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Machine Learning-Based Detection and Severity Assessment of Sunflower Powdery Mildew: A Precision Agriculture Approach[A]

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Abstract: Sunflower powdery mildew (*Golovinomyces cichoracearum* (DC.) V.P. Heluta) is a substantial threat to sunflower crops, causing significant yield loss. Traditional identification methods, based on human observation, fall short in providing early disease detection and quick control. This study presents a novel approach to this problem, utilizing machine learning for the early detection of powdery mildew in sunflowers. The disease severity levels were determined by training a Decision Trees model using matrix of soil, powdery mildew, stems, and leaf images obtained from original field images. It was detected disease severity levels of 18.14% and 5.56% in test images labeled as A and C, respectively. The model's demonstrated accuracy of 85% suggests high proficiency, indicating that machine learning, specifically the DTs model, holds promising prospects for revolutionizing disease control and diseases prevention in agriculture.

Keywords: Decision trees, Disease severity, Machine learning, Powdery mildew, Sunflower.

[A] This study does not require ethics committee approval. The article has been prepared in accordance with research and publication ethics.

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Ayçiçeğinde Küllemenin Makine Öğrenimine Dayalı Tespiti ve Şiddetinin Değerlendirilmesi: Hassas Tarım Yaklaşımı

Öz: Ayçiçeğinde külleme (*Golovinomyces cichoracearum* (DC.) V.P. Heluta), önemli ölçüde verim kaybına neden olan, ayçiçeği ürünleri için önemli bir tehdittir. Geleneksel teşhis yöntemleri, insan gözlemine dayalı olarak, erken hastalık tespiti ve hızlı kontrol sağlama konusunda yetersiz kalmaktadır. Bu çalışma, ayçiçeğinde küllemenin erken tespiti için makine öğrenimini kullanarak bu soruna yeni bir yaklaşım sunmaktadır. Orijinal alan görüntülerinden elde edilen fotoğraflara ait toprak, külleme, sap ve yaprak matrisleri ile Decision Trees (Karar Ağaçları) modeli eğitilerek hastalık şiddet seviyeleri tespit edilmiştir. Test görüntülerinde sırasıyla A ve C olarak etiketlenmiş hastalık şiddeti seviyeleri %18.14 ve %5.56 olarak belirlenmiştir. Modelin %85 oranında gösterdiği doğruluk, modelin yüksek düzeyde yetkinliğe ve özellikle Decision Trees modelinin tarım alanında hastalık kontrolünü ve hastalıkların önlenmesini devrimleştirmek için umut verici perspektiflere sahip olduğunu göstermektedir.

Anahtar Kelimeler: Karar ağaçları, Hastalık şiddeti, Makine öğrenimi, Külleme, Ayçiçeği.

Introduction

Early prediction and warning are complement for effective diseases in crop production (Li et al., 2021). Traditional plant disease diagnosis methods are based on the diagnosis of diseased plants based on human observation. However, inconsistencies arise between these observations in the detection phase from specialist to specialist (Owomugisha and Mwebaze, 2016; Wu et al., 2022). Human-centric disease detection is a time-consuming process, and yet, the demand for labor to identify plant diseases continues to increase (Wang et al., 2017; Cai et al., 2019). Plant disease severity, defined as the percentage of the plant surface affected by the disease, serves as a crucial metric for measuring disease levels (Dawod and Dobre, 2021). Therefore, a rapid and accurate diagnosis of disease severity could be instrumental in minimizing yield losses (Wang et al., 2017; Kaur et al., 2019). Advancements in visual processing techniques based on artificial intelligence and machine learning have allowed for autonomous plant disease diagnosis, significantly reducing time consumption and human resource needs (Singh et al., 2016; Nagasubramanian et al., 2019; Erdoğan et al., 2023) The production and productivity of certain herbal products, such as the sunflower (*Helianthus annuus* L.), can directly impact the economies of various nations. A member of the Compositae (Asteraceae) family (Dokken and Davis, 2007), sunflower is cultivated for its edible oil and seeds, catering to both human and animal consumption. Accounting for 11% of the global vegetable oil production, sunflower stands as a substantial source of edible oil (Lindström and Hernández, 2015). Despite its economic significance, sunflowers encounter considerable product losses due to plant diseases. One of the most prominent among these is sunflower powdery mildew (*Golovinomyces cichoracearum* (DC.) V.P. Heluta, formerly *Erysiphe cichoracearum*) (Reddy et al., 2013). This disease often infects plants around the blossoming period, leading to substantial plant death. Furthermore, early infections during dry and hot conditions result in severe damage to the plants (Park et al., 2015). While the disease affects above-ground parts of the plant, the leaves are more frequently impacted. The initial symptoms include tiny white dots on the leaves, which eventually enlarge and encompass the entire leaf, fostering the growth of numerous conidiospores. These can readily spread throughout the plant, leading to secondary infections (Mulpuri et al., 2016). Ultimately, the disease debilitates the plant by propagating both intracellularly and intercellularly in the plant tissue (Troisi et al., 2010; Lebeda and Mieslerová, 2011; Lin et al., 2019)

The primary aim of this research is to determine the severity of *G. cichoracearum* on sunflower leaves using field images. The model, which learns the main color values of soil, stems, leaves, weeds, and powdery mildew classes in the images, aims to calculate disease severity by detecting the area covered by these classes in the images. Given that the machine learning-based image processing techniques offer a more accurate and expedited detection of disease severity compared to human observation, it is anticipated that this research may contribute to the development of models that can be integrated into autonomous equipment designed for precision agriculture. As such, Decision Trees (DTs), a non-parametric supervised machine learning model, were utilized to calculate the disease severity on sunflower leaves under field conditions.

Material and Methods

Data Collection

The study was carried out on sunflowers produced in the farmland of Bursa Uludağ University Faculty of Agriculture (Figure 1). Images of sunflower leaves infected by *G. cichoracearum* were recorded using a Canon EOS 700D camera with a resolution of 5184 x 3456 pixels. A total of 1050 infected leaf images were obtained in 1 week to train the DTs model. Images were taken about 40 cm from the leaf surface. Of the dataset, 80% (840 images) was used for model training, 16% (168 images) was allocated for validation, and the remaining 4% (42 images) was set aside for testing. Test data is not included in the training.

Figure 1. A: *Sunflower cultivation area. B: The location of the area. Coordinates: lat 40°13' 33.7'' N, long 28° 51' 34.2 ''E, alt 50 m asl.*

Pathogen Identification

The initial step involved collecting infected leaves from the affected plants, followed by the careful detachment of conidia and hyphae, which are the pathogen's reproductive structures, by scraping them off the leaves. The harvested conidia and hyphae were subsequently placed on a microscope slide and examined under a microscope to determine the presence of the pathogen. The physical characteristics of the conidia, such as size, shape, and surface features, were observed under a light microscope. This data was then cross-referenced with known descriptions of *G. cichoracearum* to confirm the pathogen's presence (Cook and Braun, 2009; Reddy et al., 2013).

Flowchart

The research was carried out using Spyder (www.spyder-ide.org), an open-source, Python-integrated development environment. A machine-learning model was utilized to identify distinct image features (r, g, and b channels) in the sunflower.

I. Initially, the requisite libraries (NumPy, Pandas, Matplotlib, OpenCV), along with the mpl toolkits.mplot3d module for generating the 3D plot, were imported.

II. A pre-prepared CSV data file was then loaded into the Pandas DataFrame. This DataFrame comprises RGB values for powdery mildew, weeds, stems, soil, and healthy leaves within the plant.

III. Details of each object were presented in the 3D graph based on the RGB color space values. These areas in the images such as powdery mildew disease, weeds, stems, soil and leaf surfaces are labeled..

IV. To conduct the training of the data, the feature columns (r, g, and b) were extracted as a separate DataFrame, excluding the target column ('result') from the original DataFrame.

V. The dataset was bifurcated into X and Y for training the classification model. X contains the data, including the color data, while Y houses the accurate class labels for each data point.

VI. Subsequently, the dataset, consisting of 1050 photographs, was randomly partitioned using the train_test_split function: 80% (840 images) for model training, 16% (168 images) for validation, 16% (168 images) for validation, and the remaining 4% (42 images) were excluded from the training and reserved solely for testing.

VII. A Decision Tree classifier model was constructed.

VIII. The model underwent training.

IX. Two representative test images (A and C), not used in the training process, were uploaded.. Subsequently, classification for each pixel in the image was conducted using the DecisionTreeClassifier. The classification results were visualized on a grayscale, with each pixel assigned a color value. The outcomes were saved as an output image and displayed on the screen.

X. The severity of powdery mildew was determined by calculating the proportion of detected diseased areas.

Finally, the performance measures (accuracy, recall, precision, and f1-score) of the model trained with the Decision Tree classifier on the test dataset were calculated using the classification_report function in the sklearn library.

Classification by Decision Trees (DTs)

The study employs the Classification and Regression Tree (CART) decision tree algorithms, which are frequently utilized for identifying plant pests and diseases (Gallardo-Romero et al., 2023; Liu et al., 2023). Decision Trees (DTs) stand out among machine learning models for their distinct advantages (Mahmood et al., 2021; Khan et al., 2022; Lee et al., 2022). They are renowned for their interpretability, with their tree structures offering clarity in the decision-making process, essential in fields like healthcare (Lee et al., 2022). They are adept at managing both numerical and categorical data without significant preprocessing, and can effortlessly accommodate mixed data types or missing values (Mahmood et al., 2021). Moreover, DTs are computationally efficient, particularly with large datasets, and excel in real-time predictive tasks (Lee et al., 2018). Owing to these attributes, DTs were chosen as the preferred model for this study. Matrix values in digital images are comprised of square pixels (image elements) arranged in a grid of columns and rows. For the purposes of this research, the matrix values corresponding to soil surface, weeds, healthy leaves, stems, and powdery mildew were determined from original field images using the OpenCV library and Python programming language. These matrix values were then classified to train the Decision Tree (DT) model (Figure 2). Each pixel in a digital image possesses a certain intensity, and it is the combined interplay of red, green, and blue pixels that generates the perception of color. During the training phase, the model's accuracy was validated using the validation dataset.

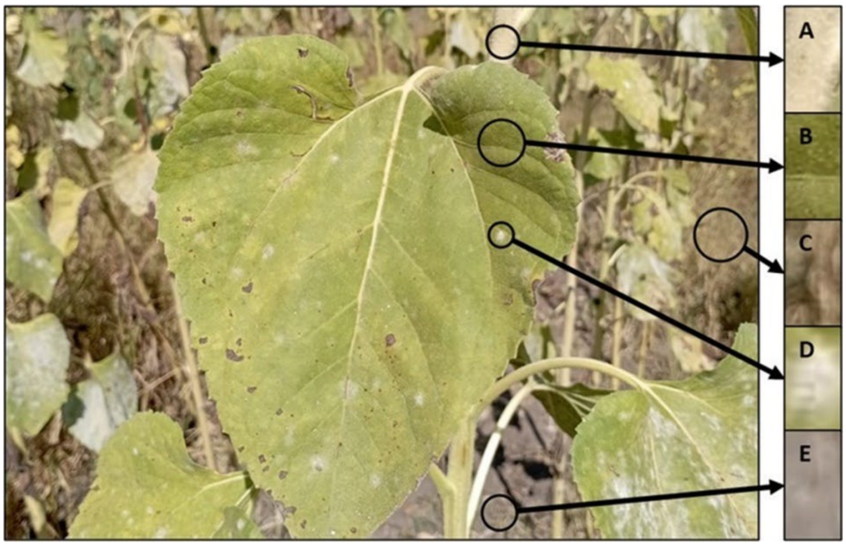


Figure 2. *Matrix values of stems (A), healthy leaf areas (B), weeds (C), infected areas of leaves (D), and soil surface (E) are classified.*

Train and Validation Datasets

During the training phase, the K-Nearest Neighbor (K-NN) approach was employed for classification of matrix values, facilitating comparisons across the X, Y, and Z axes (Jasim and Al-Taei, 2018). The classification process commences with the creation of a root node, subsequent to which the entropy value for all data trained on that node is determined (Adi et al., 2017). The dataset, consisting of 1050 photographs, was randomly partitioned using the train_test_split function: 80% (840 images) were used for model training, 16% (168 images) for validation, and the remaining 4% (42 images) were excluded from the training and reserved solely for testing. In the testing phase, areas infected by powdery mildew were visualized using a black tone, while a light grey tone was assigned to healthy leaf tissues. The grayscale values of the soil surface, weeds, healthy leaves, stems, and powdery mildew derived from field images were configured as presented in Table 1.

Table 1: Grey colours in RGB

	R (Red)	G (Green)	B (Blue)
Soil surface	60	60	60
Weeds	120	120	120
Healthy leaves	240	240	240
Stems	180	180	180
Powdery mildew disease	0	0	0

Determination of the Pathogen Severity

A rater's assessment of the disease severity is used to calculate the disease severity index (DSI), which is expressed as a percentage and is calculated as follows: DSI (%) = [sum (class frequency × score of rating class)] / [(total number of plants) × (maximal disease index)] × 100 (Bock et al., 2020). In this research, the severity was estimated by determining the pixel numbers through the classification of DTs. It was calculated by the ratio of the total pixel number of the infected leaf regions to the total pixel number of all leaf areas, including healthy regions (Goncalves et al., 2021). The severity rate and precision are calculated by Equation (1) and Eq. (2) respectively (G: Infected leaf area by *G. cichoracearum*, H: healthy leaf area, I: Severity rate (%), True Positive (TP): A True Positive is a correct identification of a positive instance in a classification task, where both the actual and predicted classes are positive. False Positive (FP): A False Positive is an incorrect identification of a negative instance as positive, where the actual class is negative, but the predicted class is positive).

$$I = \left[\frac{G}{G+H} \times 100\right] \tag{1}$$

$$Precision = \frac{TP}{TP+FP} \tag{2}$$

Evaluation of the Model

Confusion matrix, precision, recall, and F1-score are metrics used to evaluate the performance of classification models. These metrics help determine how accurately the classification model makes predictions and for which classes it is better or worse. Precision determines the proportion of instances that a classification model classifies as positive that is actually positive. Its formula is calculated as TP / (TP + FP), where TP is the number of "true positive" instances and FP is the number of "false positive" instances. Precision measures the accuracy of the classification model by keeping the false-positive rate low. Recall measure shows the ratio of the number of true positives to the number of all positive samples. Its formula is TP/(TP + FN). That is, it shows how many true positive examples a classification model finds. The F1-score measure calculates the harmonic mean of Precision and Recall values. Its formula is 2*(Precision * Recall)/(Precision + Recall). That is, it combines the accuracy and shortcomings of a classification model and evaluates them collectively under one criterion. In this study, the aforementioned performance metrics were used to assess the accuracy and effectiveness of the DTs model. This model predicts using the RGB values of the 'Soil surface', 'Weeds', 'Stems', 'Powdery mildew', and 'Healthy leaves' present in the training and validation dataset.

Results and Discussion

The soil surface, weeds, healthy leaves, stems, and powdery mildew matrix values from the original field images were used in training the non-parametric supervised machine learning model DTs. During the training process, these matrix values are clustered to compare the X, Y, and Z axes by K-Nearest Neighbor (K-Nn) method (Jasim and Al-Taei, 2018). Clustering was visualized on the X, Y and Z-axis (Figure 3). Figure 3 shows the classification within the images used for training and validation.

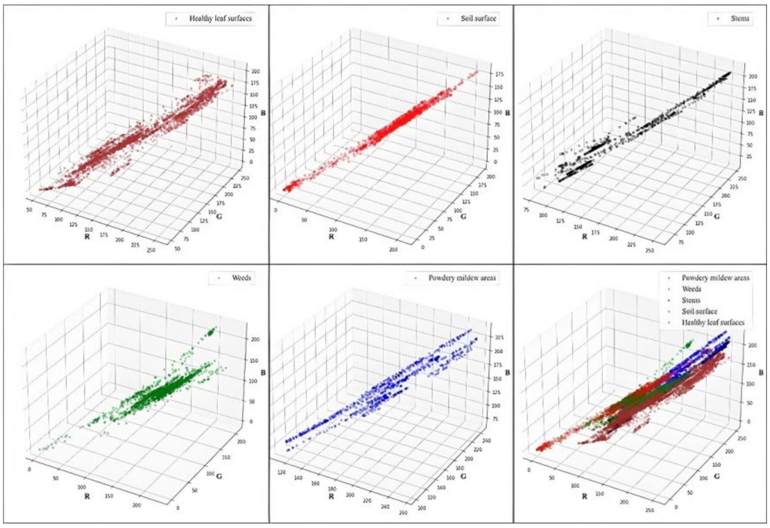


Figure 3. *Clustering of matrix values of the soil surface, weeds, healthy leaves, stems, and powdery mildew disease in the original images from the field along the X, Y and Z-axes.*

Precision, Accuracy, Recall and F1-score are metrics used to evaluate the performance of classification models. These metrics help to determine how accurately the classification model makes predictions and for which classes it is better or worse. "Precision" determines the proportion of instances that a classification model classifies as positive that is actually positive. Its formula is calculated as TP / (TP + FP), where TP is the number of "True positive" instances and FP is the number of "False positive" instances. Precision measures the accuracy of the classification model by keeping the false-positive rate low. Recall measure shows the ratio of the number of true positives to the number of all positive samples. Its formula is TP/(TP + FN). That is, it shows how many true positive examples a classification model finds. Accuracy is also a performance metric used to measure the accuracy of the model. Accuracy is the ratio of correctly classified samples to the total number of samples and is calculated by the following formula: Accuracy = (TP + TN) / (TP + TN + FP + FN). Here TN (True negative) refers to cases where the model correctly identifies true negatives, while FN (False negative) refers to cases where the model incorrectly classifies true positives as negative. For both test images with disease severity of 18.14% (A) and 5.56% (C), the "Accuracy" was 85%. This means that the accuracy of the classification model used in the study is 85%. Accuracy, Precision, Recall and F1-score metrics of the classes obtained from the test images (A and C) are given in Figure 4. and Table 2. In the evaluation of the performance criteria for all classes in the validation dataset, both Recall and Precision values are found to surpass 80%.

Table 2. Performance criteria in validation dataset.

	Precision	Recall	F1-score	Accuracy
Powdery mildew diseases	0.825	0.91	0.865	0.88
Weeds	0.815	0.705	0.755	0.85
Stems	0.68	0.695	0.685	0.72
Soil surface	0.925	0.935	0.93	0.91
Healthy leaves	0.9	0.915	0.91	0.92

In over 80% of cases, the true positives of the classes were correctly classified. In summary, the trained DTs model correctly classified over 80%. The F1-score value, which is the harmonic mean of Recall and Precision, also shows good performance for this model. However, compared to the others, the model had more difficulty in categorising the weeds and stems classes in both test images. Because the performance criteria remained at a lower level (Figure 4).

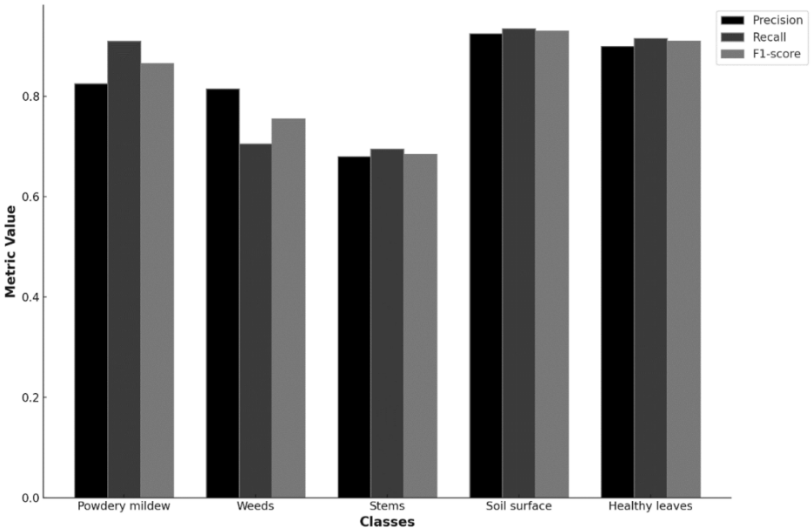
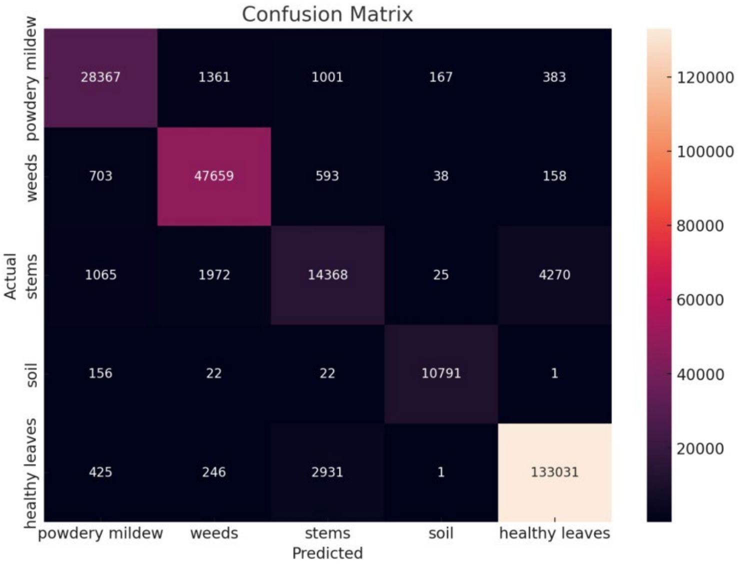


Figure 4. *Performance criteria derived from the class grouping by the DTs model.*

In Figure 5, the confusion matrix provides a critical evaluation of the classification model's performance across five distinct classes: powdery mildew, weeds, stems, soil, and healthy leaves. This matrix is pivotal for understanding not only the model's accuracy but also its specific strengths and weaknesses. The diagonal elements of the matrix signify the true positives, reflecting a high degree of accuracy in classifying healthy leaves (133,031 instances) and weeds (47,659 instances), among others. However, the off-diagonal elements reveal areas of misclassification, particularly between stems and healthy leaves (4,270 instances). The overall accuracy of 93.78% underscores the model's robustness, but the localized confusions highlight potential areas for model refinement. The confusion matrix thus serves as a nuanced diagnostic tool, offering insights into class-specific performance and guiding subsequent model optimization.



	powdery mildew	weeds	stems	soil	healthy leaves
powdery mildew	28367	1361	1001	167	383
weeds	703	47659	593	38	158
stems	1065	1972	14368	25	4270
soil	156	22	22	10791	1
healthy leaves	425	246	2931	1	133031

Figure 5. *Confusion Matrix of the Decision Tree Classifier for Classifying Plant Features.*

In the DTs model trained by applying the steps in the flowchart, test images were loaded, and classification was performed for each pixel in the image using the DecisionTreeClassifier classifier. The results of this classification were visualized in grayscale by assigning a color value to each pixel. The results were saved as an output image and displayed on the screen. The DTs model used black-toned pixels representing infected areas in the test images to estimate the powdery mildew severity. Figure 6 displays the sample images (A and C) utilized as test data.. The total pixel values of healthy leaves and powdery mildew for image A were found as 640369 and 141878, respectively. Regarding disease severity for image A, 18.14% of sunflower leaves were infected with the powdery mildew according to the DTs training results. The total pixel values of healthy leaves and powdery mildew for image C were 630765 and 37106, respectively. In terms of disease severity for image C, 5.56% of sunflower leaves were found to be infected with the powdery mildew according to the DTs training results (Figure 6).

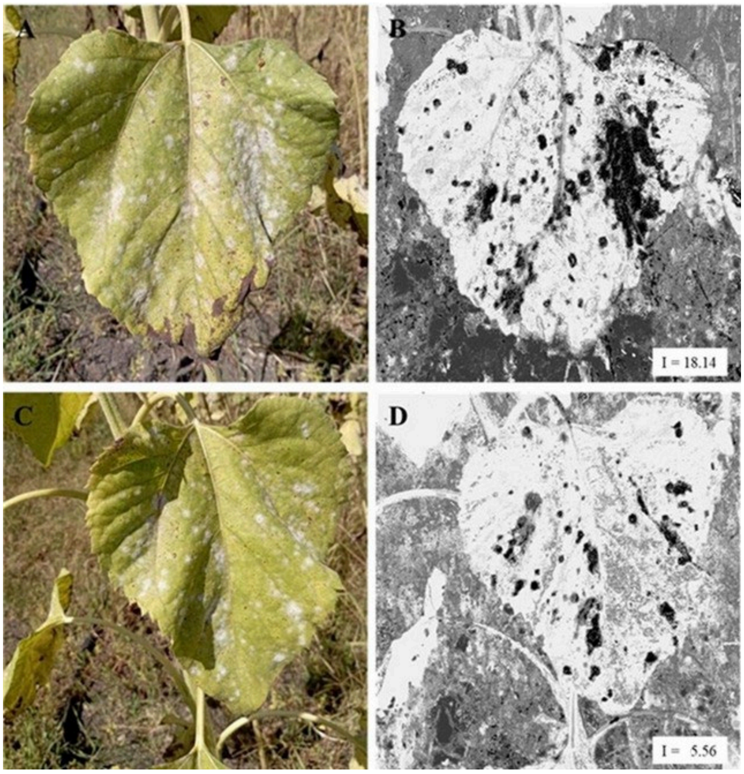


Figure 6. *The original test images (A, C) were changed to grayscale (B, D) by clustering the matrix values of the soil surface, weeds, healthy leaves, stems, and powdery mildew to determine the powdery mildew severity rate (I = 18.14 and 5.56).*

Disease severity prediction plays a crucial role in ensuring food security, controlling infections, and estimating yield losses. Traditional approaches to assessing disease severity rely heavily on visual estimation, a process that is time-consuming and subject to the observer's interpretation, potentially leading to erroneous results (Bock et al., 2010). The limitations of human observation, including rater fatigue and the inconsistencies among individual raters, have emphasized the need for a more objective, reliable, and efficient method

(Pethybridge and Nelson, 2015; Şahin et al., 2023). In this context, machine learning presents a promising alternative to human observation in determining disease severity. Machine learning techniques can reduce processing time and minimize error margins (Malik et al., 2022), essential features in timely disease control and yield preservation efforts. Various machine learning methods are available, each with its own strengths and weaknesses. Our study opted for Decision Trees (DTs) in disease severity assessment, addressing the increasing need for efficiency and reliability in this domain. DTs' ability to handle categorical data, multi-output problems, and their interpretability sets them apart from other models. Additionally, their flexible nature requires less stringent assumptions about data distribution. Despite various machine learning applications in disease detection, DTs are underutilized, signifying the novelty of our study. Our research demonstrates that DTs yield competitive results and bring unique benefits, meriting further investigation. Recent studies conducted by Esgario et al. (2020) and Ji et al. (2020) have adopted different machine learning models, including deep learning models like ResNet50, for detecting disease severity. These studies reported accuracy rates of over 85%, comparable to the accuracy rates achieved in our study (between 82% and 87%). This demonstrates that our chosen method, DTs, performs well relative to these other approaches, confirming its potential for practical application. The other studies conducted by Prabhakar et al. (2020) have explored different machine learning models for specific tasks, such as tomato leaf disease detection and severity estimation. They found that the ResNet101 model yielded the highest accuracy. While the specific focus of these studies differs from ours, their overall findings further underscore the effectiveness of machine learning in disease detection and severity estimation. In this study, we applied a machine learning-based DTs model to detect the severity of powdery mildew disease on sunflower leaves with an accuracy rate of between 82% and 87%. These results demonstrate the potential of our approach for early detection of sunflower powdery mildew disease, facilitating timely intervention before the disease spreads across the field.

Conclusion

The application of machine learning-based models in the agricultural field for the early detection of diseases, as demonstrated in this study, has the potential to significantly advance precision agriculture techniques. Precision agriculture aims to apply the right input to the right place, at the right time, and in the right amount. The data obtained from this study can facilitate precise application of treatments in the correct amount and location, thereby preventing excessive pesticide use. These models deliver prompt and consistent results, surpassing traditional human observation and disease severity prediction methods in terms of both speed and stability. Our study shows that machine learning models, especially Decision Trees (DTs), have the ability to accurately quantify the severity of damage caused by diseases and pests. This accomplishment is significant for early disease detection and intervention.

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