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Deep Neural Network-Based Identification of Fungal Diseases in Spinach Crops

George Wilson[1*], Chloe Bennett[2], Ethan Wright[1], Jack Turner[3]

Abstract

We created a software tool to help farmers rapidly identify and treat fungal infections on spinach leaves. The system relies on Deep Learning, with a particular focus on Convolutional Neural Networks (CNNs), to accurately identify fungal diseases in spinach foliage and recommend effective solutions to users. For training purposes, we assembled a dataset of images of spinach fungal disease, containing over 700 images organized into six categories: five disease types and one healthy class. Before training, all images were resized and enhanced through multiple augmentation methods to strengthen the model's performance. A sequential CNN model was developed in Keras for disease classification. After training on the prepared dataset, the model achieved an accuracy of 89.86% on the validation set. To ensure ease of use, we built a PySide2 GUI application that utilizes the trained model to analyze user-uploaded spinach leaf images. Beyond accurate disease identification, the software also recommends suitable remedies or medications for the detected condition. It also provides direct links to relevant products across multiple e-commerce platforms, enabling users to purchase the treatments they need conveniently. Overall, this solution allows users to examine infected spinach leaves, identify the specific disease, and respond effectively by applying appropriate treatments and obtaining necessary medications. By enabling quick detection and timely intervention, the tool helps safeguard spinach yields. It equips farmers to manage fungal diseases more efficiently, delivering benefits to the food, medicine, and skincare sectors.

Keywords Disease classification, Convolutional Neural Network (CNN), Fungal diseases, Spinach leaf, Remedies/medications, GUI application

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Introduction

Spinach ranks among the most important green leafy vegetables grown across India, especially in the winter months. It is highly nutritious, rich in iron, calcium, magnesium, copper, vitamins, antioxidants, and various other vital nutrients [1]. Given their commercial value, fungal diseases pose a major risk to spinach production. This study concentrates on five key fungi-related diseases [2] that frequently impact spinach crops in India and other South Asian regions. In conventional practice, farm experts rely on manual visual checks of leaves to spot infections, a process that is expensive, slow, and susceptible to mistakes. To overcome these limitations, this research introduces a Deep Learning solution based on image processing. It accepts a spinach leaf image as input, performs required preprocessing, and uses a Convolutional Neural Network (CNN) to classify the disease. This method provides a more affordable, straightforward, and rapid detection process while delivering accuracy comparable to that of experienced professionals. The training dataset for the CNN model, called "SFDNet," includes images of five major fungal leaf diseases of spinach: Anthracnose, Cercospora leaf spot, Cladosporium leaf spot, Downy mildew, and *Stemphylium* leaf spot [3], along with a healthy leaf category.

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Dataset images were sourced from multiple online locations and resized manually via an online tool [4]. Additional augmentation was performed using an open-source application [5], followed by thorough cleaning. The final dataset was split into training and validation portions. The SFDNet model was built with Keras, trained across all classes, and evaluated on the validation data [6-8]. The version showing the best validation accuracy was chosen as the final model. For practical accessibility, this model was integrated into a PySide2 desktop application. The application not only classifies diseases but also suggests appropriate remedies and supplies links to relevant medications [9-11]. This paper describes a fully automated Deep Learning system for detecting fungal diseases on spinach leaves. Compared to traditional manual inspection, it is more economical, efficient, and less prone to human mistakes. The system specifically targets the identification and classification of Anthracnose, Cercospora leaf spot, Cladosporium leaf spot, Downy mildew, and *Stemphylium* leaf spot, serving as a practical resource for spinach growers and specialists in India and neighboring South Asian countries.

Literature Review

Recognizing and grouping illnesses in crops, notably on spinach foliage, remains essential for enabling swift intervention and stopping widespread crop damage. Many investigations and tools have emerged to examine and spot issues in spinach leaves, centering on visible signs produced by fungal organisms [2]. Singh [3] and Ekman *et al.* [12] provided thorough safety protocols and extensive data on fungi-related spinach illnesses. Different methods have been suggested for identifying spinach illnesses. Sankar and S [13] described a technique based on the k-means clustering algorithm combined with specific classification tools, achieving 85% accuracy. Growers may submit spinach leaf photos via email to a service, which reviews them for illnesses and delivers warning steps. Christopher [14] explored Histogram of Oriented Gradients (HOG) for feature extraction, combined with an Artificial Neural Network (ANN), to detect illnesses on spinach leaves, achieving favorable results. Cercospora is a widespread spinach leaf disease that can spread to people and cause kidney stone issues. Ramkumar *et al.* [15] proposed a transfer-learning approach using a ResNet-50 Convolutional Neural Network (CNN) to detect Cercospora intensity in spinach leaves, with corrective steps provided.

Expert tools have likewise emerged for detecting spinach disease. Abu Al-Qumboz and Abu-Naser [16] designed an expert system implemented in CLIPS and Delphi that allows growers to enter signs for the evaluation and identification of spinach illnesses.

Lately, studies have focused on disease detection and classification from crop leaf images, often drawing on the PlantVillage dataset. Yet this collection omits photos of spinach-specific illnesses. Several works have applied CNN-based architectures trained on parts of the PlantVillage collection to achieve strong validation scores for illnesses across different crops [17-21]. A review by Boulent *et al.* [22] found that CNNs achieve significant gains in crop disease classification and detection.

For the spinach type grouping, CNN methods have also been used. Islam *et al.* [23] conducted a comparison study using architectures such as Inception3, Xception, VGG19, and VGG16 to classify spinach types native to Bangladesh, achieving accuracies of 98.68-99.79%. Sennan *et al.* [24] used image-preparation steps, including background removal, along with a new CNN architecture to group spinach leaves, achieving a total accuracy of 97.5%. KC *et al.* [25] applied adjusted DenseNet121, InceptionV3, and VGG19 setups, boosting accuracy by nearly 12% on the PlantVillage dataset via image-preparation steps such as edge- and shape-based segmentation and background removal.

Even though CNN-based techniques have delivered promising results for detecting and grouping crop diseases, the lack of spinach disease photos in the PlantVillage collection calls for custom solutions for spinach fungal disease detection.

This paper introduces a budget-friendly, precise, and simple CNN-based tool for grouping and providing treatment advice for spinach fungal diseases, suitable for spinach producers. It follows this layout: Section IV outlines the suggested system, and Section V details the approach. Section VI presents the outcomes and discusses the system, followed by Sections VII and VIII, which wrap up the effort and explore its future direction **(Figures 1-5)**.

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Figure 1. Anthracnose-affected spinach leaves.



Figure 2. Cercospora leaf spots on spinach leaves.



Figure 3. Cladosporium leaf spots on spinach leaves.

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Figure 4. Downy Mildew-affected spinach leaves.



Figure 5. *Stemphylium* leaf spots on spinach leaves.

Proposed System

An innovative system has been introduced to address the challenges faced by growers and specialists in diagnosing plant illnesses. The system uses a state-of-the-art CNN-based approach to precisely group photos of spinach leaves affected by fungal diseases. This creative answer seeks to reduce the time and effort required for illness recognition, while reducing the risk of human error that could lead to faulty diagnoses and harvest losses. The suggested system comes with an easy PySide2 program that enables spinach producers to access its functions without hassle. Through the program, users upload photos of spinach leaves and receive quick grouping results that identify the exact fungal disease affecting the crops. In addition to illness recognition, the system provides useful diagnostic data and suggests related items that support treatment or prevention of the named illnesses.

The system comprises two distinct stages, as shown in **Figure 6**. The initial stage covers the CNN-based setup, trained on a large dataset of spinach leaf photos depicting various fungal diseases. This setup uses modern image recognition methods to group new photos and accurately pinpoint the exact illness involved. Its solid precision and speed deliver trustworthy answers for users.

In the next stage, findings from the setup link smoothly into the PySide2 program. The program presents a simple screen that allows users to load spinach leaf photos and view immediate results of illness grouping. Once findings are shown, users can view full details on the spotted illness, including signs, sources, and recommended care plans.

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Moreover, the program provides a wide list of connected items, such as fungicides or avoidance steps, that users can check to manage spotted illnesses effectively. This option enhances the system's usefulness by providing real-world methods to fight and control crop diseases, ultimately helping maintain and increase spinach harvest output.

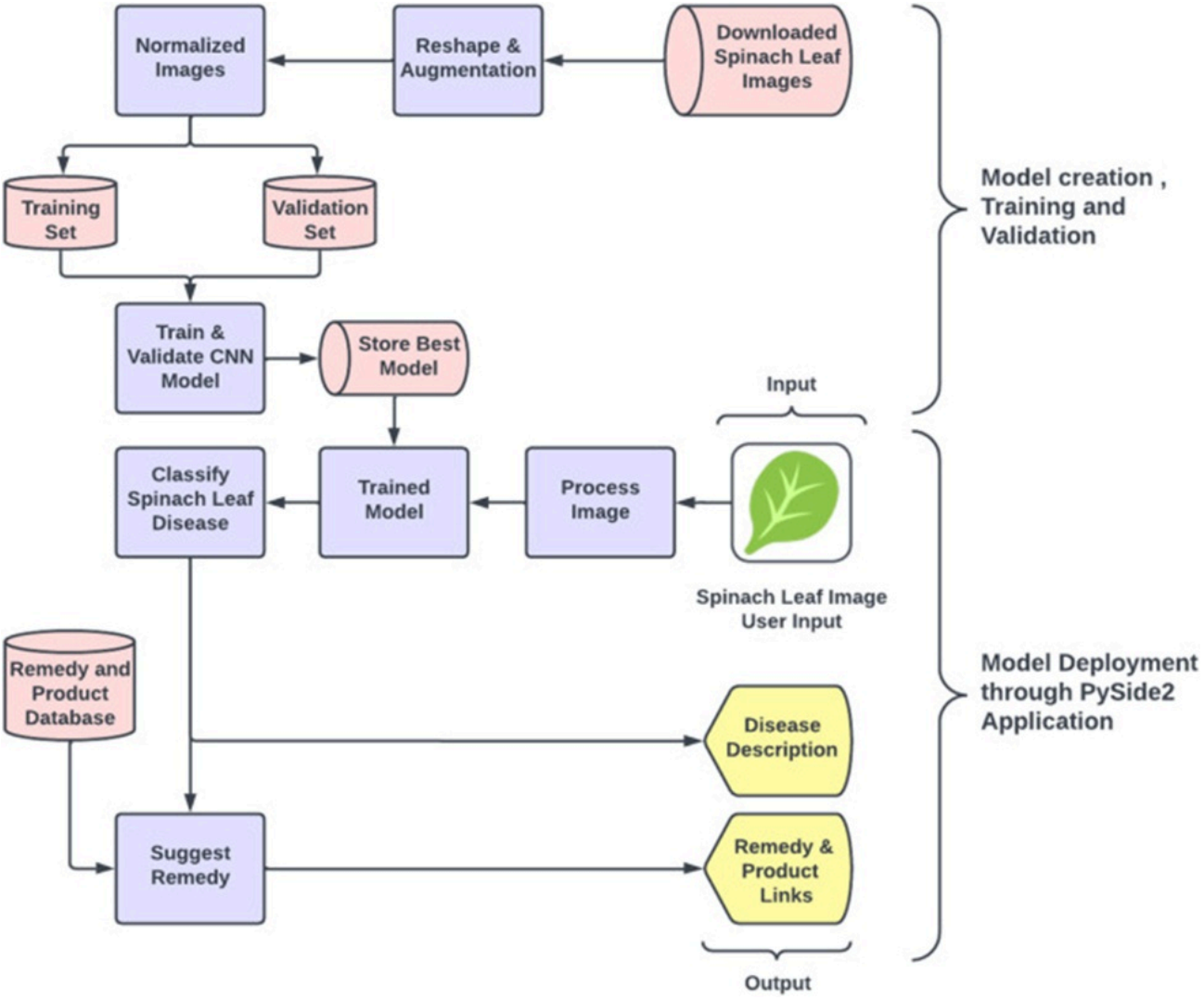

Figure 6. Overview of the proposed system.

The suggested system offers a fresh approach to crop disease recognition, especially targeting fungal diseases in spinach. Using a CNN-based approach and a simple PySide2 program, the system aims to simplify disease detection, reduce errors, and provide spinach producers with the knowledge and resources needed to fight crop diseases effectively.

Materials and Methods

The suggested platform was assembled using the following components.

Image acquisition

At the start, a photo collection of spinach leaf diseases was built by sourcing images from online platforms and from nearby farms growing spinach. This collection holds nearly 300 images across six groups (before augmentation). Group

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labels consist of Anthracnose, Cercospora leaf spot, Cladosporium leaf spot, Downy Mildew, *Stemphylium* leaf spot, and Healthy.

Image preprocessing and augmentation

Data preparation represents a vital phase during model construction. Collected photos are converted to the RGB color space and resized to 256 pixels in height and 256 pixels in width. To boost data variety and volume, augmentation approaches like horizontal/vertical flipping, rotation, and random zoom were introduced [26] via an augmentation utility [5]. Final image quantities and their distribution across groups are shown in **Table 1**.

Table 1. Image distribution in the dataset.

Disease name	No. of images
Anthracnose	130
Cercospora leaf spot	130
Cladosporium leaf spots	100
Downy mildew	140
Healthy	140
Stemphylium leaf spot	110

Problematic photos were removed, and the remaining ones were converted to a NumPy array [27]. Normalization then adjusted pixel values to a standard range of 0 to 1, improving processing speed. The entire preparation and augmentation sequence is shown in **Figure 7**.

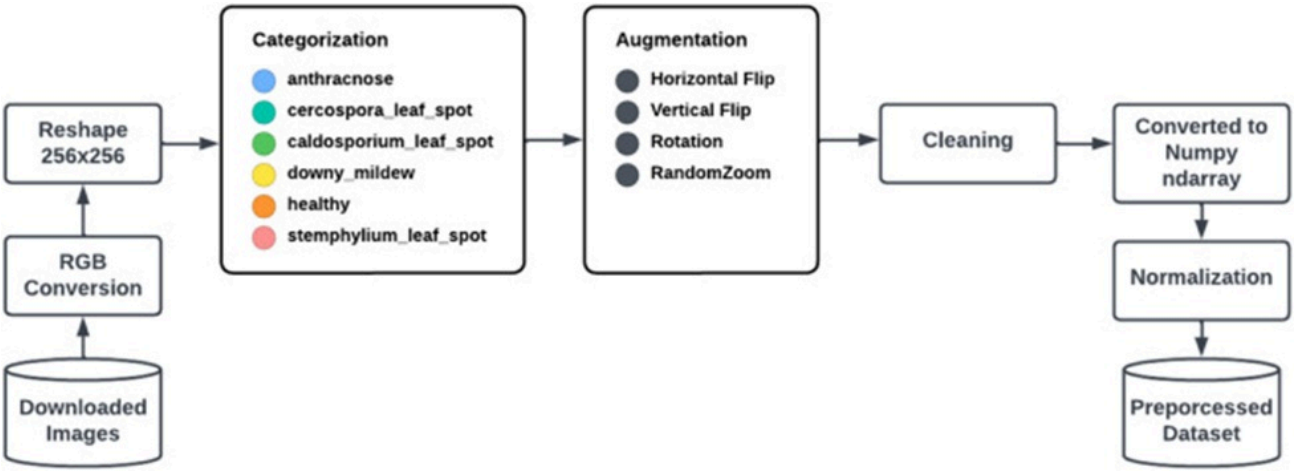

Figure 7. Image preprocessing and augmentation method.

Model development

The prepared NumPy array is split into training and validation sets to build and evaluate the proposed CNN-based model. This CNN handles both feature pulling and final grouping. Given the prepared NumPy array input, its dimensions are 256 × 256 × 3.

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A CNN is a neural network architecture that uses convolutional layers to extract image features represented as groups of filters. Dense layers then perform grouping using convolutional outputs. The full CNN layout planned for this platform is shown in **Figure 8**.

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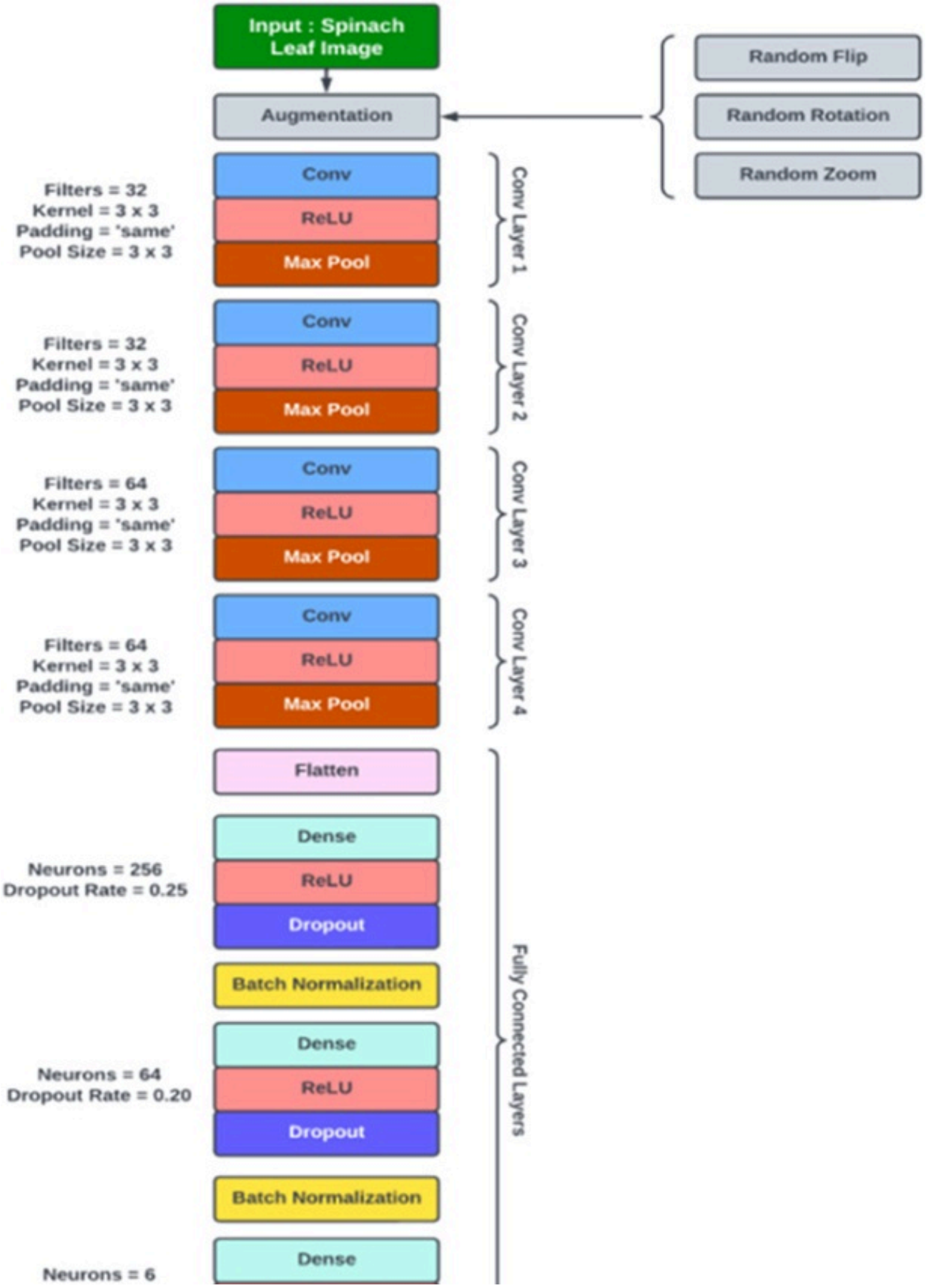

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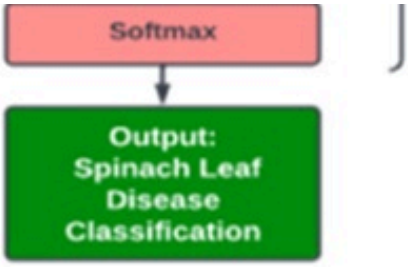

channel numbers [28].

• Convolution – Sliding filter kernels across input image data and summing dot products for each local section. This filters details and produces feature maps [28, 29]. For an n × n image and an f × f filter, the output size derives from **Eq. 1**.

$$FM_{shape} = ((n-f+1),(n-f+1)) \quad (1)$$

Where FM is the output feature map of the convolution process.

• Stride – Specifies pixel shifts of kernels over input data throughout the convolution step.

• Padding – Adds edge pixels (commonly value 0) around images during CNN processing to avoid size reduction post-convolution.

With “same” padding and f × f filters, the padding size is given by **Eq. 2**.

$$Padding_{shape} = \left(\left(\frac{f-1}{2}\right),\left(\frac{f-1}{2}\right)\right) \quad (2)$$

For convolution using padding p, filter size f × f, input n × n, and stride s, the feature map shape follows **Eq. 3**.

$$FM_{shape} = \left(\left(\frac{n+2p-f}{s}+1\right),\left(\frac{n+2p-f}{s}+1\right)\right) \quad (3)$$

• Activation function: Mechanism deciding neuron firing according to received data [30]. The model uses options such as ReLU and Softmax.

ReLU is a non-linear function that passes positive inputs unchanged and outputs 0 otherwise. ReLU follows **Eq. 4**.

$$ReLU(z) = \begin{cases} 0 \; if \; z < 0 \\ z \; if \; z \geq 0 \end{cases} \quad (4)$$

Softmax computes probability distributions for vector values scaled by relative magnitudes. Softmax uses **Eq. 5**, where x represents the input vector, K is the total number of classes, and i is the current entry.

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$$Softmax\left(\overrightarrow{z}\right)_i = \frac{exp(z_i)}{\sum_{j=1}^{K} exp(z_j)} \quad (5)$$

• Pooling: Size reduction technique sliding a two-dimensional filter over feature map channels to summarize covered regions [31]. The model uses max pooling, selecting the peak values within each region to build a new matrix [32].

• Flatten: Transforms multi-dimensional pooled maps into a single vector for fully connected layer input.

• Dense layer: Fully interconnected stage linking every neuron to all prior neurons for final image categorization [33].

• Dropout Regularization: A technique that cuts overfitting through random neuron removal during training at a set rate [34].

• Batch Normalization: Layer adjustment, rescaling, and centering batch data to accelerate and stabilize learning [35].

The proposed CNN begins with an augmentation stage that applies Random Flip, Random Rotation, and Random Zoom to incoming images. Enhanced images are fed into “Conv Layer 1” using a 3 × 3 kernel, 32 filters, a stride of 1, and “same” padding. ReLU activation follows, then 3 × 3 max pooling. Results move to “Conv Layer 2” applying the same 3 × 3 kernel, 32 filters, stride 1, and “same” padding plus ReLU and 3 × 3 max pooling.

“Conv Layer 3” and “Conv Layer 4” each apply 3 × 3 kernels with 64 filters, stride 1, and “same” padding along with ReLU and 3 × 3 max pooling. Flattened outputs from Conv Layer 4 are fed into the forward section, which consists of two dense layers: 256 neurons first, then 64 neurons. Both use ReLU, dropout rates of 0.25 and 0.20, and batch normalization afterward. The final layer comprises 6 neurons with softmax activation for multi-class classification, enabling precise identification of spinach fungal leaf disease. Consult **Figure 9** for an overview of the suggested model.

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Model: "SFDNet"

Layer (type)	Output Shape	Param #
Augmentation_Layer (Sequential)	(None, 256, 256, 3)	0
Input_layer (InputLayer)	multiple	0
Conv_1 (Conv2D)	(None, 256, 256, 32)	896
max_pooling2d_4 (MaxPooling2D)	(None, 85, 85, 32)	0
Conv_2 (Conv2D)	(None, 85, 85, 32)	9248
max_pooling2d_5 (MaxPooling2D)	(None, 28, 28, 32)	0
Conv_3 (Conv2D)	(None, 28, 28, 64)	18496
max_pooling2d_6 (MaxPooling2D)	(None, 9, 9, 64)	0
Conv_4 (Conv2D)	(None, 9, 9, 64)	36928
max_pooling2d_7 (MaxPooling2D)	(None, 3, 3, 64)	0
flatten_1 (Flatten)	(None, 576)	0
Dense_1 (Dense)	(None, 256)	147712
dropout_2 (Dropout)	(None, 256)	0
batch_normalization_2 (BatchNormalization)	(None, 256)	1024
Dense_2 (Dense)	(None, 64)	16448
dropout_3 (Dropout)	(None, 64)	0
batch_normalization_3 (BatchNormalization)	(None, 64)	256
Dense_Output (Dense)	(None, 6)	390

Total params: 231,398
Trainable params: 230,758

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Non-trainable params: 640
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Model deployment

The suggested platform uses TensorFlow to build a classifier for spinach leaf disease. Model training and validation occur in a Google Colab notebook running on cloud servers. The top version, based on validation results, is saved as a ".h5" file via the Model Checkpoint callback. This file is for download to integrate into the PySide2 setup. System data movement follows the pattern shown in **Figure 10**. Users supply a spinach leaf photo, which is reshaped, converted to NumPy arrays, and normalized. The prepared photo is sent to the trained model to predict the specific leaf disease associated with fungi. The resulting disease label triggers the remedy product recommender to suggest suitable treatments and related items.

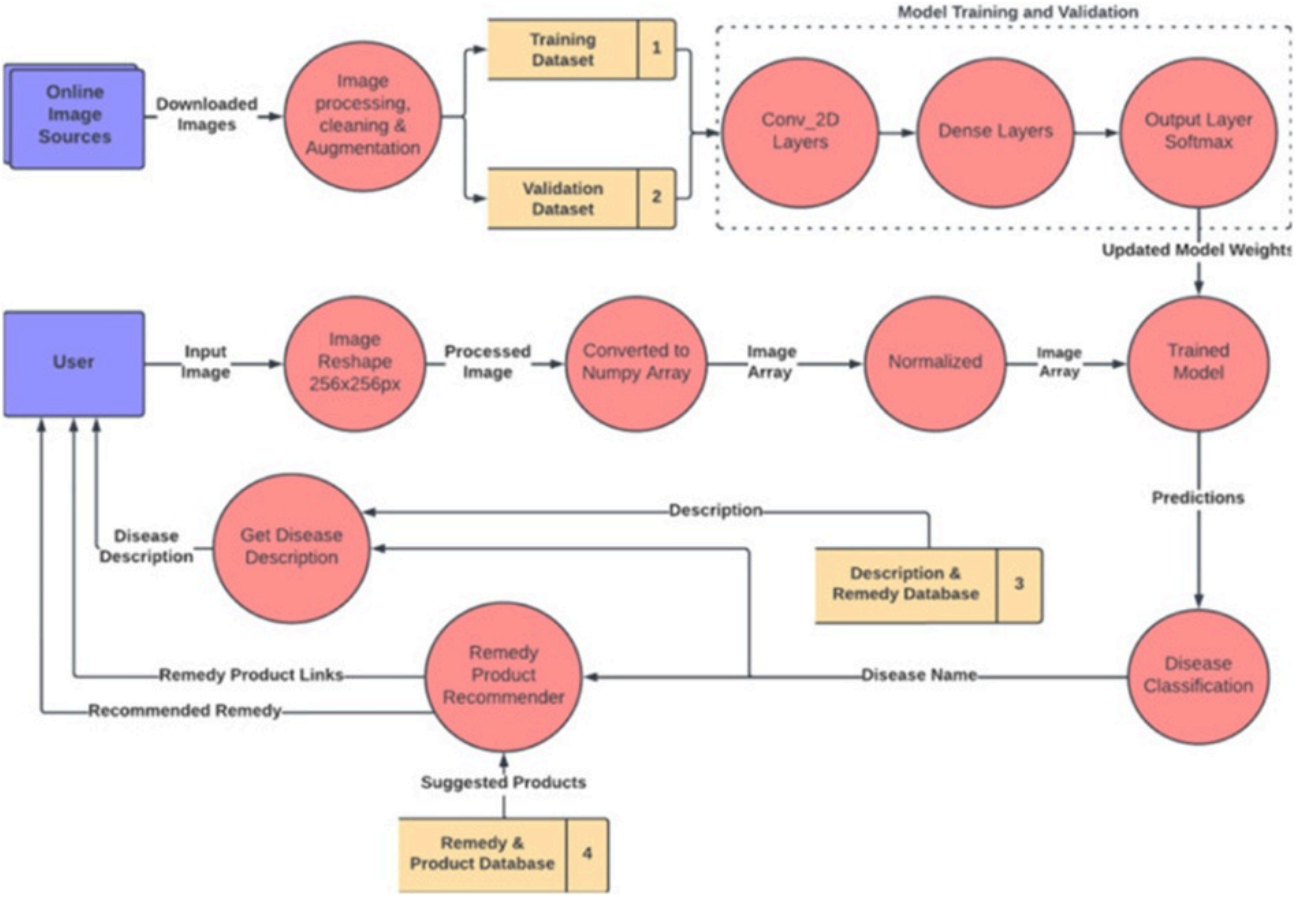

Figure 10. Data flow diagram of the proposed system.

This platform classifies spinach leaf diseases through a TensorFlow model. Creation, training, and validation occur in a Google Colab notebook running on cloud servers. The highest-accuracy validation version is saved as a ".h5" file using a ModelCheckpoint callback before integration into the PySide2 setup for everyday use.

Operations follow the flow shown in **Figure 10**, which shows data movement. A user-submitted spinach leaf photo receives reshaping, NumPy transformation, and normalization. These steps prepare the photo for review. The ready photo is fed into the trained model, which applies its patterns to forecast the presence of fungi-related leaf disease.

Once the disease label emerges, the remedy product recommender engages. It draws from this label to propose fitting treatments and database products. The recommender aims to equip users with targeted support to manage spotted leaf disease effectively.

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Anthracnose

Spinach plants are vulnerable to anthracnose, a fungal infection triggered by the pathogen *Colletotrichum Pinaceae*. The disease propagates via wind-carried spores and through water from irrigation or rainfall that splashes spores onto plants. Initial symptoms appear as small circular spots on both young and older leaves, starting with a dark olive shade [20]. As the condition progresses, the spots enlarge, shift to brown or tan, become thin and papery, and ultimately cause the entire leaf to wither. Specific weather patterns promote anthracnose development. The disease favors areas with high humidity and standing water on leaves. Temperatures between 26 and 30 °C create ideal conditions for growth.

Cercospora leaf spot

This is one of the major diseases affecting spinach cultivation. It is caused by the fungus *Cercospora beticola*, with spores dispersed by rain, wind, insects, and similar agents. The pathogen can enter leaves through open stomata and persist in infected plant debris, weeds, seeds, and soil for up to 2 years. Early signs consist of many small circular spots featuring a pale brown to off-white center surrounded by a red border. During sporulation, the spots enlarge, fuse, and turn gray, leading to leaf death and significant foliage reduction. Ideal conditions for spread include elevated humidity and temperatures between 25 and 30 °C [21].

Cladosporium leaf spot

Another common leaf spot infection in spinach is caused by the fungus *Cladosporium variabile*, which primarily persists inside seeds. Spores spread through wind and rain. Affected leaves show brownish, circular spots measuring about 0.2 inches across, which later develop velvety, dark green spore layers. Nearby spots often coalesce, creating larger, uneven lesions. The disease thrives in cool, moist settings with temperatures of 15 to 20 °C and relative humidity exceeding 80% [22].

Downy mildew

Organisms in the Oomycota group trigger this widespread, highly infectious, and damaging fungal disease of spinach. The wind carries spores formed in the morning during the day. Initial symptoms include irregular yellow patches on the upper leaf surface and purplish-gray growth on the lower leaf surface. In advanced phases, the spots expand, turn tan, and dry out. The disease develops best in cool, damp conditions with temperatures between 15 and 21 °C [23].

Stemphylium leaf spot

Various *Stemphylium* species, including *Stemphylium botryosum*, *Stemphylium* sp, and *Stemphylium beticola*, cause this fungal leaf spot condition. Symptoms present as light gray to tan-green spots measuring 0.15-1.3 cm. Larger spots tend to have irregular outlines and become dry and papery in later stages. Prolonged leaf wetness from frequent rains, combined with moderate temperatures of 17 to 23 °C, strongly favors disease development [24, 25].

Model creation, training, and validation

RGB spinach leaf photos from five illness groups and the healthy group were obtained and prepared. At first, the photos were resized to 256 x 256. Image augmentation methods were then applied to enlarge the dataset. Any unwanted photos were removed from the collection. The prepared dataset was converted to a NumPy array and scaled for subsequent steps. The dataset is split into training and validation sets to support training and validation of a CNN-based model.

To monitor the setup's results and keep the best version, a model checkpoint callback was configured. This callback watched validation precision and stored the setup version with the top precision as the best one.

To sum up, the preparation stages covered resizing, augmentation, and tidying of the RGB spinach leaf photos. The finished dataset was then converted to a NumPy array, scaled, and split into training and validation sets. The model

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checkpoint callback made sure the best version of the CNN-based setup was saved based on validation precision.

Model deployment through a PySide2 application

This Python tool features a clean, straightforward interface, as illustrated in **Figure 11**. It loads a previously saved model file at startup. Users input a leaf photo, which is converted to RGB mode, resized to 256 pixels in both height and width, and converted to a NumPy array. Normalization occurs next, after which the loaded model performs the prediction. The model sorts the supplied image among six possible disease types. Following the outcome, the tool retrieves data from a dedicated remedies and products database. It then presents the user with targeted disease details if available, including linked remedies and shopping links.

The main screen **(Figure 11a)** allows users to start the tool and select a photo of a spinach leaf via the “Browse for Picture” option. After selection, activating the “Predict” button begins the identification sequence. Results include the recognized disease label, the CNN model’s certainty level, and a brief overview of that disease type. Pressing “See More” launches a “Disease Details” panel **(Figure 11b)** filled with broad details on the identified issue. Contents feature a sample image, the formal disease title, responsible fungi or pathogens, common signs, and preferred environmental factors that promote its growth and transmission. This panel aims to provide users with thorough information.

Activating the “Cure” button opens a “Remedy Details” panel **(Figure 11c)** listing known solutions for the detected disease. It additionally shows associated product links. Selecting any link opens the default browser in a new tab to the matching product page. In summary, the tool delivers a practical, insightful experience for individuals seeking to detect and manage fungal issues on spinach leaves.

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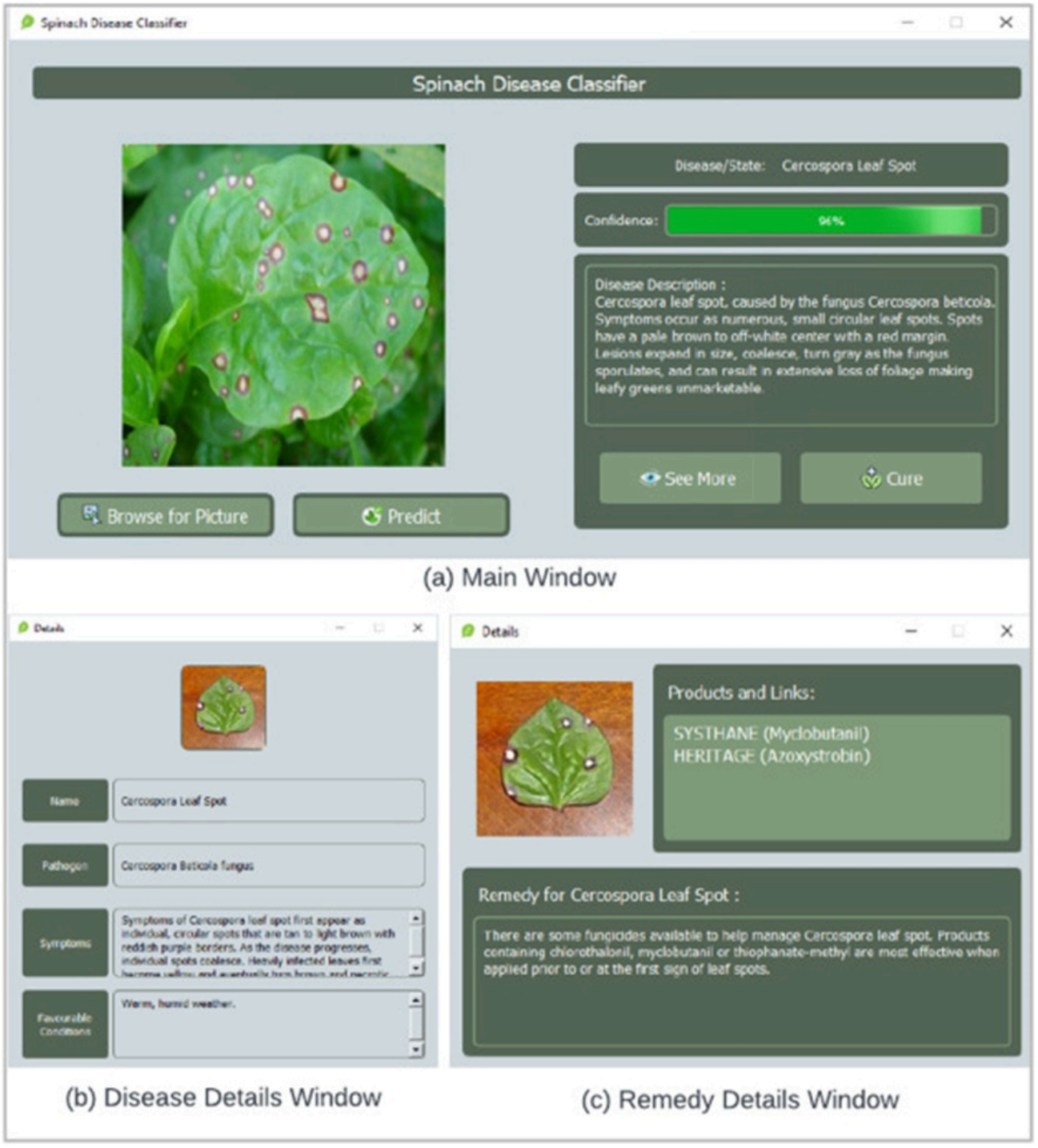

Figure 11. Windows in the PySide2 Application (a) Application home screen predicting the “Cercospora” disease accurately, (b) Disease Details Window of the predicted disease, (c) Remedy Details window of the application about the predicted disease.

Results and Discussion

This section presents an evaluation of the classifier’s effectiveness using training and validation image sets derived from the initial collection.

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The suggested CNN model, called “SFDNet”, operates with a learning rate of 0.01 and a batch size of 32. It applies the Softmax activation function with the ‘Adam’ optimizer and trains for 300 epochs. Model hyperparameters appear in **Table 2**.

Table 2. Hyperparameters of the “SFDNet” model.

Hyperparameter	Value
Learning Rate	0.001
Optimizer	Adam
Batch Size	32
Activation Function	Softmax
Epoch	300

Training and test data split

The proposed “SFDNet” model is trained and validated using an 80:20 split. The random state parameter remains fixed at 20. **Table 2** shows how the data are distributed across the training and validation sets, along with the target label for each disease category.

Accuracy of the proposed model

Accuracy reflects the correctness of predictions, while loss or error indicates the gap between expected and real outcomes. The network seeks to raise accuracy and lower loss. Accuracy and loss curves in **Figures 12 and 13** result from training and validating the model on the respective datasets.



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Figure 12. Model accuracy graph.

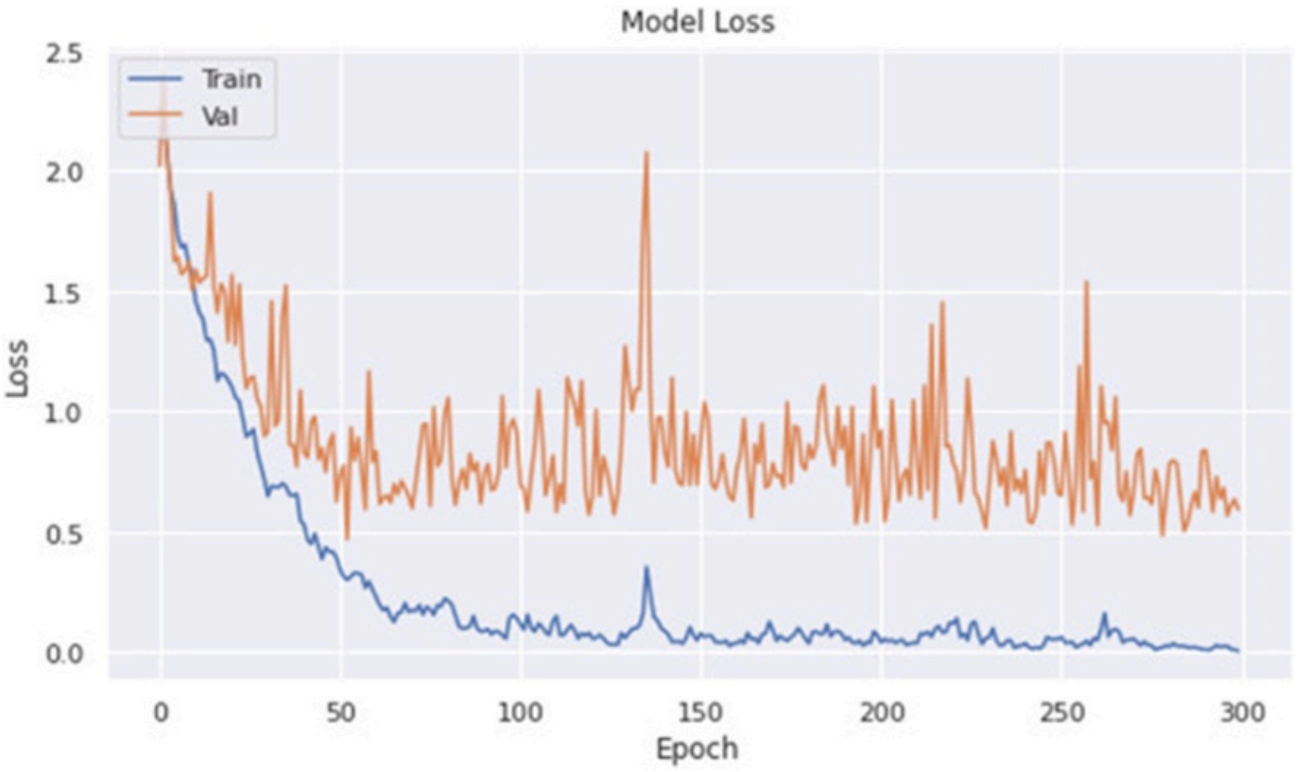

Figure 13. Model loss graph.

The accuracy curve in **Figure 12** plots training and validation accuracy against Epoch. The figure shows that both the training and validation accuracies increase with the number of epochs. Our model "SFDNet" achieves a peak validation accuracy of 89.86% and avoids overfitting, as the validation accuracy line remains close to the training accuracy line. One additional note is that the validation accuracy curve shows more fluctuations than the training accuracy curve.

In the training and validation loss versus epoch plot in **Figure 13**, both the validation and training losses decline steadily with increasing epochs and approach their minima near the 300th epoch.

For a CNN classifier, assessment relies on a confusion matrix. This matrix records the model's predictions as True Positive (TP), False Positive (FP), True Negative (TN), and False Negative (FN). The confusion matrix supports the calculation of several metrics, such as Accuracy, Precision, Recall, and F1-Score, to assess overall model quality.

For any given class, accuracy equals the ratio of correctly predicted cases to total cases. It follows **Eq. 6**.

$$Accuracy = \frac{TP+TN}{TP+TN+FP+FN} \quad (6)$$

Precision equals the ratio of correctly predicted positive cases to all predicted positive cases. It follows **Eq. 7**.

$$Precision = \frac{TP}{TP+FP} \quad (7)$$

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For a specific class, recall equals the ratio of correctly predicted positive cases to the total number of actual positive cases. It follows **Eq. 8**.

$$Recall = \frac{TP}{TP+FN} \quad (8)$$

The F1-Score is the balanced average of recall and precision, taking into account both FP and FN. It follows **Eq. 9**.

$$F1 = 2 \times \left(\frac{Precision \times Recall}{Precision + Recall} \right) \quad (9)$$

The confusion matrix for spinach leaf disease prediction on the validation set is shown in **Figure 14**. Predicted and actual classes link to their target labels in **Table 3**.

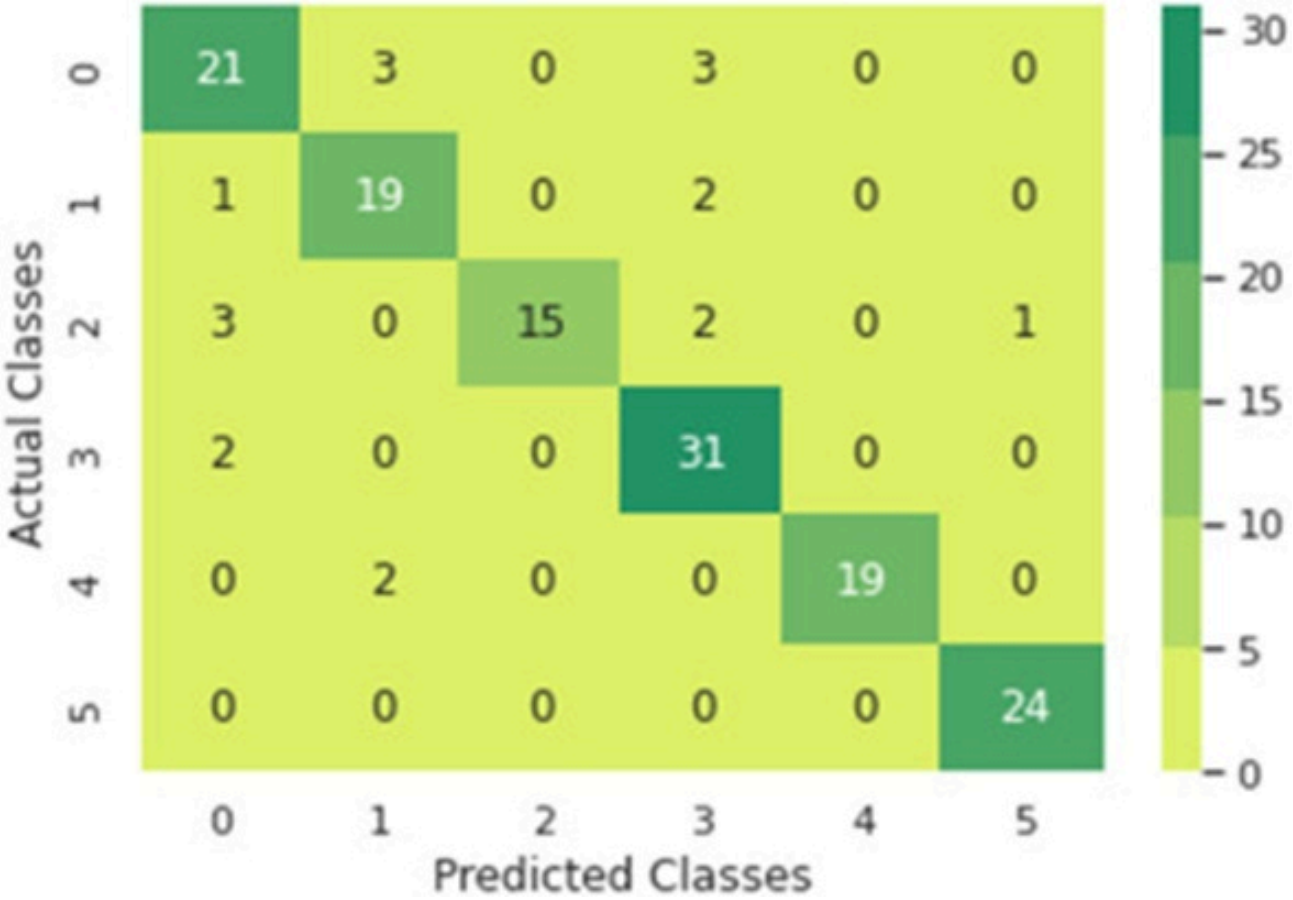

Figure 14. Confusion Matrix of “SFDNet” model on validation set.

Table 3. Distribution of image data into training and validation sets.

Disease name	Total images	For the training set	For the test set	Target label
Anthracnose	130	103	27	0

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Cercospora Leaf Spot	130	108	22	1
Cladosporium Leaf Spots	100	79	21	2
Downy Mildew	140	107	33	3
Healthy	140	119	21	4
Stemphylium Leaf Spot	110	86	24	5

The classification report for our model “SFDNet” on the validation set is shown in **Figure 15**. It lists evaluation metric values for each disease category. Results show that the average accuracy of the CNN model in the proposed system is 89.86%, while the average F1-score, recall, and precision are 0.90 each.

	precision	recall	f1-score	support
anthracnose	0.82	0.85	0.84	27
cercospora_leaf_spot	0.87	0.91	0.89	22
cladosporium_leaf_spot	0.83	0.95	0.89	21
downy_mildew	0.91	0.88	0.89	33
healthy	1.00	0.86	0.92	21
stemphylium_leaf_spot	1.00	0.96	0.98	24
accuracy			0.90	148
macro avg	0.91	0.90	0.90	148
weighted avg	0.90	0.90	0.90	148

Figure 15. Classification Report of “SFDNet” model on Validation Set.

Conclusion

To summarize, this paper introduces an original deep learning method for detecting major fungal diseases on spinach leaves. The suggested system applies a Convolutional Neural Network (CNN) model trained and tested on a collection of spinach leaf disease images gathered from multiple web sources. The CNN model achieves 89.86% accuracy on the validation set, demonstrating its ability to classify spinach leaf diseases correctly.

To overcome limited data, image augmentation methods, along with Dropout layers and Batch Normalization, were used to prevent overfitting during training. This approach promotes strong performance on new spinach leaf images.

Moreover, the CNN model integrates smoothly into the Spinach Disease Classification and Cure Recommendation System built with PySide2. This connection allows spinach growers to quickly identify specific fungi-caused diseases on spinach leaves and receive appropriate treatments.

By delivering a practical, approachable solution for disease detection in spinach farming, the system offers notable benefits to agriculture. It gives growers a simple tool for fast disease recognition, supporting quick responses that limit infection spread and reduce financial damage. The proposed system shows promising results for detecting key fungi-related diseases in spinach leaves. It adds a useful resource to agriculture by strengthening disease control methods and promoting lasting spinach production. Future studies could expand the dataset, add more disease types, and test additional deep learning architectures to improve accuracy and usefulness.

Future efforts offer multiple opportunities to refine and broaden the suggested spinach disease detection and cure recommendation system. These directions can further strengthen the accuracy, features, and real-world value of the software tool.

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First, increasing the dataset size is a key step to boosting the trained model's ability to generalize and remain stable. Gathering a larger, more varied set of spinach leaf images that cover additional disease types and examples would enable the model to identify a wider range of conditions correctly. Working with farming research centers, growers, and web services could help build a complete dataset.

Second, testing other deep learning architectures and designs could reveal alternative approaches to disease grouping. Although the Convolutional Neural Network (CNN) model in this work achieved solid accuracy, alternatives such as ResNet, Inception, or EfficientNet might yield superior results. Testing and comparing various models would help select the best structure for spinach disease grouping.

Third, adding instant disease-spotting and tracking features could increase the software tool's usefulness. Using computer vision methods and integrating with cameras or drones would enable the system to provide growers with immediate alerts on disease outbreaks and support ongoing observation of spinach fields. Live information would allow faster responses and better control over infection spread.

In addition, adding location and weather information to the disease-spotting system could improve diagnostic precision. Factoring in area-specific conditions, such as temperature, humidity, and rainfall, would allow the model to adjust forecasts based on common diseases in that area. This tailored approach could improve disease recognition and guide appropriate treatments.

Also, adding user input and interactions could support ongoing refinement of the system. Letting growers share comments on disease groupings and treatments would help sharpen the model and gradually improve its results. User comments could highlight practical issues, guiding the creation of specific fixes.

Finally, building ties with farming groups, government agencies, or online shopping sites could widen the software tool's influence and availability. Such links could help integrate the system with existing farming tools, making it easier for more growers to reach. Linking with shopping platforms would provide direct access to trusted products and simplify obtaining recommended treatments.

Overall, continued development of the spinach disease detection and cure recommendation system should focus on expanding the dataset, testing other deep learning architectures, adding live tracking, including location and weather data, incorporating user input, and forming alliances to broaden use. Tackling these points will help the software tool advance and deliver strong assistance to growers fighting fungal diseases in spinach farming.

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Conflict of interest

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Ethics statement

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