learning techniques. Section 3 describes the proposed framework. Finally, in Section 4, we report the obtained results, and in Section 5, we discuss the future implications of our work.

## 2 Related Work

Over the recent years, numerous studies have been undertaken to identify and diagnosis plant diseases by utilizing feature extraction in conjunction with machine learning approaches. A framework based on multiclass support vector machines was described by Jadhav et al.<sup>[6]</sup> for identifying soybean disease. To begin with, infected regions were extracted using *k*-means clustering technique on images of healthy and diseased leaves, and then GLCM-based features and RGB color-based statistical properties were merged and used as features for the SVM classifier which outperformed with an accuracy of 90.20%. Khan et al.<sup>[7]</sup> proposed the use of a deep neural network, especially the back propagation neural network (BPNN) to identify and classify walnut fungal infections. Before extracting relevant features using color moments and GLCM, preprocessing techniques such as downsizing, intensity improvement, and histogram equalization have been used. The performance of the BPNN classifier was 95.3% accurate. The extreme learning machine (ELM) was employed to perform the classification of plant diseases<sup>[8–10]</sup>. The proposed method by Aqel et al.<sup>[8]</sup> begins by establishing the regions of interest (RoI) based on the *k*-means method. As a result, their method outperformed by an accuracy of 94%. Hyperspectral images based features were used in Refs. [9, 10]. As proposed by Lu et al.<sup>[9]</sup>, ten GLCM-based features merged with more than 900 local binary patterns (LBP)-based features were used to train an

ELM classifier. Their approach achieved an accuracy of approximately 92.3%. Devi et al.<sup>[11]</sup> proposed the use of synthetic features to improve the classification accuracy of plant diseases. A hybrid learning model that incorporates both GLCM-based and synthetically generated features as an input of a convolutional neural network (CNN) was used. The performance of the CNN was then compared to that of the SVM and the ELM algorithms, and it was determined that CNN achieved the highest accuracy of 92.6%. Shin et al.<sup>[12]</sup> compared two machine learning models (artificial neural network (ANN) and SVM) as well as three feature extraction algorithms (histogram of oriented gradient (HOG), speedup robust features (SURF), and GLCM) to detect powdery mildew on strawberry leaves. Experiments reveal that SURF+ANN performs the best, with an accuracy of 90.38%. To perform plant disease detection and classification, Kumar et al.<sup>[13]</sup> suggest the Adaboost algorithm in conjunction with k-means clustering and Otsu's thresholding for ROI detection. After that, features were computed using GLCM and the proposed classifier outperformed with an accuracy of 85%. As reported by Panchal et al.<sup>[14]</sup>, random forest method is used to classify infected part of the leaves, the latter is detected using a combination of k-means clustering algorithm and HSV dependent classification. The proposed framework reached a remarkable accuracy of 98%. Other ML methods like neuro-fuzzy logic classifier was proposed by Rao and Kulkarni<sup>[15]</sup> to conduct the classification of plant disease based on the combination of multiple features such as GLCM, complex gabor filter, curvelet and image moments.

Despite recent advances in technology, little research is being conducted in the field of early identification and classification of date palm disease. Alaa et al.<sup>[16]</sup> reported that the classification of some diseases like blight spots and leaf spots is possible by using CNN. The proposed system has reached an accuracy of 97.9%. Magsi et al.<sup>[17]</sup> demonstrated that it is possible to diagnose sudden decline syndrome illness utilizing ML and feature extraction approaches. They suggested a three-steps method based on image preprocessing, feature extraction using both color and texture descriptors, and a CNN-based classification method. According to Al-Shalout and Mansour<sup>[18]</sup>, CNN exhibits encouraging results in the identification and classification of date palm diseases. However, to execute identification or classification tasks, the deep learning approach necessitates the use of large and well-annotated datasets, which requires

considerable effort and attention. Therefore, machine learning combined with feature extraction technique may be adopted as a resort to perform the sub-mentioned tasks.

### 3 Experimental Methodology

We propose a WSD stage-wise classification system based on feature extraction and two types of machine learning algorithms. The architecture of the proposed system is shown in Fig. 2, which consists of the three major phases including data preprocessing, feature extraction, and models training and performance evaluation. In what follow, we will describe each of these phases.

#### 3.1 Dataset

The dataset utilized in the context of this work is a public dataset<sup>[19]</sup> composed of more than 2000 labeled date palm leaflet images. This dataset presents three main classes which are (1) healthy, (2) brown spots disease, and (3) white scale disease. Since we are investigating WSD, only the images from the two classes (1) and (3) were used. The latter comprises pictures of leaflets that have been infested at three different stages. Figures 3

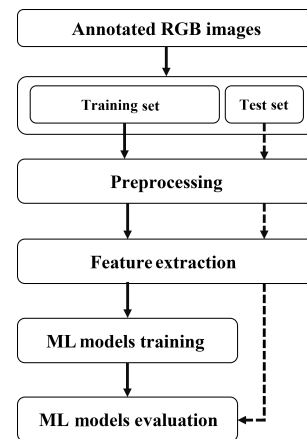


Fig. 2 System architecture.

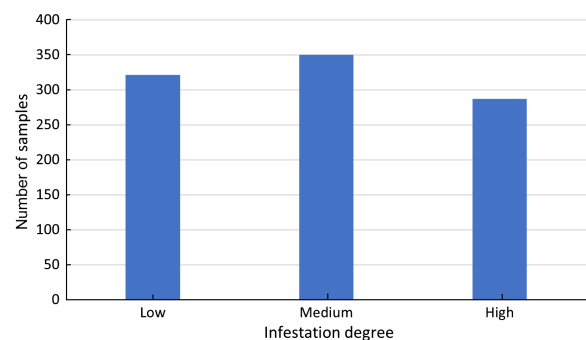


Fig. 3 Initial number of samples per infestation degree.

and 4 illustrate the number of WSD-infected leaflets per stage and some representative samples from each class, respectively. Finally, the dataset is divided into a training set which represents 80% of the entire dataset, and the remaining 20% is used for testing purposes.

### 3.2 Data preprocessing

The two difficulties we faced are as follows. (1) The classes in the dataset are imbalanced. Given the number of images in the class of healthy leaflets, the latter is dominant, accounting for around 56% of the dataset as illustrated in Fig. 5. (2) The very low sample size per class which will have a significant effect on the learning process. To address the sub mentioned issues, we choose to use data augmentation techniques<sup>[20]</sup> on both majority and minority classes.

We performed numerous modifications on the images, such as zooming, rotation, horizontal flipping, width and height shifting. Finally, we created a set of augmented images by combining these transformations. Table 1 summarizes the distribution of the samples

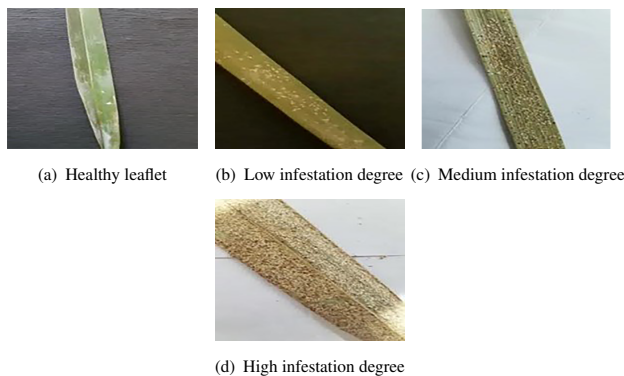


Fig. 4 Samples of healthy and infected leaflets.

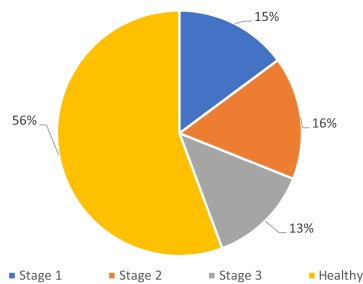


Fig. 5 Distribution of images per class.

Table 1 Distribution of samples in the training set and testing set.

Dataset	Healthy	Infected by white scale disease			Total
		Stage 1	Stage 2	Stage 3	
Training set	1258	1219	1264	1197	4938
Testing set	340	336	312	301	1289

per class in the training set and the testing set. Other preprocessings such as down sampling, color mode conversions from RGB to grayscale and from RGB to HSV, and normalization were performed to prepare the dataset for the feature extraction phase.

### 3.3 Feature's extraction

In image processing, feature extraction means the quantification of certain features as opposed to utilizing all of the information at the pixel level. The fundamental objective is to decrease the dimensions by generating a collection of expressive values characterizing the entire image. Consequently, computational time and used memory will be optimized. Therefore, this technique is widely utilized for classification, object detection, and recognition tasks<sup>[21]</sup>. In the context of this study, two descriptors were examined. The first one is a set of 80 GLCM-based texture features, and the second is the combination of nine statistical HSV color moment based features and the already extracted GLCM-based features. More details about the process of feature extraction are tackled in Sections 3.3.1 and 3.3.2.

#### 3.3.1 Gray level co-occurrence matrix (GLCM)

To recognize the regions of interest (RoI), the analysis of image textures proved to be efficient<sup>[22]</sup>. One way to extract the texture properties from an image is to calculate second order statistical values introduced by Harlick et al.<sup>[23]</sup> which requires the study of the relation between two pairs of pixels in terms of space<sup>[24]</sup>. In the context of this work, we decided to investigate the potential of gray level co-occurrence matrix (GLCM) in characterizing textures presented in healthy and WSD infected leaflets images. We did calculate the five statistical measures, namely, energy, correlation, dissimilarity, homogeneity, and contrast, proposed by Conners and Harlow<sup>[25]</sup> from the GLCM and used them as texture features. The chosen statistical measures<sup>[26]</sup> are described bellow. To define a sufficient variety of spatial relations between the image's pixels, we suggested the use of four different distances  $d$  (i.e., 1, 3, 6, and 9) and four different orientations  $\theta$  (i.e.,  $0$ ,  $\pi/4$ ,  $\pi/2$ , and  $3\pi/4$ ). For each pair  $(d, \theta)$ , the already mentioned statistical measures were computed. As a result, an 80 GLCM-based texture features vector is produced. The choice of various distances is justified by the fact that this value is critical for the image classification task. To incorporate the texture patterns, the distance value must be large enough. At the same time, it must be small enough to maintain the local

characteristic of spatial dependency<sup>[24]</sup>.

In what follows,  $P_{i,j}$  represents the element  $(i, j)$  of the normalized symmetrical GLCM,  $N$  is the number of the gray levels in the image,  $\mu$  represents the GLCM mean calculated as shown in Eq. (1), and  $\sigma^2$  is the GLCM intensities variance computed using the Eq. (2).

$$\mu = \sum_{i,j=0}^{N-1} iP_{i,j} \quad (1)$$

$$\sigma^2 = \sum_{i,j=0}^{N-1} P_{i,j}(i - \mu)^2 \quad (2)$$

Energy indicates the grey level homogeneity between the pixels of an image: if the intensities of the grey level in adjacent pixels (pairs) are similar, the energy is low; otherwise, it is high<sup>[24]</sup>. It can be computed using the Eq. (3). Correlation measures the linearity and the predictability between a pair of pixels. Significant and non significant values mean the existence and nonexistence of this relationship, respectively. Equation (4) is used to calculate this measure. The dissimilarity is used to interpret the distance between a pair of pixels<sup>[27]</sup>. Equation (5) demonstrates how this measure is calculated.

$$\text{Energy} = \sum_{i,j=0}^{N-1} (P_{i,j})^2 \quad (3)$$

$$\text{Correlation} = \sum_{i,j=0}^{N-1} P_{i,j} \frac{(i - \mu)(j - \mu)}{\sigma^2} \quad (4)$$

$$\text{Dissimilarity} = \sum_{i,j=0}^{N-1} |i - j| P_{i,j} \quad (5)$$

Homogeneity quantifies how near the elements distribution in the GLCM is to its diagonal<sup>[27]</sup>. Finally, the contrast measure represents the intensity between adjacent pixels. The inexistence of variation means that the contrast is irrelevant<sup>[27]</sup>. Homogeneity and contrast values are calculated using Eqs. (6) and (7), respectively.

$$\text{Homogeneity} = \sum_{i,j=0}^{N-1} \frac{1}{1 + |i - j|^2} P_{i,j} \quad (6)$$

$$\text{Contrast} = \sum_{i,j=0}^{N-1} |i - j|^2 P_{i,j} \quad (7)$$

### 3.3.2 Combination of texture-based and color-based features

HSV (i.e., hue, saturation, and value) is a color model that is believed to be an alternative to the RGB color representation. HSV is more consistent with the way

human vision processes colors. It shows enhanced color abstraction by differentiating the saturation and the value channels<sup>[28]</sup>. Color moments are probabilistic measurements that describe the distribution of an image's color channels<sup>[28]</sup>. In this research, we opted for the extraction of three statistical measures for each channel (i.e., mean, standard deviation, and skewness), yielding a total of nine color-based features. The used measures are detailed bellow.

- Mean. It calculates the average of pixel intensities in a color channel, it can be computed using Eq. (8).

$$\mu_c = \frac{1}{N'} \sum_{i,j=1}^N C_{i,j} \quad (8)$$

- Standard deviation (SD). It measures the deviations between each observation and the mean. Equation (9) is used to compute the SD of a given channel  $C$ .

$$\sigma_c = \left( \frac{1}{N'} \sum_{i,j=1}^N (C_{i,j} - \mu_c)^2 \right)^{\frac{1}{2}} \quad (9)$$

- Skewness. It calculates the symmetry of a color channel distribution. Equation (10) demonstrates how this measure is computed.

$$s_c = \left( \frac{1}{N'} \sum_{i,j=1}^N (C_{i,j} - \mu_c)^3 \right)^{\frac{1}{3}} \quad (10)$$

where  $C_{i,j}$  represents the value of pixel at the position  $(i, j)$  regarding the channel represented by  $C$ , whereas  $N'$  is referring to the total number of pixels.

The obtained color-based characteristics of the image are represented by the vector given in Eq. (11). This set of features was combined with extracted GLCM features to form a vector that represents the healthy and infected date palm leaflets.

$$F_{\text{colors}} = [\mu_H, \sigma_H, s_H, \mu_S, \sigma_S, s_S, \mu_V, \sigma_V, s_V] \quad (11)$$

### 3.4 Machine learning models

Machine learning (ML) is a subset of artificial intelligence (AI) that enables computers to automatically learn and improve with experience<sup>[29]</sup>. To fulfill this purpose, three main approaches are proposed, namely, supervised learning, unsupervised learning, and reinforcement learning. In supervised learning, the learning process is based on previous examples: models are trained using labeled dataset (i.e., each input is paired with an output), during which the model acquires knowledge about the various types of data. After training, the model is evaluated using a portion of the training set and then used to perform either a regression

or a classification task<sup>[30]</sup>. To apply appropriate WSD degree of infestation classification task, we have trained and evaluated several ML models, namely, classical ML models like SVM and CNN, and ensemble-based learning models such as random forest and LightGBM.

### 3.4.1 Supervised classical ML algorithms

In the context of this study, two supervised machine learning models were investigated, namely, multiclass SVM and KNN. SVM uses hyperplanes to separate data into several classes whose boundary is as far as possible from the data points (i.e., maximum margin)<sup>[28]</sup>. KNN algorithm classification approach is based on learning data from neighbors (i.e., closet objects). To classify an unseen object, KNN classifier calculates similarity<sup>[31]</sup> between learned patterns and test ones in a predefined range  $k$ <sup>[32]</sup>.

### 3.4.2 Ensemble learning algorithms

When multiple models, like classifiers, are systematically generated and merged in order to tackle a specific computational task, this is referred to as ensemble learning, this can be done by adopting various strategies such as bagging and boosting<sup>[33]</sup>. Random forest (RF) is a bagging technique that generates a collection of decision trees from a randomly chosen subset of the training set, then it aggregates the votes (i.e., majority voting) from the various decision trees to determine the final prediction<sup>[30]</sup>. LightGBM is a decision tree based gradient boosting framework. The classification task becomes quicker while maintaining high accuracy thanks to the integration of two techniques: exclusive feature bundling (EFB) and gradient-based one side sampling (GOSS)<sup>[34]</sup>.

### 3.4.3 Model reliability and finetuning

To avoid the overfitting<sup>[35]</sup> problem, and to assess the effectiveness and the reliability of the different ML models, we opted for a five-fold cross validation technique and a hyperparameters finetuning process to find the optimal hyperparameters which were applied during the training phase of each model.

### 3.4.4 Evaluation metrics

Accuracy, Precision, Recall, F1-score, and confusion matrix are the evaluation metrics chosen to assess the ML models performance. For a given class, accuracy is defined as the proportion of well classified samples out of the total number of samples in that class. This metric is calculated using Eq. (12).

$$\text{Accuracy} = \frac{\text{TP} + \text{TN}}{\text{TP} + \text{FP} + \text{TN} + \text{FN}} \times 100\% \quad (12)$$

True positives (TP) mean that the model predicted the positive class correctly. In the same way, the true negatives (TN) indicate that the model has correctly predicted that the class is negative. In contrast, a false positive (FP) means that the model mispredicts the positive class. And a false negative (FN) means that the model wrongly predicts that the class is negative.

Precision, Recall, and F1-score are calculated using Eqs. (13)–(15), respectively.

$$\text{Precision} = \frac{\text{TP}}{\text{TP} + \text{FP}} \quad (13)$$

$$\text{Recall} = \frac{\text{TP}}{\text{TP} + \text{FN}} \quad (14)$$

$$\text{F1-score} = \frac{2 \times \text{Precision} \times \text{Recall}}{\text{Precision} + \text{Recall}} \quad (15)$$

In the context of this work, class-wise metrics were computed, and arithmetic mean of individual class (macro average) were calculated for each of the already mentioned metrics (i.e., Recall, Precision, and F1-score). Finally, confusion matrices were used to analyze and interpret the performance of the different investigated ML models.

## 4 Result

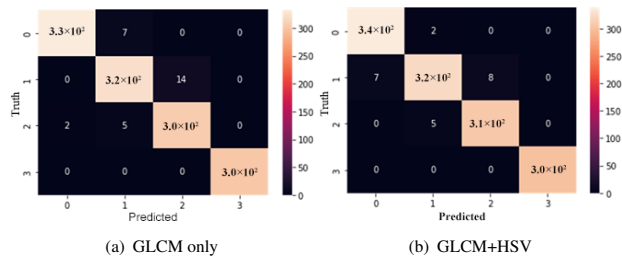
In this study, we proposed a framework for automatically classifying WSD into its three degrees of infestation. For this purpose, machine learning models are applied on two datasets which are GLCM-based texture features and combined GLCM and HSV color moments features. To fulfill the objectives, four ML models were applied including SVM, KNN, RF, and LightGBM. To assess the performance of each algorithm, several stage-wise metrics are used. Table 2 presents the performance of SVM classifier. An accuracy of 97.83% was obtained when using GLCM-based texture features only and 98.29% on combined texture and color GLCM+HSV features which is mainly due to the detailed statistical information provided by the chosen features. The incorporation of HSV features has slightly improved the accuracy by approximately 0.5%.

When looking at the confusion matrices of the SVM classifier (Fig. 6), it is evident that all susceptible images are correctly classified when using combined GLCM+HSV features. However, there are some first level infestation samples (class 1) that are misclassified as healthy (class 0) or as a second level infestation (class 3). This is mainly due to their similarity in terms of the diseases visual patterns. However, level 3 infestation samples are successfully classified (100% of accuracy) because of their distinctive color and texture properties.



**Table 2 Performance comparison of SVM classification on GLCM only and GLCM+HSV features.**

Class	Precision		Recall		F1-score	
	GLCM only	GLCM +HSV	GLCM only	GLCM +HSV	GLCM only	GLCM +HSV
Healthy	0.99	0.98	0.98	0.99	0.99	0.99
White Stage 1	0.96	0.98	0.96	0.96	0.96	0.97
scale Stage 2	0.96	0.97	0.98	0.98	0.97	0.98
disease Stage 3	1.00	1.00	1.00	1.00	1.00	1.00
Macro average	0.98	0.98	0.98	0.98	0.98	0.98



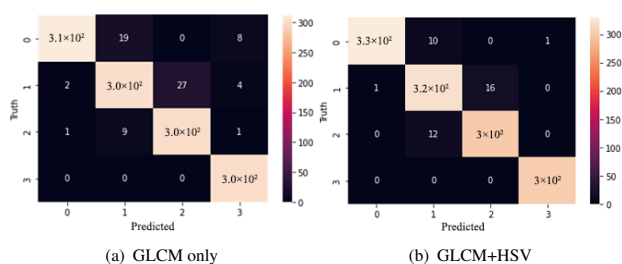
**Fig. 6 Confusion matrices of SVM classifier. 0–3 indicate healthy, low infestation degree, medium infestation degree, and high infestation degree, respectively. The color metric scale represents the number of prediction in the confusion matrices.**

Similarly, Table 3 summarizes the KNN performance using the same class-wise metrics. KNN classifier achieves 94.49% of accuracy on GLCM features dataset and 96.90% of accuracy when using the GLCM+HSV-based features. The introduction of color descriptors improves the accuracy by 2.55%.

KNN classification confusion matrices are shown on Fig. 7 where the distribution of well-classified and misclassified images is illustrated. Again, samples

**Table 3 Performance comparison of KNN classification on GLCM only and GLCM+HSV features.**

Class	Precision		Recall		F1-score	
	GLCM only	GLCM +HSV	GLCM only	GLCM +HSV	GLCM only	GLCM +HSV
Healthy	0.99	1.00	0.92	0.97	0.95	0.98
White Stage 1	0.92	0.94	0.90	0.95	0.91	0.94
scale Stage 2	0.92	0.95	0.96	0.96	0.94	0.96
disease Stage 3	0.96	1.00	1.00	1.00	0.98	1.00
Macro average	0.95	0.97	0.95	0.97	0.95	0.97



**Fig. 7 Confusion matrices of KNN classifier.**

from the the first class (low degree of infestation) were incorrectly classified sometimes as a class two (medium degree of infestation), other times as healthy. This is mainly because the three classes’ patterns are characterized by solid invariances in texture and color.

Tables 4 and 5 summarize the performance of RF and LightGBM classifiers, respectively. When tested using GLCM features only, RF outperformed with an overall accuracy of 91.93% while LightGBM reached 92.63%. The performance of both models will be remarkably increased when tested on combined GLCM and HSV features. RF model outperformed by an average accuracy of 95.42% and an accuracy of 97.52% has been attained by LightGBM.

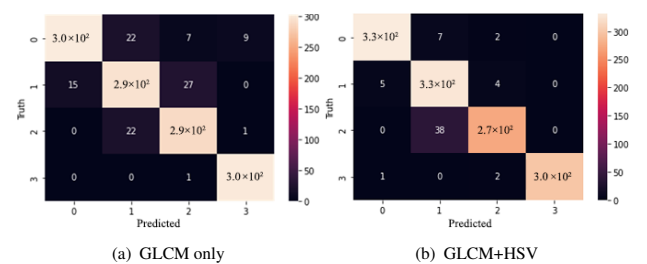
RF and LightGBM classification confusion matrices are shown in Figs. 8 and 9, respectively. It is clearly remarkable that the introduction of HSV features improves the discriminative ability of both classifiers. However, some samples are misclassified (first and second stage of infestation). As discussed before, this

**Table 4 Performance comparison of Random Forest classification on GLCM only and GLCM+HSV features.**

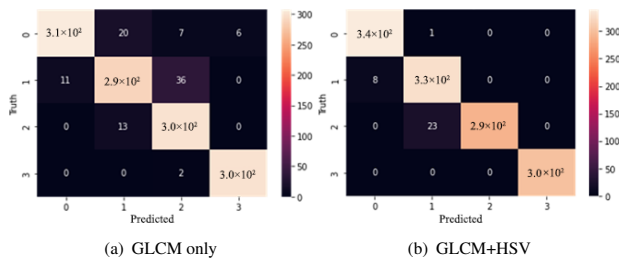
Class	Precision		Recall		F1-score	
	GLCM only	GLCM +HSV	GLCM only	GLCM +HSV	GLCM only	GLCM +HSV
Healthy	0.95	0.98	0.89	0.97	0.92	0.98
White Stage 1	0.87	0.88	0.88	0.97	0.87	0.92
scale Stage 2	0.89	0.97	0.93	0.88	0.91	0.92
disease Stage 3	0.97	1.00	1.00	0.99	0.98	0.99
Macro average	0.92	0.96	0.92	0.95	0.92	0.95

**Table 5 Performance comparison for LightGBM classification on GLCM only and GLCM+HSV features.**

Class	Precision		Recall		F1-score	
	GLCM only	GLCM +HSV	GLCM only	GLCM +HSV	GLCM only	GLCM +HSV
Healthy	0.97	0.98	0.90	1.00	0.93	0.99
White Stage 1	0.90	0.93	0.86	0.98	0.88	0.95
scale Stage 2	0.87	1.00	0.96	0.93	0.91	0.96
disease Stage 3	0.98	1.00	0.99	1.00	0.99	1.00
Macro average	0.93	0.98	0.93	0.97	0.93	0.97



**Fig. 8 Confusion matrices of RF classifier.**



**Fig. 9** Confusion matrices of LightGBM classifier.

is mainly due to the high invariance between the two classes.

The performance comparisons of the investigated classifiers in terms of overall Accuracy, Precision, Recall, and F1-score are presented in Table 6. It is observed from the results that SVM outperformed with highest precision of 0.92, recall of 0.91, and an accuracy of 98.29% when using the combined GLCM and HSV features. After SVM, LightGBM achieved the highest accuracy of 97.52%. The performance of KNN is better as compared to the performance of RF. Both traditional and ensemble-based machine learning show good results in classifying the degree of infestation by WSD when trained on merged texture and color features. The introduction of HSV color moments contributes to increasing the accuracy. This contribution varies from an insignificant percentage as remarked in SVM classifier performance to an important percentage for the LightGBM model with about 5.28% of improvement.

## 5 Discussion

This study presented a framework for automatically classifying the degree of infestation caused by date palm WSD at different stages. As a preliminary step, annotated images of both healthy and sick date palm leaflets were divided into training and testing sets, then augmentation technique was performed to balance the dataset. As a third step, preprocessing techniques such as down sampling, data normalization, and color conversion were applied on the augmented data. Following that, GLCM-based features and HSV color moments, were

extracted and used to train and test various classical and ensemble-based machine learning algorithms, namely: SVM, KNN, RF, and LightGBM. Finally, techniques such as cross validation and finetuning were considered to evaluate the reliability and effectiveness of the models and a numerous class-wise metrics were used to evaluate their accuracy.

We ran two sets of trials to see how adding HSV characteristics affected classification accuracy. The first assesses solely GLCM features, whereas the second trains ML models using the combined GLCM+HSV features. As a result, SVM works perfectly on merged color and texture-based features, with an accuracy of roughly 98.3%. Experiments also prove that the incorporation of HSV characteristics improves overall classification accuracy.

The main objective of this research is to demonstrate the strength of machine learning when combined with machine vision for the identification and categorization of date palm diseases. The latter requires the availability of a sufficient yet high-quality amount of carefully annotated image datasets. Unfortunately, such data is almost non-existent for essential oasis tree farming system, which makes it impossible to test the effectiveness of the proposed system on data other than what is available.

As a future work, we propose the investigation of other texture and color features, and the application of other preprocessing approaches, such as segmentation that may help to improve the performance of the suggested architecture. Also required is the investigation of other machine learning models, particularly for identifying and diagnosing date palm diseases, which are critical components of phoeniculture. In addition, with the support of experts in the field, images of various palm diseases must be collected and appropriately annotated to permit the application of contemporary artificial intelligence technologies, such as deep learning techniques, to detect and categorize several date palm diseases.

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**Table 6** Performance comparison of all classifiers.

Model	Precision		Recall		F1-score		Accuracy (%)	
	GLCM	GLCM+HSV	GLCM	GLCM+HSV	GLCM	GLCM+HSV	GLCM	GLCM+HSV
SVM	0.98	0.98	0.98	0.98	0.98	0.98	97.83	98.29
KNN	0.95	0.97	0.95	0.97	0.95	0.97	94.49	96.90
RF	0.92	0.96	0.92	0.95	0.92	0.95	91.93	95.42
LightGBM	0.93	0.98	0.93	0.97	0.93	0.97	92.63	97.52



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