



Efficient Faba Bean Leaf Disease Identification through Smart Detection using Deep Convolutional Neural Networks

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ABSTRACT

Background: Legumes, such as lentils, field peas, Faba beans and chickpeas, are high in vitamins, fiber, important minerals and protein and can help avoid obesity and cardiovascular illnesses. They also contribute to ecosystem services, such as nitrogen fixation and resilience to environmental stresses. Despite a 60% increase in global pulse production from 2000 to 2021, a demand-supply gap, especially in South Asia, raises concerns about nutritional access. Since illnesses are currently an issue to the food security of faba beans, machine learning is required for efficient disease identification.

Methods: This research employs Convolutional Neural Networks (CNNs) for robust Faba bean leaf disease identification. The CNN model is trained with diverse images representing specific diseases. The study focuses on diseases like Chocolate Spot, Faba Bean Gall, Rust and Healthy leaves. Image processing involves resizing, grayscale conversion and labeling. The CNN architecture includes eight convolutional layers, four max-pooling layers and three dropout layers. The model is trained using 80% of the dataset, validated using 20% and tested for accuracy.

Result: The CNN model achieves an accuracy of 99.37% during training and 89.69% during validation after 75 epochs. Confusion matrix and classification report illustrate the model's performance. It shows high precision, recall and F1 scores for each class, indicating balanced performance. Chocolate Spot and Rust exhibit the highest precision and F1 scores. The overall accuracy is 91%, comparable to other studies on Faba bean disease detection. The study presents a CNN-based disease identification system for Faba beans, demonstrating high accuracy and balanced performance across different diseases. The model's effectiveness is comparable to other advanced techniques. The research highlights the potential of machine learning in optimizing disease management for Faba beans. Future work could explore a broader range of diseases and incorporate hybrid machine learning algorithms for further improvement.

Key words: Augmentation, Convolutional neural network, Disease classification, Hyperparameter.

INTRODUCTION

Legumes such as chickpeas, Faba beans, lentils and field peas (often referred to as "poor man's meat" due to their richness in protein, essential elements, dietary fiber and vitamins) play a crucial role in preventing health issues like cardiovascular diseases and obesity when included in daily diets (Crujeiras *et al.*, 2010; Bouchenak and Lamri-Senhadj, 2013). Also, they have significant contributions in providing ecosystem services, such as nitrogen fixation, deep root systems and resilience to environmental stresses involving carbon sequestration and mitigation of greenhouse gas emissions, reducing groundwater pollution and enhancing crop resilience in the face of climate change (Hazra *et al.*, 2020; Jena *et al.*, 2022). Faba beans are vital contributors to global food security and provide essential nutrients to human and livestock diets (Kwon *et al.*, 2018).

Though the global pulse production saw a surge between 2000 and 2021 with a 60% increase, surpassing the world population growth (30%), the persistent demand-supply gap, especially in South Asia, is a concerning issue (CGAIR, 2023). This scarcity has led to rising local prices, indicating potential challenges in meeting the nutritional demands of the growing population. Additionally, the increased reliance on pulse imports, coupled with the susceptibility of legumes to diseases in rainfed conditions,

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raises concerns about the stability of the global supply chain. Balancing the surge in production with effective disease management strategies becomes crucial for ensuring sustained access to this vital source of nutrition.

This research aims to develop a robust and reliable Faba bean leaf disease identification system using a convolutional neural network. Training the model with diverse images will enable it to detect patterns indicative of specific diseases. This tool will assist farmers in making accurate and data-driven decisions to mitigate the impact of diseases on Faba bean crops. This study anticipates enhancing

agricultural productivity, optimizing resource utilization and securing global food supplies.

Related work

Legume plants are frequently affected by diseases caused by different microorganisms like fungi, bacteria, viruses and parasites. These diseases limit the full potential of these plants, leading to significant losses in yield. Sometimes, the losses can be as high as 100% in the absence of effective crop management practices (Darai *et al.*, 2017; Jones, 2020; Urva, 2021).

Subsequently, researchers are turning towards technological solutions for the early and accurate identification of crop diseases. Various automated methods, categorized as direct and indirect, have been proposed for disease detection. Among the indirect methods, are optical imaging techniques, such as fluorescence and hyperspectral imaging which provide valuable insights into the physiological and morphological changes in legume plants caused by diseases. For example, parameters like morphological changes and transpiration rates are measured using these techniques to identify diseases and predict crop health (Suárez *et al.*, 2022). Over time, the analysis of the large datasets generated by these imaging technologies has seen an increase in the use of machine learning algorithms, particularly from the year 2010 (Chen *et al.*, 2020). Deep learning techniques such as Convolutional Neural Networks (CNNs) have emerged as powerful tools in the field of image-based disease detection in plants (Min *et al.*, 2024). CNNs are a class of deep learning models designed for pattern recognition in visual data, making them well-suited for tasks like plant disease identification. CNNs employ convolutional layers to automatically extract relevant features from images. This feature extraction capability is crucial for discerning subtle visual cues indicative of diseases, such as discoloration, lesions, or abnormal growth patterns. A model based on deep learning is suggested for identifying plant species and classifying plant leaf diseases. Convolutional Neural Networks (CNNs) are neural networks that are highly layered and usually contain basic function layers such as convolution layers, pooling layers and a classification layer. The first practical use of a modern Convolutional Neural Network was proposed as LeNet-5. CNNs vary in terms of how these basic layers are structured and packaged, as well as the approach used to train the network. Aside from the legume crop, artificial intelligence has been used in many other fields, such as big data analysis and animal research (Na *et al.*, 2024; Kim and Kim, 2023; Porwal *et al.*, 2024; Wasik and Pattinson 2024).

In addition to CNN, various models often integrate multiple approaches where the strengths of different methods are combined to achieve improved accuracy and reliability (Cho, 2024). These systems are known as hybrid systems. Hybrid systems may incorporate traditional image processing techniques, such as segmentation and morphological operations, alongside deep learning methods like CNNs and can fuse information from various sources,

including spectral, spatial and temporal data, to enhance the overall disease detection process. Bedi and Gole (2021) came up with a way to automatically detect Bacterial Spot disease in peach plants using their leaf images. Their method involved a combination of a convolutional autoencoder (CAE) and CNN, resulting in a hybrid system. With just 9,914 training parameters, their model achieved an impressive 99.35% training accuracy and 98.38% testing accuracy. The main advantage of this approach was that it required fewer training parameters, which ultimately reduced the analysis time. Abed *et al.* (2021) proposed a framework that detects bean leaves and diagnoses diseases within the detected leaves using a pre-trained ResNet34 encoder. Five different deep-learning models were evaluated to identify the healthiness of bean leaves. The effectiveness of the suggested framework was assessed utilizing a dataset comprising 1295 images categorized into three classes. The Densenet121 model demonstrated superior performance, achieving a CAR of 98.31%, Sensitivity of 99.03%, Specificity of 96.82%, Precision of 98.45%, F1-Score of 98.74% and an AUC of 100%. These findings collectively emphasize the significant impact of cutting-edge technologies and machine learning in enhancing disease management processes. For instance, Manschadi *et al.* (1998) utilized a model that was created for beans cultivated in cooler climates with ample water and nutrients. Through subsequent updates incorporating region-specific features and validation using field data from northern Syria, where beans were subjected to varying water levels, the refined model demonstrated accurate predictions of bean growth and yield in drought-prone areas. This highlighted the importance of accounting for regional nuances in optimizing predictive models for plant diseases. The present study extends the application of deep CNNs to address disease detection challenges, emphasizing a tailored approach for Faba beans.

MATERIALS AND METHODS

The method used for building a Deep Convolutional Neural Network (CNN) model for Faba bean leaf disease identification is described in the following sections. It is divided into several significant segments, the first of which is the gathering of images for deep neural network classification.

Dataset

The CNN model requires a sizable dataset to be processed. In this work, the data is captured with the help of agricultural experts. The Dataset contains 8021 images of faba bean leaf images captured in the fields, the detail is summarized in Table 1. It is separated into four categories: three disease categories and one healthy category. The disease groups include Healthy, Rust, Faba Bean Gall and Chocolate Spot leaf images (Fig 1 and Table 1). In this study, the entire dataset was split into training, testing and validation data in an 80:20 ratio.

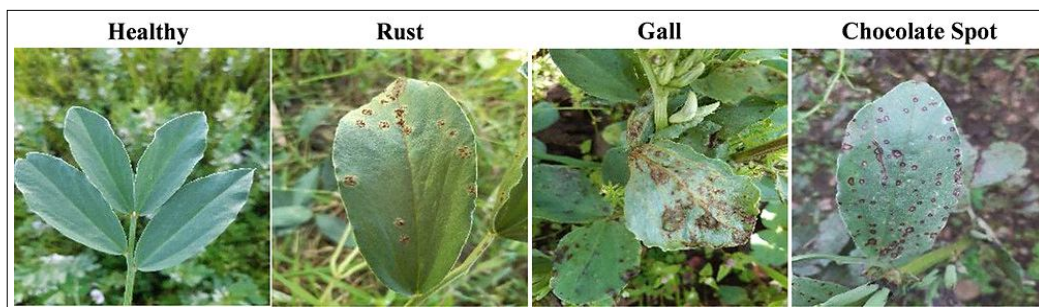


Fig 1: Images from faba beans leaf dataset (a) Healthy (b) Rust (c) Gall and (d) Chocolate spot images.

Table 1: Classification of diseases in Faba beans.

Class	Dataset	Description
Healthy	2019	Leaves are healthy under favorable conditions.
Rust	2000	It is caused by a fungal pathogen known as <i>Uromyces viciae-fabae</i> .
faba bean gall	2000	It is swiftly proliferating due to plant debris and a soil-borne pathogen.
Chocolate spot	2002	It is caused by the fungus <i>Botrytis fabae</i> .

Image processing and labelling

Image pre-processing was used to enhance or modify the raw images that the CNN classifier needed to process before training the model. Images acquired from various sources might have various dimensions, so it would be necessary to resize and rescale the pictures to make sure that the dimensions of the images are the same. Considering the computational cost of handling larger-sized images, this procedure is essential for consistency as well as for speeding up the training process. Scaling the data to a standardized size and format is essential before putting it into the network. It is standard procedure to use 224×224 input images in reliable models. A meaningful comparison with state-of-the-art models is facilitated by aligning the image size of our network with these standard dimensions.

So, the images were first resized to 224×224 pixels to normalize its size. The pictures were then converted to grayscale. For the explicit learning of the training data features, a significant amount of training data is needed at this pre-processing stage. The next stage involved sorting the photos of Faba bean leaves according to type and labeling each photo with the appropriate disease acronym. In this instance, the test collection and training dataset displayed four classes (Table 1).

Training dataset

This step involved applying the Convolutional Neural Network

Table 2: Hyper-parameter of CNN model.

Parameter	Description
No. of convolution layer	8 (32 and 64 Filters)
No. of max pulling layer	4
Dropout rate	0.25 and 0.4
Network weight assigned	Uniform
Activation function	Relu
Learning rate	0.00001
Epoch	75
Batch size	32

(CNN) process to generate a model for performance evaluation using image data as input. The steps involved in normalizing images of Faba bean leaves are depicted in Fig 2.

Convolutional neural network (CNN) model

In the CNN model, images can be efficiently filtered by the convolution operation because of its matrix structure. A convolutional layer, input layer, fully connected layer, pooling layer, drop-out layer and a final linked dataset classification layer are among the layers used in the Convolutional Neural Network for data training. An order of operations is mapped onto the input test set by each layer. Table 2 provides the details of the critical architectural and training parameters of a Convolutional Neural Network (CNN) employed in this study.

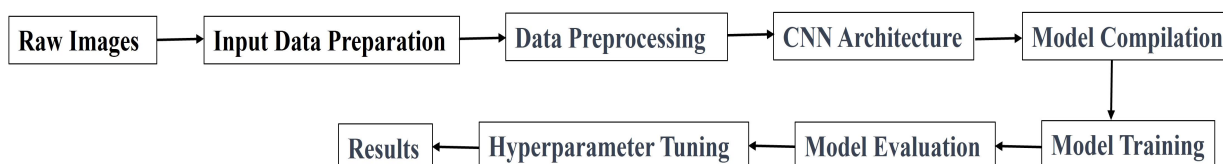


Fig 2: Classification of CNN model.

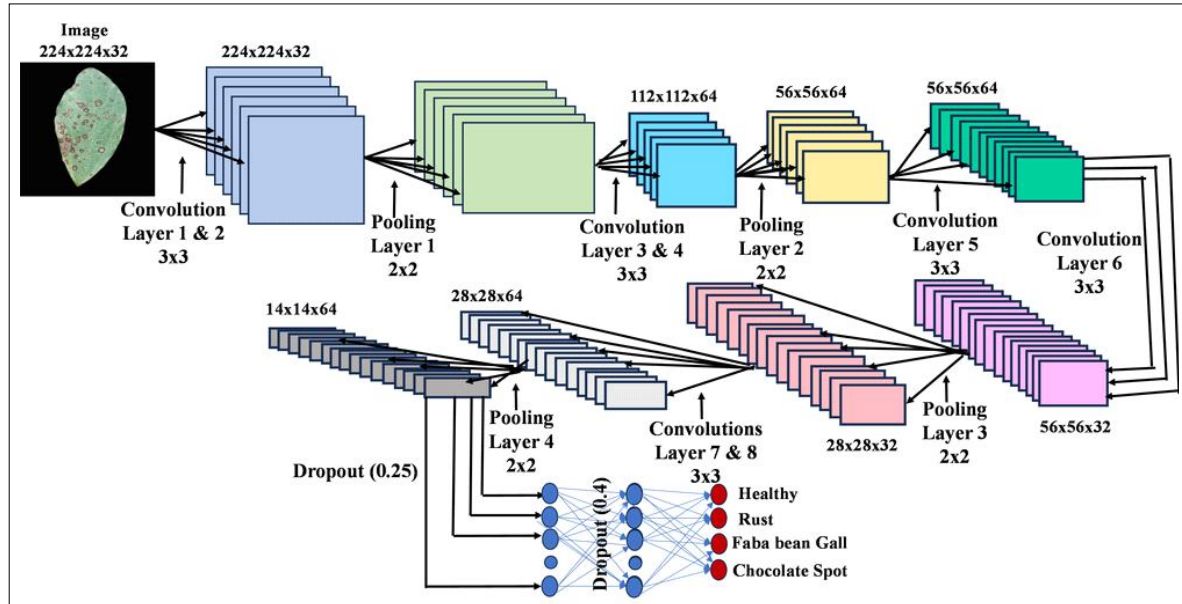


Fig 3: CNN model Architecture with convolution and pooling layer specifications.

The CNN incorporated eight convolutional layers, each employing 32 and 64 filters to extract intricate features from input data. The architecture is further enriched with four max-pooling layers to down-sample spatial dimensions effectively. Dropout, a regularization technique, is strategically applied with rates of 0.25 and 0.4 in specific layers, enhancing the model's generalization ability. Uniform weight assignment, Rectified Linear Unit (ReLU) activation function and a low learning rate of 0.00001 contribute to the network's stability. The training regimen spans 75 epochs, each involving a batch size of 32 instances. Fig 3 visually presents the comprehensive architecture.

Feature extraction process

The present work employs a Convolutional Neural Network (CNN) to classify Faba bean leaf diseases. The study is conducted within the Jupyter Notebook environment of the Anaconda platform. There are four different classes in the categorization test. The Sequential API from the Keras package is utilized in the construction of the neural architecture. The input shape parameter is set to (224, 224, 3), reflecting the dimensions of the RGB input images, after a Conv2D layer is initialized with 32 filters of 3×3 dimensions. A crucial component of feature extraction is the introduction of non-linearity to the model through the subsequent use of the Rectified Linear Unit (ReLU) activation function. After the convolutional layer, a MaxPooling2D layer with a 2×2 pool size is deliberately included to improve feature abstraction and enable spatial dimension downsampling. This pattern of architecture is repeated twice, this time with extra Conv2D layers that have 64 and 128 filters, respectively, along with max-pooling and ReLU activation. The ability to extract spatial information hidden in the input images and capture complex structure are made possible

by these layers. The addition of a flattening layer, which converts the three-dimensional feature maps into a single one-dimensional vector, marks an important change. Then, a dense layer with 128 neurons that uses ReLU activation acts as a feature aggregator, adding a substantial amount of complexity to the model. A Dropout layer with a dropout rate of 0.5 is purposefully inserted into the architecture to fix the overfitting problem. This layer effectively improves the model's capacity for generalization by methodically deactivating 50% of neurons during the training phase.

Convolution layer

Convolution is a type of specialized linear operation that involves multiplying a filter and an input matrix element by element, followed by a summation at each location in a feature map. A 3×3 kernel is used for the entire input matrix. The output value in the corresponding position of the output tensor, also known as a feature map, is obtained by summing the element-wise products of each kernel element and the corresponding input tensor element at each location. Over a two-dimensional input image (I) and two-dimensional kernel (K), the convolution operation is defined as follows:

$$S_{(i,j)} = I * K(i, j) = \sum_{x=0}^{m-1} \sum_{y=0}^{n-1} I_{(i+x, j+y)} K_{(x, y)}$$

Where

m and n = Kernel (K) coordinates.

i and j = Image (I) coordinates.

After every convolution operation with $W_{\text{output}} \times H_{\text{output}} \times D_{\text{output}}$, the output size of the convolution layer is calculated as follows:

$$W_{\text{output}} = \frac{W_{\text{input}} - F + 2P}{S} + 1$$

$$H_{\text{output}} = \frac{H_{\text{input}} - F + 2P}{S} + 1$$

$$D_{\text{output}} = K$$

Where

K = Number of filters applied to the image matrix.

F = Filter size.

P = Number of zero paddings.

S = Number of stride sizes.

Pooling layer

Max-pooling is the most popular type of pooling technique. It reduces the number of parameters in the network and eases computational demands by surveying larger image areas, which lowers the resolution of an output from a convolutional layer. The idea behind max-pooling is that the network recognizes unique elements like edges, curves and circles for a given image. The hypothesis states that more activated pixels have higher values. As a result, max-pooling chooses the most active pixels, forward-propagating these high values while eliminating less active pixels with lower values.

Performance evaluation parameters

a) Accuracy

The ratio of the total number of accurate predictions including both true positives and true negatives to the total number of predictions is one of the most widely used performance evaluation metrics. It usually indicates whether a model is being trained correctly and provides an estimate of its general performance. The following is the accuracy calculation formula:

$$\text{Accuracy} = \frac{TP+TN}{TP+TN+FP+FN}$$

TP = True positive.

TN = True negative.

FP = False positive.

FN = False negative.

b) Precision

The frequency of accurate model predictions is indicated by this parameter. The calculation involves dividing the total number of positive labels by the number of accurate positive predictions.

$$\text{Precision} = \frac{TP}{TP+FP}$$

c) Recall or sensitivity

It calculates the classifier's completeness. It is the proportion between the total number of positive reviews in the dataset and the number of correctly predicted positive observations. Discovering the most positive labels is the aim of computing these metrics. The following is the recall calculation formula:

$$\text{Recall} = \frac{TP}{TP+FN}$$

d) F1 Score

An F1-score of 1 indicates perfect performance, while a score of 0 indicates complete failure. The following formula is used to get the F-measure:

$$\text{F1-Score} = \frac{2 * \text{Precision} * \text{Recall}}{\text{Precision} + \text{Recall}}$$

Steps used in algorithm

- Collect the color images of the leaf of faba beans.
- Utilize a convolutional neural network (CNN)-based segmentation to generate a mask from the given color image.
- Overlay the original color image with the generated mask to produce a new masked image.
- Divide the masked image into smaller regions known as tiles (K_{tiles}).
- Classify each tile (K_{tiles}) from the masked image into the category of "Faba bean."
- Identify and analyze the classified tiles (K_{tiles}) to pinpoint regions indicative of a diseased part of the leaf.
- Conclude the process, having completed the steps for disease detection.

RESULTS AND DISCUSSION

The Convolutional Neural Network (CNN) framework used in this study consisted of eight convolutional layers with 32 and 64 filters, four Max-pooling layers, three dropout layers with 0.25 and 0.4 settings and two fully-connected layers with 1024 hidden nodes and four output nodes, as shown graphically in Fig 4. A total of 1,11,69,476 training parameters are included in the overall architecture.

Table 3: Classification accuracies, precision, F1 score and support.

Classification	Precision	Recall	F1-score	Support
Chocolate spot	0.90	0.90	0.90	80
Faba bean Gall	0.85	0.86	0.86	80
Healthy	0.93	0.95	0.94	80
Rust	0.96	0.93	0.94	80
Accuracy			0.91	320
Macro Avg	0.91	0.91	0.91	320
Weighted Avg	0.91	0.91	0.91	320

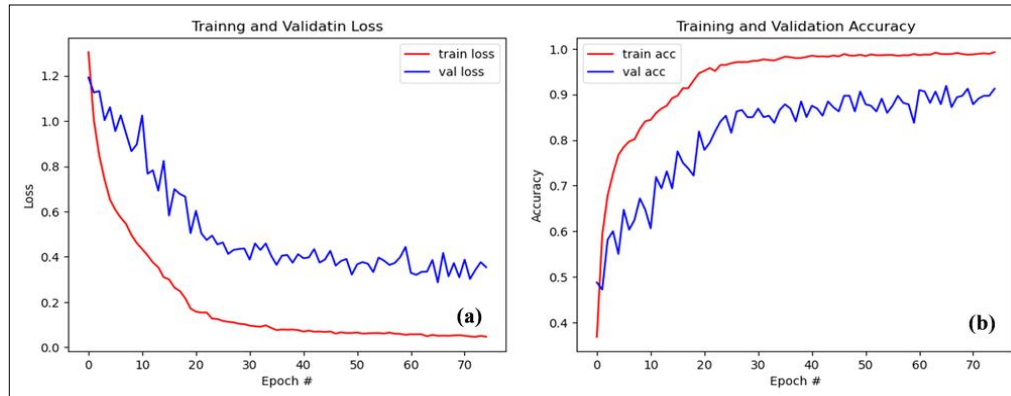


Fig 4: (a) Training loss vs validation loss (b) Training accuracy vs validation accuracy.

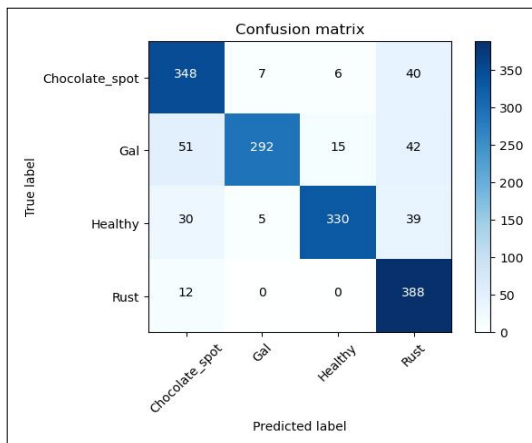


Fig 5: Confusion matrix with faba bean test data for categories: Chocolate spot, Faba bean Gall, Healthy and Rust.

The training and validation loss comparison is shown in Fig 4 (a) and the training accuracy and validation accuracy comparison is shown in Fig 4 (b). It is evident that, after 75 epochs, an accuracy rate of 99.37% has been achieved during the training phase. While the accuracy rate for validation phase is 89.69%. Thus, it is sensible to conclude that, under the research methodology, more iterations would result in higher data accuracy. It is worth noting that the number of epochs rises proportionally with the lengthening of the training phase.

Confusion matrix performance

For a particular set of test data, the confusion matrix is a matrix that is used to assess the extent to which the classification models perform. Fig 5 displays the confusion matrix with faba bean test data for the following categories: Chocolate spot, Faba bean Gall, Healthy and Rust. It shows the performance of the presented algorithm on the testing dataset as a visual representation. The confusion matrix shows the values of true positives, true negatives, false positives and false negatives for each class.

Classification report

Table 3 shows the classification performance the present model with metrics such as precision, recall and F1-score. It was observed that the model performed well on the classification task.

The model is well-balanced in terms of precision and recall with few false positives or false negatives. Hence, the model is able to accurately identify the correct class for most of the images. The accuracies in present study were comparable with other studies on disease detection in Faba beans. Slimani *et al.* (2023) obtained precision of 95.1% by using YOLOv8 for classification of rust disease in faba bean fields of eastern Morocco. Other performance indicators were also high and almost equivalent to the present study with mean Average Precision (mAP), recall and F1 score of 93.7%, 90.3% and 92%, respectively. In another study, Salau *et al.* (2023) achieved accuracies of 92.1% and 98.14% with raw and preprocessed data, respectively.

In the present study, the average precision, recall and F1-score were all high (around 0.91), indicating that the model could accurately identify the correct class for most of the images. However, the model performed slightly better in some classes than others. Chocolate Spot and Rust had the highest precision and F1 scores, while Faba Bean Gall had a slightly lower recall. This could be due to several factors, such as the number of images in each class or the inherent difficulty of distinguishing between certain classes.

CONCLUSION

This study addresses a recent area of research in digital image processing by using a convolutional neural network (CNN) technique to identify diseases of the Faba bean leaf. The basic processes of image acquisition, preprocessing, representation, interpretation and recognition are followed by all digital image processing methods, including CNN. This entails channel ordering, pixel value normalization, resizing the dimensions and image data augmentation. Following preprocessing, a Canny edge detector was used to segment those images and determine the region of interest. Using

the segmented images, the model is trained to produce representative features. the developed classifier's robustness using F1-score, accuracy, precision and recall is assessed. For this study, four disease classes-Chocolate Spot, Faba Bean Gall, Rust and Healthy are taken into account.

High recall, F1-scores and precision for each category-Chocolate Spot, Faba Bean Gall, Healthy and Rust-indicate that the classification model performs well across a number of classes. The precision and recall metrics show how well the model predicts each class, while the former emphasizes how well it captures instances of each category. The model's ability to produce accurate predictions across the whole dataset is indicated by its overall accuracy of 91%. With unweighted and weighted evaluations, respectively, the macro and weighted averages provide additional evidence for the model's resilience. All of these metrics confirm that the model is dependable in correctly categorizing examples within the specified classes, offering insightful information about its overall effectiveness and emphasizing its potential for real-world use.

LIMITATIONS AND FUTURE WORK

This study was limited to four distinct diseases that affect Faba bean leaves. But it's important to recognize that faba beans are vulnerable to several diseases that affect not just the leaves but also the stems and roots. It is therefore recommended that future research examine a wider range of illnesses that could impact various faba bean parts. Furthermore, the concatenated model's fully connected layer classifier was employed in this study. To compare and improve the overall performance of the model, hybrid machine learning algorithms, such as support vector machines, random forests and decision trees can be used in the future.

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Authors' contributions

All authors contributed toward data analysis, drafting and revising the paper and agreed to be responsible for all the aspects of this work.

Data availability statement

The database generated and /or analysed during the current study are not publicly available due to privacy, but are available from the corresponding author on reasonable request.

Declarations

Author(s) declare that all works are original and this manuscript has not been published in any other journal.

Conflict of interest

The authors declare that they have no conflicts of interest to report regarding the present study.

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