Plant Disease Classification Using Deep Learning: Technical Report

Hosted Demo: https://plant-disease-prediction-516848219617.asia-south1.run.app

Github Link: https://github.com/DerickDavies/plant-disease-prediction-keras

Abstract

This report presents the development and implementation of a deep learning model for plant disease classification using a convolutional neural network (CNN) architecture. The model achieves 98.51% accuracy on the training set and 95.99% accuracy on the validation set, demonstrating its effectiveness in identifying 38 different classes of plant diseases.

1. Introduction

Plant diseases can significantly impact agricultural yield and food security. Early detection and classification of plant diseases using machine learning techniques can help in timely intervention and crop protection. This project implements a deep learning solution using TensorFlow to classify plant diseases from images.

2. Dataset

Link to dataset used: https://www.kaggle.com/datasets/vipoooool/new-plant-diseases-dataset

This dataset is recreated using offline augmentation from the original dataset. This dataset consists of about 87K RGB images of healthy and diseased crop leaves which is categorized into 38 different classes. The total dataset is divided into 80/20 ratio of training and validation set preserving the directory structure. A new directory containing 33 test images is created later for prediction purpose.

2.1 Dataset Overview

- Training samples: 70,295 images
- Validation samples: 17,572 images
- Number of classes: 38
- Image specifications: RGB, resized to 128x128 pixels

38 classes defined are as follows:

No.	Plant Species	Disease/Condition
1	Apple	Apple Scab
2	Apple	Black Rot
3	Apple	Cedar Apple Rust
4	Apple	Healthy
5	Blueberry	Healthy
6	Cherry	Powdery Mildew
7	Cherry	Healthy
8	Corn (Maize)	Cercospora Leaf Spot/Gray Leaf Spot
9	Corn (Maize)	Common Rust
10	Corn (Maize)	Northern Leaf Blight
11	Corn (Maize)	Healthy
12	Grape	Black Rot
13	Grape	Esca (Black Measles)
14	Grape	Leaf Blight (Isariopsis Leaf Spot)
15	Grape	Healthy
16	Orange	Haunglongbing (Citrus Greening)
17	Peach	Bacterial Spot
18	Peach	Healthy
19	Pepper (Bell)	Bacterial Spot
20	Pepper (Bell)	Healthy
21	Potato	Early Blight
22	Potato	Late Blight
23	Potato	Healthy
24	Raspberry	Healthy
25	Soybean	Healthy
26	Squash	Powdery Mildew
27	Strawberry	Leaf Scorch
28	Strawberry	Healthy
29	Tomato	Bacterial Spot

30	Tomato	Early Blight
31	Tomato	Late Blight
32	Tomato	Leaf Mold
33	Tomato	Septoria Leaf Spot
34	Tomato	Spider Mites/Two-spotted Spider Mite
35	Tomato	Target Spot
36	Tomato	Yellow Leaf Curl Virus
37	Tomato	Mosaic Virus
38	Tomato	Healthy

2.2 Data Preprocessing

- Standardized image dimensions: 128 x 128 pixels
- Color mode: RGB (3 channels)
- Training and validation Images loaded using with the following parameters:
    - batch_size = 32 (optimal for memory management)
    - shuffle = True (prevents learning order-based patterns)
    - interpolation = "bilinear" (good balance of quality and speed)

3. Model Architecture

The implemented CNN architecture consists of multiple convolutional blocks with increasing filter sizes:

Layer (type)	Output Shape	Parameters
conv2d (Conv2D)	(None, 128, 128, 32)	896
conv2d_1 (Conv2D)	(None, 126, 126, 32)	9,248
max_pooling2d (MaxPooling2D)	(None, 63, 63, 32)	0
conv2d_2 (Conv2D)	(None, 63, 63, 64)	18,496
conv2d_3 (Conv2D)	(None, 61, 61, 64)	36,928
max_pooling2d_1 (MaxPooling2D)	(None, 30, 30, 64)	0
conv2d_4 (Conv2D)	(None, 30, 30, 128)	73,856
conv2d_5 (Conv2D)	(None, 28, 28, 128)	147,584

max_pooling2d_2 (MaxPooling2D)	(None, 14, 14, 128)	0
conv2d_6 (Conv2D)	(None, 14, 14, 256)	295,168
conv2d_7 (Conv2D)	(None, 12, 12, 256)	590,080
max_pooling2d_3 (MaxPooling2D)	(None, 6, 6, 256)	0
conv2d_8 (Conv2D)	(None, 6, 6, 512)	1,180,160
conv2d_9 (Conv2D)	(None, 4, 4, 512)	2,359,808
max_pooling2d_4 (MaxPooling2D)	(None, 2, 2, 512)	0
dropout (Dropout)	(None, 2, 2, 512)	0
flatten (Flatten)	(None, 2048)	0
dense (Dense)	(None, 1500)	3,073,500
dropout_1 (Dropout)	(None, 1500)	0
dense_1 (Dense)	(None, 38)	57,038

Model Summary Statistics:

- Total parameters: 7,842,762 (29.92 MB)
- Trainable parameters: 7,842,762 (29.92 MB)
- Non-trainable parameters: 0 (0.00 B)

1. Input Layer: 128x128x3
2. Convolutional Blocks:
   - Block 1: Two Conv2D layers (32 filters) + MaxPooling
   - Block 2: Two Conv2D layers (64 filters) + MaxPooling
   - Block 3: Two Conv2D layers (128 filters) + MaxPooling
   - Block 4: Two Conv2D layers (256 filters) + MaxPooling
   - Block 5: Two Conv2D layers (512 filters) + MaxPooling
3. Regularization: Dropout (0.25)
4. Flatten Layer
5. Dense Layer: 1500 units with **ReLU** activation
6. Dropout Layer (0.4)
7. Output Layer: 38 units with **Softmax** activation

3.1 Model Configuration

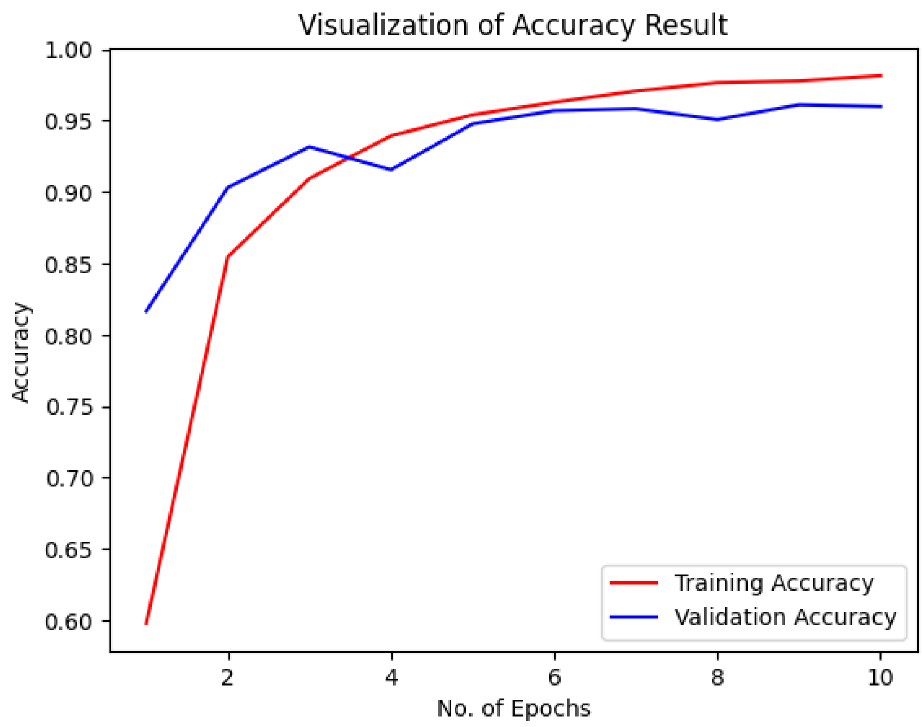
- Optimizer Used: Adam (learning rate = 0.0001 – Set low so as to prevent the overshooting of loss function)
- Loss function used: Categorical Cross-entropy
- Metrics: Accuracy
- Training epochs: 10

4. Results and Analysis

4.1 Model Performance

Particular	Performance
Training Accuracy	98.51%
Training Loss	0.0445
Validation Accuracy	95.99%
Validation Loss	0.1447

Accuracy Visualization:



Model evaluation using Precision, Recall, F1-Score and Support:

Class	Precision	Recall	F1-Score	Support
Apple___Apple_scab	0.96	0.92	0.94	504
Apple___Black_rot	0.93	1.00	0.96	497
Apple___Cedar_apple_rust	0.98	0.95	0.96	440
Apple___healthy	0.97	0.94	0.95	502
Blueberry___healthy	0.93	0.98	0.96	454
Cherry_(including_sour)___Powdery_mildew	0.95	0.98	0.97	421
Cherry_(including_sour)___healthy	0.96	0.99	0.97	456
Corn_(maize)___Cercospora_leaf_spot Gray_leaf_spot	0.87	0.96	0.91	410
Corn_(maize)___Common_rust_	0.99	0.99	0.99	477
Corn_(maize)___Northern_Leaf_Blight	0.97	0.89	0.93	477
Corn_(maize)___healthy	0.99	1.00	0.99	465
Grape___Black_rot	0.98	0.98	0.98	472
Grape___Esca_(Black_Measles)	0.99	0.99	0.99	480
Grape___Leaf_blight_(Isariopsis_Leaf_Spot)	0.98	1.00	0.99	430
Grape___healthy	0.97	0.99	0.98	423
Orange___Haunglongbing_(Citrus_greening)	0.99	0.98	0.98	503
Peach___Bacterial_spot	0.93	0.97	0.95	459
Peach___healthy	0.96	0.99	0.97	432
Pepper,_bell___Bacterial_spot	0.89	0.99	0.94	478
Pepper,_bell___healthy	0.94	0.96	0.95	497
Potato___Early_blight	0.96	0.99	0.97	485
Potato___Late_blight	0.98	0.94	0.96	485
Potato___healthy	0.96	0.95	0.96	456
Raspberry___healthy	1.00	0.98	0.99	445
Soybean___healthy	0.99	0.96	0.98	505

Squash___Powdery_mildew	0.99	0.98	0.98	434
Strawberry___Leaf_scorch	0.97	0.98	0.98	444
Strawberry___healthy	0.98	0.99	0.99	456
Tomato___Bacterial_spot	0.98	0.96	0.97	425
Tomato___Early_blight	0.93	0.89	0.91	480
Tomato___Late_blight	0.92	0.93	0.92	463
Tomato___Leaf_Mold	0.97	0.94	0.95	470
Tomato___Septoria_leaf_spot	0.96	0.84	0.90	436
Tomato___Spider_mites Two-spotted_spider_mite	0.97	0.94	0.95	435
Tomato___Target_Spot	0.88	0.89	0.88	457
Tomato___Tomato_Yellow_Leaf_Curl_Virus	0.98	0.99	0.99	490
Tomato___Tomato_mosaic_virus	0.97	1.00	0.98	448
Tomato___healthy	1.00	0.89	0.94	481
Accuracy	-	-	0.96	17572
Macro Avg	0.96	0.96	0.96	17572
Weighted Avg	0.96	0.96	0.96	17572

4.2 Training Dynamics

- The model showed consistent improvement across training epochs with minimal signs of overfitting, demonstrated by:
    - Small gap between training and validation accuracy
    - Stable learning curve
    - Effective dropout regularization (0.25 and 0.4)

4.3 Model Evaluation

- The model demonstrates robust performance across classes, as evidenced by:
    - High precision and recall scores across categories
    - Strong performance on the validation set
    - Effective generalization with minimal overfitting

5. Technical Implementation Details

- Framework: TensorFlow
- Key Libraries:
    - tensorflow
    - matplotlib
    - pandas
    - seaborn
    - scikit-learn

6. Conclusions

The implemented CNN model demonstrates strong performance in plant disease classification, achieving high accuracy on both training and validation sets. The model's architecture, with its multiple convolutional layers and dropout regularization, effectively captures the relevant features for disease classification while preventing overfitting.