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Machine Learning Algorithms for Early Detection of Legume Crop Disease

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ABSTRACT

Background: Legume crops are an essential component of global agriculture and are widely supplied for human consumption, livestock feed and soil improvement due to their vital nutritional nature. The economic and nutritional significance of legumes is threatened by a multitude of diseases that can cause substantial yield losses. Traditional methods for disease detection, relying on visual inspection, are often subjective and inefficient, leading to delayed intervention.

Methods: This study investigates the utilization of machine learning algorithms for the early identification of diseases affecting legume crops. A comprehensive evaluation is conducted on machine learning algorithms, namely Support Vector Machines (SVM) and Convolutional Neural Networks (CNN) with respect to the domain of disease detection. Through a comparative analysis of their performance across different environmental conditions and phases of crop development, this study also explores their strengths and weaknesses.

Result: The findings and comparative examination offered significant perspectives on the potential of machine learning algorithms in the realm of early legume crop disease detection. In addition to enhancing crop health and disease management, the research provides support for sustainable agricultural practices and possesses the capacity to augment environmental sustainability and food security through the application of machine learning techniques.

Key words: Augment environmental sustainability, Convolutional neural networks (CNN), Machine learning, Support vector machines (SVM).

INTRODUCTION

Agriculture stands as the fundamental pillar of human society, ensuring nourishment, financial stability and ecological equilibrium. Legumes are now crucial components of the agricultural landscape and play a vital role in the worldwide food supply (Gamage *et al*., 2023). Generally, Legumes including soybeans, peas, lentils and chickpeas, are renowned for their exceptional nutritional value, characterized by their high protein content, dietary fiber and essential nutrients. As a result, they are crucial elements in both human and cattle diets (Hernández-López *et al*., 2022). Additionally, their exceptional ability to repair atmospheric nitrogen improves soil fertility and promotes sustainable agriculture through the implementation of crop rotation strategies (Hirel *et al*., 2011 and Ladha *et al*., 2022). The ability to fix nitrogen is advantageous for both the environment and crop rotation techniques. Although legume crops hold significant agricultural value, they are susceptible to illnesses caused by a variety of pathogens (Zahran, 1999). However, these crops are consistently facing formidable challenges from diseases initiated by a diverse array of pathogens, encompassing fungi, bacteria and viruses. The presence of these pathogens collectively poses a significant threat to the long-term health and productivity of leguminous crops (Dell'Olmo *et al*., 2023). These diseases present a significant risk to the economic feasibility and nutritional stability of agriculture. Infections can result in diminished agricultural yields, decreased crop quality, heightened production expenses and, in extreme instances, total crop collapse (Stagnari *et al*., 2017). Moreover, the utilization of chemical remedies for disease management entails detrimental environmental repercussions and poses hazards to human health (Godde *et al*., 2021 and Abebe, 2022). Legume crop diseases exhibit a range of symptoms that are challenging to visually distinguish and their swift dissemination across extensive agricultural areas adds complexity to early management (Orchi *et al*., 2022).

The study investigates the use of machine learning algorithms to detect legume crop diseases at an early stage. Here, the potential of artificial intelligence, data analysis and predictive modeling is extensively utilized to tackle this problem. Reliable machine learning models that can effectively detect diseases in legume crops at an early stage are modelled. This is achieved by integrating data from several sources, including crop plant photos, sensor data and weather data. The potential of machine learning in agriculture resides in its capacity to automate the analysis of extensive datasets, raise the speed and precision of

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disease identification, diminish the dependence on manual labor and amplify the possibility of early intervention. Machine learning techniques: Convolutional Neural Networks (CNN) and Support Vector Machines (SVM), are employed for effective disease identification. The detection is performed using algorithms under varying environmental conditions and stages of crop growth. The comparison of the strengths and weaknesses of different machine learning algorithms in the context of disease detection in legume crops is pursued.

Literature survey

Conventional disease detection procedures, which rely on visually examining and manually intervening, are both time-consuming and require a significant amount of effort. The constraints of these traditional methods require a fundamental change in approach towards inventive and technology-oriented alternatives (Alzubaidi *et al*., 2021 and Vanlauwe *et al*., 2019). These crops are commonly afflicted by several illnesses, including fungal infections such as soybean rust produced by *Phakopsora pachyrhizi*, viral infections like Bean common mosaic virus and bacterial diseases caused by pathogens like *Xanthomonas axonopodis* (Pérez-Pizá *et al*., 2023; Cho, 2024). The pernicious characteristic of these diseases is their capacity to interfere with crop growth and development, resulting in stunted growth, diminished yields and, in severe instances, substantial crop losses (Panth *et al*., 2020). The identification of illnesses in legume crops has depended on visual examination and manual scrutiny. Nevertheless, these approaches have various constraints. These methods are fundamentally subjective as they depend on the knowledge and judgment of human observers (Najjar, 2023). Additionally, they often lead to delayed disease identification, frequently occurring after apparent symptoms have already appeared. Furthermore, the process of manually inspecting is demanding in terms of manpower and is not as effective in large-scale agricultural activities (Ngugi *et al*., 2021). The aforementioned issues have created an urgent demand for enhanced automated, precise and prompt disease detection systems in legume crop cultivation. Machine learning has become a transformative tool in agriculture, providing several uses for identifying diseases, managing crops and implementing precision agriculture (Andrew *et al*., 2022). Machine learning algorithms have the potential to significantly transform disease identification in agriculture, enabling more efficient monitoring and management of diseases (Rani *et al*., 2022). These algorithms have the ability to automate the processing of extensive datasets, such as crop photos, sensor data and weather data (Durai and Shamili, 2022). Machine learning enhances disease management systems by decreasing dependence on manual labor and enabling timely intervention, resulting in improved efficiency and effectiveness. Machine learning has gained significant attention in recent years for its potential applications in agriculture, particularly in the early detection of diseases (Rodrigues *et al*., 2023; Gong *et al*., 2019). Prior research has investigated the application of machine learning algorithms in many crops, such as cereals, fruits and vegetables. Although there has been significant advancement in the sector, it is crucial to emphasize that legume crops have not garnered the same level of focus as staple crops such as rice, wheat and maize when it comes to disease detection using machine learning (Sadenova *et al*., 2023). However, there is ongoing research exploring the application of machine learning, namely Convolutional Neural Networks (CNNs), for identifying diseases in legume crops like soybeans and peas based on images. These investigations have shown the capacity for prompt and precise identification of diseases (Jadhav *et al*., 2021).

MATERIALS AND METHODS

Data sources

The primary dataset utilized in this study is derived from the Plant Village dataset, which was gathered under controlled circumstances. This dataset has a total of 54,306 photos depicting both damaged and healthy plant leaves (Mohanty *et al*., 2016). This study utilized a total of 14,195 leaf photos obtained from the PlantVillage database as experimental data. The dataset consisted of images representing 10 different leaf diseases, which affect 10 different crop species (Fig 1).

Data preprocessing and cleaning

In order to improve the segmentation of lesion photos, the background segmentation of the images available in Plant Village is chosen to categorize the severity of the disease (Mohanty *et al*., 2016). During the image acquisition process, the unevenness of scene brightness occurs as a result of leaves obstructing each other and variations in illumination circumstances. This is primarily due to the excessive intensity of light in the bright regions of the image, coupled with inadequate brightness levels in the dark regions. Consequently, certain crucial aspects cannot be emphasized or concealed, significantly compromising the visual and practical significance of these images. Hence, it is imperative to partition the affected regions of diseased leaves. Nevertheless, the uneven lighting in the photographs adversely affected the segmentation quality. The problem was addressed by employing an adaptive adjustment algorithm for nonuniform illumination images, which relies on a two-dimensional (2-D) gamma function (Yuan *et al*., 2022). The expression is as stated:

$$O(x,y)= 255\ [F(x,y)/255]^{\gamma},\ \gamma= (1/2)^{m-1(x,\ y)/m} \qquad ...(1)$$

In this context, O (x, y) represents the brightness value of the corrected output image, while F (x, y) refers to the input image. The index value γ is used for brightness enhancement and contains information about the illumination components of the image. I (x, y) represent the estimated illumination component and m represents the mean luminance of the illumination component.

Selection of machine learning algorithms

Convolutional Neural Networks (CNNs) were selected for their inherent capacity to independently extract hierarchical characteristics from picture data, making them highly suitable for the purpose of disease detection through image analysis. CNN possesses robust feature extraction capabilities through the construction of many filters (Andrew *et al*., 2022). These filters were then utilized to extract representative features from the input data, layer by layer. It utilized a combination of sparse connections and parameter weight sharing to down-sample the data dimension in time and space. This approach significantly reduces the number of training parameters and effectively prevents over-fitting of the algorithm. The CNN model utilizes the back-propagation (BP) algorithm to modify the model parameters. Its excellent capacity to adjust to image scaling, tilting and translation makes it highly suitable for applications in image recognition and related tasks. (Fig 2) illustrates a fundamental architecture of a Convolutional Neural Network (CNN).

Support Vector Machines (SVM) is a supervised Machine Learning (ML) algorithm utilized for both classification and regression tasks. The process of finding out the correct hyperplane for classification with the help of support vectors, that is, the points of each class present at the margin is the basic principle of SVMs. The components of SVM model are depicted in (Fig 3).

Model training and validation

The annotated data from the dataset is utilized to train machine learning models. In order to ensure strong model performance, it is crucial to divide the dataset into several subsets, which consist of training, validation and test sets. This facilitates a thorough assessment of the model's performance. In order to evaluate the model's efficacy and minimize the potential for over fitting, well-established techniques such as k-fold cross-validation was utilized. This method involves partitioning the data into several subsets, known as folds, then repeatedly training and testing the model using different combinations of these folds. This technique facilitates the assessment of the model's coherence and ability to apply to a wide range of data samples. During this iterative phase, the hyper parameters is optimized and model architecture enhanced.

Fig 1: Leaf image samples of the raw dataset, consisting of 10 leaf diseases from 10 different crops (Plant Village database).

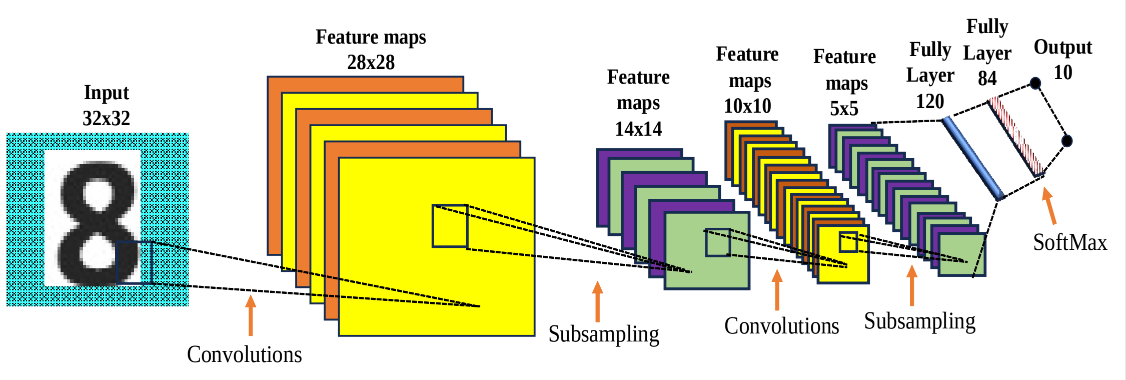

Fig 2: The sketch of structure of the convolutional neural network (CNN).

Performance comparison of different machine learning algorithms

The ability of the chosen machine learning methods, namely Support Vector Machines (SVM) and Convolutional Neural Networks (CNN) was assessed to accurately detect diseases by taking into account key assessment metrics such as accuracy, precision, recall, F1-score and other relevant indicators.

RESULTS AND DISCUSSION

Accuracy is a quantitative measurement that assesses the overall accuracy of a model's predictions. It provides a comprehension of the ratio of instances that were accurately classified. Precision is the ratio of true positive predictions to all positive predictions, which measures the model's ability to minimize false positives (Powers, 2020). Sensitivity measures the model's ability to correctly identify positive cases among all the real positive occurrences, indicating its effectiveness in reducing false negatives. The F1-Score is a quantitative measure that computes the harmonic mean of precision and recall. It is particularly advantageous for handling uneven class distributions (Powers, 2020). Depending on the specific research aims, one may consider using additional metrics such as Area Under the Receiver Operating Characteristic Curve (AUC-ROC), Mean Absolute Error (MAE), or Root Mean Square Error (RMSE) (Feby *et al*., 2020).

Convolutional neural networks (CNNs) have remarkable efficacy in disease detection via image analysis, as they automatically extract relevant features from images and show significant potential for accurate classification. The overall process flowchart of the CNN based analysis is depicted in (Fig 4). Image categorization has made significant advancements, with the development of diverse model designs in the past decade. The majority of these deep learning models were suggested within the framework of the "Large Scale Visual Recognition Challenge" (ILSVRC). The models encompass popular architectures such as AlexNet, GoogleNet, VGG and ResNet, which have been extensively utilized for image categorization across several application domains. Table 1 provides a concise overview of utilized pre-existing CNN designs. It presents the specific architecture employed in each study, along with the accompanying outcomes.

The accuracy percentages offered for various neural network architectures provide information about each performance on a particular task, most likely image categorization. It is important to remember that these outcomes depend on the environment in which they are

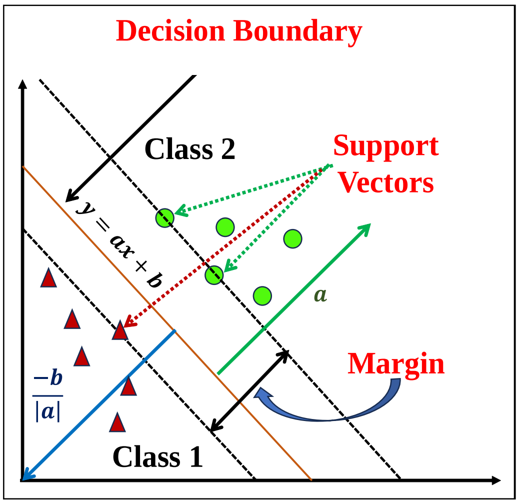

Fig 3: Components of support vector machine (SVM) Learning for classification and regression tasks.

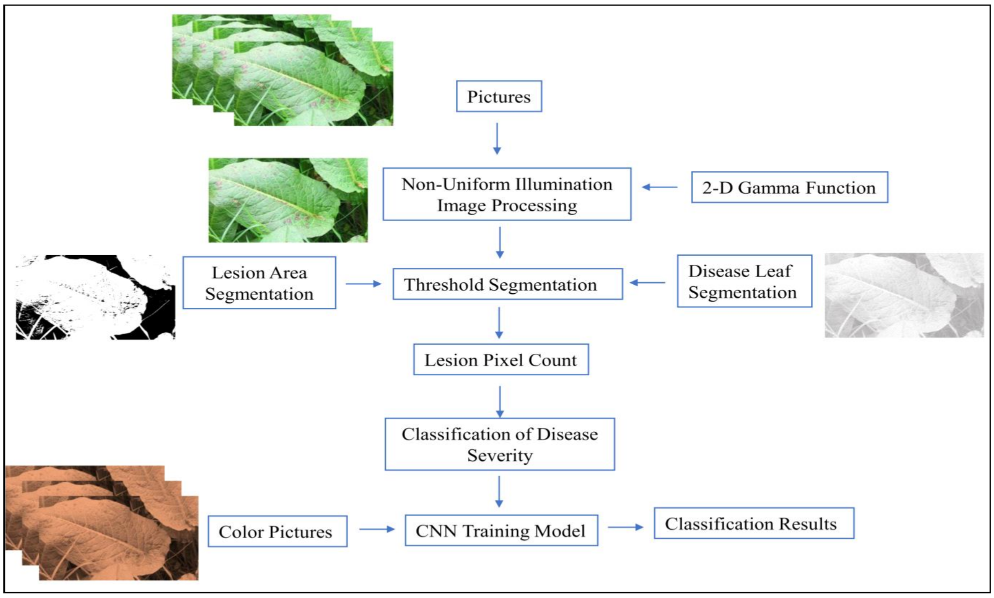

Fig 4: Overall process flowchart of CNN-based analysis.

examined and are affected by several variables, including the training approach, the dataset employed and the particular evaluation criteria. On the one hand, high precision levels, ranging from 98.3% to 99.6%, are demonstrated by architectures like AlexNet, GoogleNet (Inception) and LeNet. In image identification tasks, these models have proven to be robust; in the initial stages of deep learning, AlexNet and GoogleNet were especially prominent. An older architecture called LeNet is very good at recognizing handwritten digits. These models appear to be capable of making accurate predictions on a wide range of images based on their high accuracy percentages. However, the accuracy percentages of ResNet, VGGNet and FPN are significantly lower, ranging from 48.2% to 54.9%. Given ResNet's huge influence in resolving deep network training issues, its decreased accuracy may come as unexpected. But accuracy simply doesn't give a whole view; computing efficiency and model complexity are other important factors. The differences in reported accuracy emphasize the importance it is to selecting a model that is customized to particular needs and datasets, keeping in mind both practical and performance factors.

The support vector machine (SVM) is a model that constructs a hyperplane to effectively divide two classes (and can even be extended to handle multi-class situations). SVM selects the optimal hyper-plane to separate the data by maximizing the margin between the nearest support vectors of each class (Domingues *et al*., 2022). SVM can effectively handle non-linear data by utilizing the kernel trick technique. The SVM kernel is a mathematical function that converts a low-dimensional input space into a higher-dimensional space where the data points can be separated by a straight line (Domingues *et al*., 2022). Hence, Support Vector Machines (SVM) can exhibit great efficacy in areas with a high number of dimensions. The application of Support Vector Machines (SVM) as the machine learning algorithm for identifying diseased legume plants was showcased in (Table 2). The SVM-based classification and regression methods usually utilize linear, polynomial and RBF kernels in the context of agriculture.

Both polynomial and linear models show a noteworthy accuracy of 90.0% in the classification domain, indicating their effectiveness in differentiating between classes. An R-squared value of 0.45 for a linear model indicates a reasonable level of predictive power. Examining classification tasks in more detail reveals that linear models perform similarly to polynomial models, with a high accuracy of 91.0%. According to these findings, polynomial models show similar performance in classification tasks, while linear models consistently perform well in regression and classification cases. Decisive factors including interpretability, computing efficiency and the particulars of the dataset under study may influence the decision between polynomial and linear models. Certain applications may require substantial amounts of annotated data and computational resources, resulting in a high resource burden. Support Vector Machines (SVMs) have shown effectiveness in tasks involving binary classification, robustness when dealing with high-dimensional data and the capability to establish clear decision boundaries. Multi-class classification jobs are prone to hyperparameter sensitivity and potential challenges, which is one of its disadvantages. The data analysis provides a thorough assessment of the research findings and their implications, with a specific focus on performance metrics, visualization methods and a comparison of machine learning algorithms used in detecting diseases in legume crops.

Several crucial insights regarding the application of machine learning algorithms to the early detection of legume crop maladies are revealed by the analysis of results. The results presented in this study indicates that the disease detection capabilities of chosen machine learning algorithms-Convolutional Neural Networks (CNN), Support Vector Machines (SVM) are promising. The performance metrics of these algorithms, namely F1-score, recall, accuracy and precision, serve as indicators of their ability to accurately classify legume crops as diseased or healthy. The accuracy of the algorithms is validated through the interpretation of the confusion matrices and the visualization of disease detection outcomes, which also unveil regions in which diseases were detected with efficacy.

Although this study has yielded favorable results, it is imperative to recognize and address its inherent limitations. These include the sensitivity of certain algorithms, such as SVM, to hyperparameters and the possibility of model overfitting, particularly with limited datasets. Moreover, although the research employed a heterogeneous dataset, it might have omitted certain environmental conditions or disease scenarios, thereby limiting the findings' applicability.

Table 1: Performance of convolutional neural networks (CNN) architecture.

Architecture	Results
GoogleNet	98.3%
AlexNet	98.3
CaffeNet	96.3%
VGG16	98.0%
ResNet	49.4%
VGGNet	48.2
LeNet	99.6%
FPN	54.9%
Inception V3	62.1%
InceptionResNet V2	98.96

Table 2: Performance of support vector machine.

Classification/Regression	Type	Results
Classification	Polynomial	90.0%
Classification	Linear	90.0%
Regression	Linear	R^2= 0.45
Classification	Linear	91.0%
Classification	Polynomial	91.0%

In addition, practical implementation may present obstacles, including the availability of high-quality data and the computational demands of particular algorithms.

Future investigation is needed to gather datasets that are more diverse in nature, encompassing a broader spectrum of environmental conditions and disease scenarios. This will serve to strengthen and extrapolate the models' capabilities. Hyperparameter tuning is an area that warrants additional investigation in order to enhance the efficacy of machine learning algorithms, especially in scenarios involving parameter sensitivity such as support vector machines (SVM). Evaluate the feasibility and expandability of the constructed models in relation to their application in agricultural practices, taking into account the obstacles associated with gathering data and allocating computational resources. Examine the viability of ensemble models as a means to improve the accuracy and dependability of disease detection by combining the strengths of multiple algorithms.

CONCLUSION

The present study examined the utilization of machine learning algorithms in the context of early legume crop disease detection. The study involved data analysis and the selection of convolutional neural networks (CNN) and support vector machines (SVM) techniques. The findings underscore the capability of these algorithms to precisely identify maladies in legume crops, shedding light on their efficacy in classification, merits and demerits. In summary, this study showcases the considerable capabilities of machine learning in the timely identification of maladies affecting legume crops, underscoring the criticality of implementing it in the agricultural sector. These results make a valuable contribution to the advancement of technology and sustainability in the field of crop disease management and agricultural practices.

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Consent for publication

The author has provided their consent for publication in the journal 'Legume Research'.

Availability of data and materials

Not Applicable.

Conflict of interest statement

There is no conflict of interest.

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