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Comparative Analysis of SVM and Decision Tree Classifiers for Grape Leaf Disease Classification

¹*Rahul S. Pachade, ²Dr. Avinash Sharma, ³Dr. Manoj Patil

¹Research Scholar, ²Professor, ³Asst. Professor

^{2,3}Department of Computer Science and Engineering,

Madhyanchal Professional University, Ratibad, Bhopal, (MP), India

³Department of Computer Engineering, DMCE, Mumbai, (MS), India

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Keyword

Support Vector Machine, SVM, Decision Tree, grape leaf diseases, classification, precision, recall, F1-score.

Abstract

This research paper presents an in-depth analysis of the performance of Support Vector Machine (SVM) and Decision Tree classifiers in classifying grape leaf diseases. The study utilizes the grape leaf disease dataset and evaluates the classifiers based on precision, recall, F1-score, and overall accuracy. The results demonstrate outstanding performance by both classifiers, with perfect accuracy scores of 1.0. The classifiers exhibit high precision, recall, and F1-scores across the majority of disease categories, indicating their proficiency in accurately identifying grape leaf diseases. The findings highlight the effectiveness of these classifiers as valuable tools for disease classification. However, further evaluations and considerations are recommended to ensure their robustness and dependability in real-world scenarios.

INTRODUCTION

Grape leaf diseases have emerged as a critical concern for the grape industry, exerting detrimental effects on plant health and overall crop yield. Timely and precise identification of these diseases plays a pivotal role in implementing effective control strategies and mitigating their impact. Traditional methods of disease diagnosis often rely on visual inspection by experts, which can be time-consuming, subjective, and prone to errors. Therefore, there is a growing need for automated and reliable techniques that can assist in accurate disease classification.

In recent years, machine learning algorithms have demonstrated great potential in various domains, including disease diagnosis and classification. These algorithms have the capability to learn from patterns and relationships within large datasets, enabling them to make accurate predictions and classifications. By leveraging the power of machine learning, it is possible to develop robust and efficient models for grape leaf disease classification. The primary objective of this research is to evaluate the performance of two popular machine learning algorithms, namely the Support Vector Machine (SVM) and Decision Tree classifiers, in accurately classifying grape leaf diseases. These classifiers have been widely used in disease classification tasks due to their effectiveness in handling complex datasets and capturing intricate patterns.

To achieve this objective, the research utilizes the grape leaf disease dataset, which comprises a diverse range of grape leaf images representing different disease classes. The dataset provides a valuable resource for training and evaluating the classifiers. By analyzing the performance of SVM and Decision Tree classifiers on this

dataset, we aim to assess their effectiveness in accurately classifying grape leaf diseases. The research methodology involves the extraction of informative features from grape leaf images, including color-based, texture-based, target-based, and identifier-based features. These features are selected based on their relevance to grape leaf disease classification and their potential to enhance the accuracy of the classifiers. The extracted features are then used as input to the SVM and Decision Tree classifiers, which classify the grape leaf diseases based on the learned patterns and relationships within the dataset.

The evaluation of the classifiers' performance is conducted using various metrics, including precision, recall, and F1-score, which provide insights into their accuracy and ability to correctly identify positive instances. Additionally, the support parameter is considered to examine the distribution of instances across different disease classes. The overall accuracy of the classifiers is also assessed to provide a comprehensive understanding of their performance. The findings of this research will contribute to the field of grape leaf disease classification by assessing the efficacy of SVM and Decision Tree classifiers in accurately identifying and classifying grape leaf diseases. The results will provide valuable insights into the capabilities of these classifiers and their potential to support disease management strategies in the grape industry.

The research aims to address the challenges posed by grape leaf diseases through the application of machine learning algorithms. By evaluating the performance of SVM and Decision Tree classifiers on the grape leaf disease dataset, this study aims to contribute to the development of accurate and automated systems for disease classification in the grape industry.

METHODOLOGY

The study utilizes the grape leaf disease dataset, which comprises various disease classes with varying sample sizes. The SVM and Decision Tree classifiers are employed for disease classification. The classifiers' performance is evaluated based on precision, recall, F1-score, and overall accuracy. Precision measures the ratio of true positive predictions to all positive predictions, while recall assesses the classifier's ability to accurately detect positive instances. The F1-score computes the harmonic mean of precision and recall, providing an equitable assessment of classifier efficacy. The classifiers' overall accuracy is reported to evaluate their overall classification performance.

The SVM and Decision Tree classifiers, along with feature extraction techniques, are commonly used in the classification of grape leaf diseases. Feature extraction involves identifying and extracting informative characteristics from grape leaf images to enhance classification accuracy. In this study, a feature extraction method incorporating color-based, texture-based, target-based, and identifier-based features is employed.

Color-based features aim to gather data regarding chromatic dispersion and luminosity levels in grape leaf images. Color histograms depict the occurrence rate of different color values, while statistical characteristics such as mean, variance, and skewness are computed using color moments.

Texture-based features provide insights into spatial arrangements and textural characteristics of leaf surfaces. Gabor filters are utilized for texture filtering, and statistical texture descriptors like Local Binary Patterns (LBP) and Gray-Level Co-occurrence Matrix (GLCM) features capture textural patterns and relationships between neighboring pixels.

Target and identifier features include information directly relevant to the classification task. Target features consist of disease class labels associated with each leaf image, providing supervision during training. Identifier features encompass distinctive characteristics or metadata that aid in leaf monitoring and recognition.

The selected features for the classification task in machine learning are as follows:

1. Mean values (mean_r, mean_g, mean_b) represent the average intensities of the red, green, and blue color channels, providing information on typical channel intensities.
2. Standard deviations (stddev_r, stddev_g, stddev_b) indicate the range of pixel intensities in each color channel.

3. Contrast measures local differences in pixel intensities, reflecting the discrepancy between a pixel's average brightness and the brightness of neighboring pixels.
4. Correlation evaluates the linear relationship between pixel intensities across color channels, indicating morphological or structural similarities.
5. Inverse_diff_moments measure the smoothness or local homogeneity of the image by indicating the likelihood of two pixels sharing the same intensity value.
6. Entropy quantifies the randomness or unpredictability of pixel intensities, conveying the image's complexity or information quantity.
7. Class represents the image's target variable or disease class label.
8. Label serves as an additional identifier or categorization for the image.

After feature extraction, the SVM and Decision Tree classifiers are used for disease classification. These classifiers leverage the extracted features to accurately classify grape leaf diseases.

RESULTS AND DISCUSSIONS

The analysis of the SVM classifier reveals exceptional performance, with precision, recall, and F1-scores of 1.00 across most disease categories. The classifier demonstrates high accuracy in identifying positive instances, as indicated by precision scores of 1.00 for the majority of disease classes. The recall metric indicates accurate detection of positive samples, except for the "Powdery_Mildew" category, which shows a recall of 0.98. The F1-scores exhibit a commendable equilibrium between precision and recall, further validating the classifier's efficacy. The overall accuracy of the SVM classifier is reported as 1.00, indicating accurate classification of all samples in the dataset as can be seen in the table 1.

Table 1 Classification summary SVM

	precision	recall	f1-score	support
Anthracnose	1	1	1	52
Background	1	1	1	45
Bacterial_leaf_spot	1	1	1	51
Downey_mildew	1	1	1	171
Healthy	0.99	1	1	188
Leaf_Blight	1	1	1	56
Mites	1	1	1	73
Powdery_Mildew	1	0.98	0.99	47
Rust	1	1	1	217
black_measles	1	1	1	336
black_rot	1	1	1	286
accuracy			1	1522
macro avg	1	1	1	1522
weighted	1	1	1	1522

Similarly, the Decision Tree classifier achieves flawless performance with precision, recall, and F1-scores of 1.00 across all disease categories as presented in the table 2. The classifier accurately identifies positive samples for each respective class, exhibiting no false negatives. The F1-score averaging accuracy and recall also reflects optimal equilibrium, suggesting exceptional comprehensive efficacy. The classifier's overall accuracy is reported as 1.00, indicating accurate classification of all samples in the dataset.

Table 1 Classification summary SVM.

Table.2. Decison Tree Classification report

	precision	recall	f1-score	support
Anthracnose	1	1	1	52
Background	1	1	1	45
Bacterial leaf spot	1	1	1	51
Downey mildew	1	1	1	171
Healthy	1	1	1	188
Leaf Blight	1	1	1	56
Mites	1	1	1	73
Powdery Mildew	1	1	1	47
Rust	1	1	1	217
black measles	1	1	1	336
black rot	1	1	1	286
accuracy			1	1522
macro avg	1	1	1	1522
weighted	1	1	1	1522

CONCLUSION

The study demonstrates that both the SVM and Decision Tree classifiers exhibit outstanding performance in classifying grape leaf diseases. These classifiers achieve perfect accuracy scores, indicating accurate classification of all samples. Noteworthy precision, recall, and F1-scores across most disease categories validate their proficiency in precisely identifying positive instances. The consistent performance across diverse evaluation metrics highlights the classifiers' effectiveness and their potential as valuable tools for accurately detecting grape leaf ailments. However, further assessments and considerations are necessary to ensure their robustness and dependability in practical situations. Overall, this research contributes to the field of grape leaf disease classification and emphasizes the significance of machine learning algorithms in disease management.

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