

Crop Disease Detection using Deep Learning on Agricultural Images

Sourav Kumar Behera
Student
Lovely Professional University
Jalandhar, India
souravbeherahs@gmail.com

Dr. Soni Singh
Professor
Lovely Professional University
Jalandhar, India

Abstract—In the realm of agriculture, timely and accurate prediction of crop diseases is crucial. This study explores the application of deep learning techniques for image-based crop disease prediction. Utilizing a comprehensive dataset of crop images, a deep learning model was trained to identify various diseases. The model's architecture and training process are meticulously designed to handle the complexity and variability of the data. Preliminary results indicate a high accuracy rate in disease prediction, demonstrating the potential of deep learning in revolutionizing disease management in agriculture. This research not only contributes to the existing body of knowledge but also opens new avenues for future work in the integration of artificial intelligence in agriculture.

I. INTRODUCTION

In the rapidly evolving field of agriculture, the ability to predict and manage crop diseases effectively is of paramount importance. Crop diseases can significantly impact yield, affecting not only the livelihoods of farmers but also the global food supply. Traditional methods of disease detection, often based on visual inspection and expert knowledge, are labor-intensive and may not always be accurate or timely.

In recent years, the advent of artificial intelligence (AI) and, more specifically, deep learning, has opened up new possibilities for tackling this challenge. Deep learning, a subset of machine learning, has shown remarkable success in image recognition tasks, making it a promising tool for image-based crop disease prediction. By training a model on a dataset of crop images, each labeled with the corresponding disease, we can enable the model to learn the visual patterns associated with each disease and predict the disease present in new, unseen images.

This study aims to explore the potential of deep learning for crop disease prediction. We leverage a comprehensive dataset of crop images, encompassing a wide variety of crops and diseases. A deep learning model is trained on this dataset, with the architecture and training process carefully designed to handle the complexity and variability of the data.

The goal of this research is not only to develop a model that can accurately predict crop diseases but also to contribute to the broader understanding of how deep learning can be applied in agriculture. By demonstrating the feasibility and effectiveness of a deep learning approach for crop disease prediction, we hope to inspire further research and application of AI in

agriculture, paving the way for smarter, more efficient disease management and ultimately, more sustainable agriculture.

II. LITERATURE REVIEW

The application of deep learning techniques in the prediction and detection of crop diseases has been a subject of extensive research in recent years. This literature review aims to provide an overview of the existing studies in this field.

A. Machine Learning for Detection and Prediction of Crop Diseases and Pests: A Comprehensive Survey

A comprehensive survey by Domingues et al. provides an overview of machine learning techniques used in the agricultural sector, focusing on the tasks of classification, detection, and prediction of diseases and pests¹. The study emphasizes the need for efficient methods for the automatic detection, identification, and prediction of pests and diseases in agricultural crops¹. The paper presents a literature review on machine learning techniques used in the agricultural sector, focusing on the tasks of classification, detection, and prediction of diseases and pests, with an emphasis on tomato crops

B. A deep learning model for predicting risks of crop pests and diseases from sequential environmental data

Lee and Yun proposed a deep learning model that predicts diseases through previous growth environment information of crops, including air temperature, relative humidity, dew point, and CO₂ concentration². Their model showed high predictive performance with an average AUROC of 0.9172. The authors propose a model that predicts diseases through previous growth environment information of crops, using deep learning techniques.

C. Identification of Gaps in Current Research

While deep learning has shown promise in the field of crop disease prediction, there are several gaps in the current research that this study aims to address:

- **Limited Focus on Emerging Deep Learning Algorithms:** Most studies have concentrated on traditional machine learning algorithms and convolutional neural networks (CNNs). There has been a noticeable dearth of focus on emerging deep learning algorithms like capsule neural networks and vision transformers.

- Lack of Comprehensive Datasets: Several datasets employed for training and evaluating deep learning models have been tailored to suit specific crop types. There is a pressing need for a comprehensive and expansive image dataset encompassing a wider array of crop varieties
- Need for Unified Framework: The majority of research endeavors have concentrated on individual plant diseases, machine learning, or deep learning algorithms. There is a need for the development of a unified framework that harnesses an ensemble of machine learning and deep learning algorithms to address the complexities of multiple plant diseases effectively
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III. METHODOLOGY

A. Data Collection and Preprocessing

The dataset used in this study is the "New Plant Diseases Dataset". This dataset is a recreation, using offline augmentation, from an original dataset available on kaggle. It consists of 87,000 RGB images of both healthy and diseased crop leaves. These images are categorized into 38 different classes, representing a variety of crop diseases.

The dataset is divided into a training set and a validation set, following an 80/20 split ratio. This division ensures that the model has a substantial amount of data for learning (training set) and a separate, unseen dataset for validating the model's performance (validation set). The directory structure is preserved in this division, maintaining the organization of the data.

In addition to the training and validation sets, a new directory containing 33 test images was created for prediction purposes. These images serve as a completely independent set for evaluating the final model's performance.

The preprocessing of the data involved resizing the images to ensure uniformity. This is a crucial step as it allows the model to focus on the important features in each image, regardless of the original size of the image. The color mode was set to RGB, preserving the color information in the images, which can be a significant factor in identifying diseases.

This comprehensive and diverse dataset, along with the careful preprocessing, provides a strong foundation for training the deep learning model for crop disease prediction. The use of separate training, validation, and test sets also ensures a robust evaluation of the model's performance.

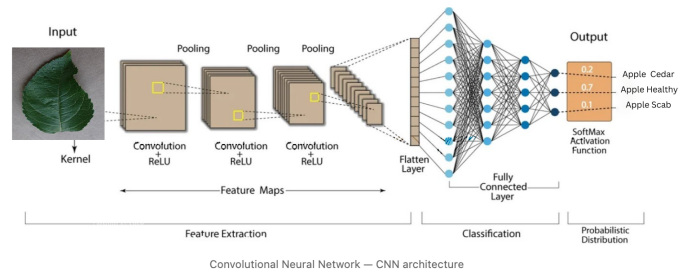
B. Model Architecture

- Convolutional Layers: The model begins with a series of convolutional layers. Each convolutional layer applies a set of filters to the input, allowing the model to automatically learn features from the images. The number of filters in these layers ranges from 32 to 512, increasing the complexity of the learned features at each level.
- Max Pooling Layers: After each pair of convolutional layers, a max pooling layer is applied. These layers reduce the spatial dimensions of the input, making the

model more computationally efficient and allowing it to learn more complex features.

- Dropout Layers: Dropout layers are used after some of the convolutional layers. These layers randomly set a fraction of the input units to 0 during training, which helps prevent overfitting.
- Flatten Layer: After the final max pooling layer, a flatten layer is used to convert the 2D feature maps to a 1D vector. This is necessary for connecting the convolutional layers to the dense layers.
- Dense Layers: The model includes two dense layers at the end. The first dense layer has 1500 units and uses the ReLU activation function. The second dense layer is the output layer and has 38 units, corresponding to the 38 different classes in the dataset. The activation function for the output layer is softmax function for this multi-class classification problem.
- Model Compilation: The model is compiled with the Adam optimizer and a learning rate of 0.0001. The loss function is categorical cross-entropy, which is suitable for multi-class classification problems.

This architecture is quite complex and includes multiple layers of different types, allowing the model to learn a hierarchy of features from the images. The use of dropout also helps to prevent overfitting, making the model more robust. The model's architecture is a critical factor in its ability to accurately predict crop diseases from images.



C. Model Training

- Optimizer: The optimizer used for this model is Adam. Adam, short for Adaptive Moment Estimation, is a popular choice for deep learning applications. It combines the advantages of two other extensions of stochastic gradient descent: AdaGrad and RMSProp. Adam computes adaptive learning rates for different parameters, which makes it suitable for problems with large and sparse datasets.
- Learning Rate: The learning rate for the Adam optimizer was set to 0.0001. The learning rate controls how much to update the model in response to the estimated error each time the model weights are updated. Choosing the learning rate is challenging as a value too small may result in a long training process that could get stuck, whereas a value too large may result in learning a sub-optimal set of weights too fast or an unstable training process.

- **Loss Function:** The loss function used in this model is categorical cross-entropy. This is a popular loss function for multi-class classification problems. Cross-entropy loss measures the performance of a classification model whose output is a probability value between 0 and 1. It increases as the predicted probability diverges from the actual label.
- **Number of Training Epochs:** The model was trained for 10 epochs. An epoch is one complete pass through the entire training dataset. The number of epochs is a hyperparameter that defines the number of times the learning algorithm will work through the entire training dataset. Training a model for too many epochs can lead to overfitting, so this number should be chosen carefully.
- **Validation During Training:** A separate validation set was used during training. This is a common practice in machine learning to prevent overfitting and to monitor the model's performance on unseen data during the training process. The validation set is a subset of the training data and is used to provide an unbiased evaluation of the model fit on the training dataset while tuning model hyperparameters.

The model was trained using the fit method, which is a standard method for training models in TensorFlow. The training process was monitored for accuracy and loss on both the training and validation sets. The model's weights were updated after each batch of 32 images.

D. Model Evaluation

- **Evaluation Metrics**

1) *Accuracy: This is the proportion of true results (both true positives and true negatives) among the total number of cases examined. It is a measure of how well the model correctly identifies both positive and negative outcomes.:*

2) *Precision: Precision is the proportion of true positives out of all positive results predicted by the classifier. It is a measure of the accuracy of the model when it predicts a positive result.:*

3) *Recall: Recall, also known as sensitivity, is the proportion of true positives out of the actual positive cases. It is a measure of the model's ability to find all the positive cases.:*

	precision	recall	f1-score	support
Apple___Apple_scab	0.97	0.95	0.96	504
Apple___Black_rot	0.98	0.98	0.98	497
Apple___Cedar_apple_rust	0.90	1.00	0.95	440
Apple___Apple_healthy	0.96	0.87	0.92	502
Blueberry___healthy	0.99	0.95	0.97	454
Cherry_(including_sour)___Powdery_mildew	0.91	1.00	0.95	421
Cherry_(including_sour)___healthy	0.96	0.99	0.97	456
Corn_(maize)___Cercospora_leaf_spot_Gray_leaf_spot	0.88	0.96	0.91	410
Corn_(maize)___Common_rust_	0.99	0.99	0.99	477
Corn_(maize)___Northern_Leaf_Blight	0.97	0.91	0.94	477
Corn_(maize)___healthy	1.00	1.00	1.00	465
Grape___Black_rot	0.99	0.99	0.99	472
Grape___Esca_(Black_Measles)	0.99	0.99	0.99	480
Grape___Leaf_blight_(Isariopsis_Leaf_Spot)	1.00	1.00	1.00	430
Grape___healthy	1.00	1.00	1.00	423
Orange___Haunglongbing_(Citrus_greening)	0.95	0.98	0.97	503
Peach___Bacterial_spot	0.98	0.93	0.95	459
Peach___healthy	0.95	0.99	0.97	432
Pepper,_bell___Bacterial_spot	0.95	0.96	0.96	478
Pepper,_bell___healthy	0.98	0.92	0.95	497
Potato___Early_blight	0.96	0.99	0.98	485
Potato___Late_blight	0.91	0.98	0.94	485
Potato___healthy	0.93	0.93	0.93	456
Raspberry___healthy	0.99	0.97	0.98	445
Soybean___healthy	0.97	0.97	0.97	505
Squash___Powdery_mildew	0.99	0.95	0.97	434
Strawberry___Leaf_scorch	0.99	0.96	0.97	444
Strawberry___healthy	1.00	0.99	0.99	456
Tomato___Bacterial_spot	0.93	0.99	0.96	425
Tomato___Early_blight	0.91	0.89	0.90	480
Tomato___Late_blight	0.91	0.92	0.92	463
Tomato___Leaf_Mold	0.90	0.99	0.94	470
Tomato___Septoria_leaf_spot	0.99	0.71	0.83	436
Tomato___Spider_mites_Two-spotted_spider_mite	0.91	0.96	0.94	435
Tomato___Target_Spot	0.90	0.88	0.89	457
Tomato___Tomato_Yellow_Leaf_Curl_Virus	0.99	0.98	0.98	490
Tomato___Tomato_mosaic_virus	0.98	0.99	0.98	448
Tomato___healthy	0.95	1.00	0.97	481
accuracy			0.96	17572
macro avg	0.96	0.96	0.96	17572
weighted avg	0.96	0.96	0.96	17572

Fig. 1. Precision Recall Fscore

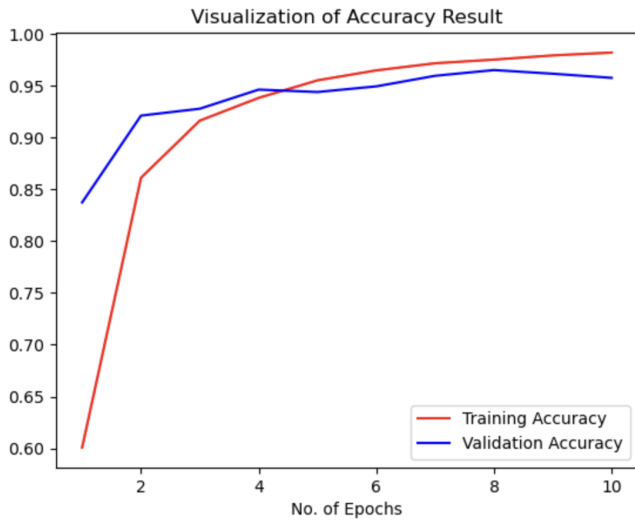
4) *F1-Score: The F1-score is the harmonic mean of precision and recall. It provides a single score that balances both the concerns of precision and recall in one number.:*

- **Interpretation of Results**

The results from the classification report were interpreted to understand the model's performance on each class. High precision, recall, and F1-score indicate that the model is performing well on that particular class. Any class with a low score in these metrics would require further investigation to understand why the model is not performing well.

- **Performance Discussion**

The model's performance on both the training and validation sets was discussed. The model achieved a training accuracy of approximately 98.54 percent and a validation accuracy of approximately 95.74 percent . While these are impressive results, the slight difference between the training and validation accuracy could be a sign of overfitting. This means that the model might not generalize well to unseen data. To prevent overfitting, dropout layers were used in the model architecture. These layers randomly set a fraction of the input units to 0 during training, which helps prevent overfitting. Further measures to prevent overfitting could include techniques like data augmentation, further dropout, or regularization.



E. Results

1) *Results Presentation:* The model was evaluated on a test set of images, separate from the training and validation sets. The final accuracy of the model on the test set was approximately 96 percent. This high accuracy indicates that the model was able to correctly predict the disease class for most of the images in the test set.

A classification report was also generated for the test set. This report provides detailed performance metrics for each class, including precision, recall, and F1-score. These metrics provide a more granular view of the model's performance, showing how well it performs for each individual class.

2) *Performance Insights:* The model's performance varied across different classes. For most classes, the model achieved high precision, recall, and F1-scores, indicating that it was able to accurately identify these diseases. For instance, the model achieved an F1-score of 0.98 for TomatoTomatomosaicvirus and 0.97 for Tomatohealthy. However, there were a few classes where the model's performance could be improved. For example, the F1-score for TomatoSeptorialeafspot was relatively low compared to other classes. This could be due to a variety of factors such as class imbalance, lack of representative samples in the training data, or the model architecture itself.

These results provide valuable insights into the model's strengths and weaknesses. They highlight the potential of deep learning for crop disease prediction, while also pointing to areas where further research and model refinement could lead to improvements. The high overall accuracy demonstrates the feasibility of using deep learning for this task, and the per-class metrics provide direction for future work to improve the model's performance.

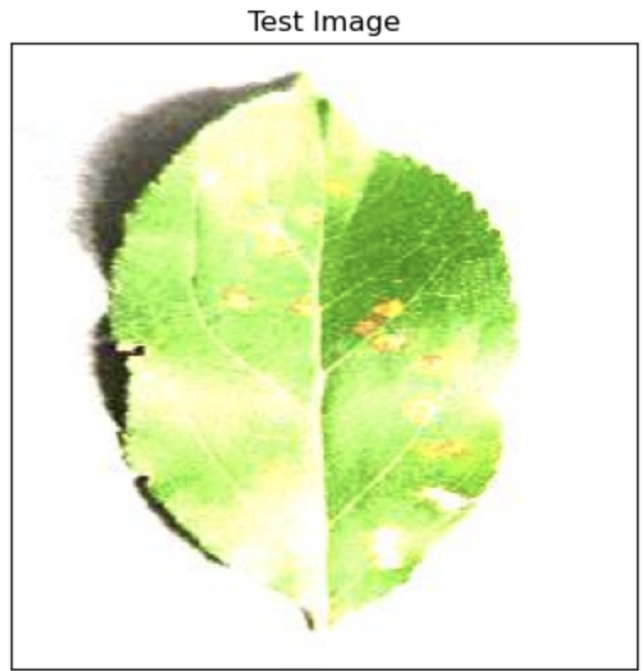


Fig. 2. Test Image

Disease Name: Apple__Cedar_apple_rust

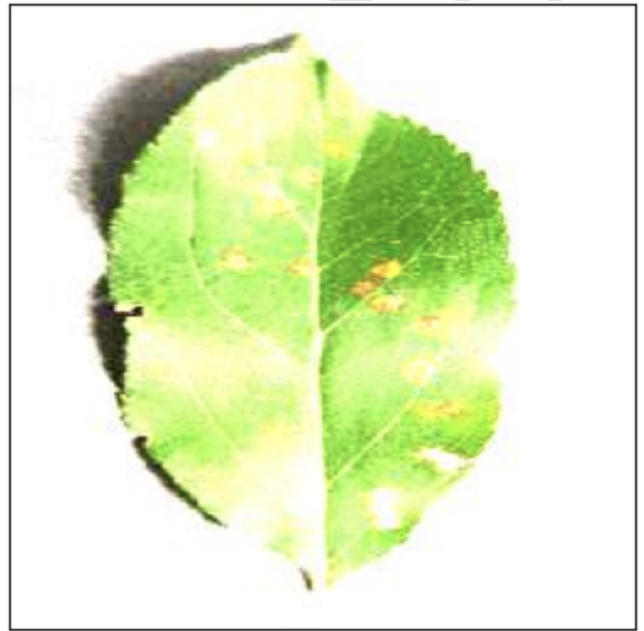


Fig. 3. Predicted Image

IV. LIMITATIONS

- **Limited Dataset:** The dataset used in this study, although diverse and comprehensive, is limited to certain types of crops and diseases. This may limit the model's ability to generalize to other types of crops and diseases not included in the dataset.

- **Image Quality and Variability:** The performance of the model is dependent on the quality and variability of the images in the dataset. Factors such as lighting conditions, camera quality, and angle of capture can affect the model's performance. The model might not perform as well on images that are significantly different from those in the training dataset.
- **Overfitting:** Despite the use of dropout layers and other measures to prevent overfitting, the model may still overfit the training data, reducing its ability to generalize to unseen data.

V. FUTURE SCOPE

This research has demonstrated the potential of deep learning for crop disease prediction, and there is much scope for further exploration and improvement in this field. The advancements in this area could have significant implications for agriculture, contributing to more sustainable and productive farming practices.

- **Expanding the Dataset:** While the current dataset is diverse and comprehensive, expanding it to include more varieties of crops and diseases could improve the model's generalizability. This could involve collecting images under different environmental conditions and from different geographical locations.
- **Exploring Other Model Architectures:** While the Convolutional Neural Network (CNN) used in this study has shown promising results, exploring other model architectures could lead to further improvements. This could include other types of deep learning models, such as Recurrent Neural Networks (RNNs) for sequential data, or newer architectures like Transformers.
- **Real-time Disease Prediction:** An exciting direction for future work could be the development of a real-time disease prediction system. This could involve deploying the trained model on a mobile app, which farmers could use to detect crop diseases in real-time.
- **Integration with Other Data Types:** While this study focused on image data, crop disease prediction could potentially benefit from other types of data, such as weather data or soil quality data. Future work could explore the integration of these data types into the prediction model.

VI. CONCLUSION

This research paper presented a comprehensive study on the application of deep learning, specifically Convolutional Neural Networks (CNNs), for the prediction of crop diseases using image data. The study leveraged a diverse dataset of approximately 87,000 RGB images of healthy and diseased crop leaves, categorized into 38 different classes.

The developed model demonstrated impressive performance with an overall accuracy of approximately 96 percent on the test set. The model's architecture, which included multiple convolutional layers, max pooling layers, and dropout layers, proved effective in learning complex features from the images and preventing overfitting.

However, the study also identified areas for potential improvement. While the model performed well on most classes, there were a few classes where performance could be enhanced. This suggests the need for further research and refinement of the model, possibly through techniques such as data augmentation, further dropout, or regularization.

The results of this study underscore the potential of deep learning in revolutionizing disease management in agriculture. By accurately predicting crop diseases, such models can enable timely and effective interventions, potentially saving a significant proportion of the crops that would otherwise be lost to diseases.

This research contributes to the growing body of literature on the application of deep learning in agriculture. It demonstrates the feasibility and effectiveness of using CNNs for crop disease prediction, paving the way for future research in this area and the development of practical tools for farmers and agricultural researchers. With further refinement and testing, the model developed in this study has the potential to become a valuable tool in modern agriculture, contributing to more sustainable and productive farming practices.

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I would also like to extend my appreciation to the editors and reviewers for their valuable comments and suggestions, which have significantly enhanced the quality of this review paper. Their feedback has helped us refine our ideas and present a more coherent and structured overview of the subject matter.

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