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Generalising Across Different Crop Diseases With InceptionCNN

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Abstract: This Plant diseases have a significant impact on the agriculture of the world and lead to decreased crop productivity, food quality, and economic productivity as a result. Following is an automated pathogen detection system for plant diseases using an Inception-type convolutional neural network (InceptionCNN) in PyTorch. The model was trained on an original Kaggle-based New Plant Dataset containing 38 classes of healthy and diseased plant leaf images. We performed the appropriate preprocessing (duplicate deletion, stratified data splitting, normalization, and augmentations) to improve generalization and robustness of our models. We offer a multi-scale architecture of multi-scale convolutional branches utilizing 1×1, 3×3, and 5×5 filters among others to select a collection of lesion patterns and disease structures. Adam optimization, scheduling of the learning rate, dropout regularization, and class imbalance reduction were utilized as the training method. Experimental results demonstrate optimal performance with 99.24% validation accuracy and minimal validation loss. These evaluation metrics involved measured performance accuracy, recall, F1 score, confusion matrix analysis, and Grad-CAM visualizations which helped enable consistent classification of the disease under the categories. Our proposed framework represents a scalable, accurate and reproducible approach to the intelligent plant disease detection and lays the groundwork to future AI-related precision agriculture applications.

Keywords: Plant disease detection; Convolutional Neural Network; Deep Learning; Precision Agriculture; Plant Protection

I. INTRODUCTION

This document is a template. An electronic copy can be downloaded from the conference website. For questions on paper guidelines, please contact the conference publications committee as indicated on the conference website. Information about final paper submission is available from the conference website. Plant diseases impact global agriculture including decreasing crop production, reduction of food quality, and significant economic losses. Expert interpretation and laboratory checking based manual methods for disease identification are prone to man-error. They are costly, time-consuming, and have limited availability for many farmers. Innovations in image-based classification schemes have made it possible for automated plant disease identification based on computer vision and deep learning techniques to be deployed through the recent breakthroughs in computer vision and deep learning technology as well. In this work, we show the development of an InceptionCNN model in PyTorch over multiclass disease classification for plants. It's applied to a Kaggle database, with 38 classes of healthy & diseased plant leaves. Inception-style convolutional branches: 1×1, 3×3 and 5×5 filters are used to obtain information about multi-scale features and complex disease. We performed the preprocessing of the model such as data augmentation methods, the stratified data splitting method, batch normalization, and dropout to make the model generalizable and avoid overfitting. Among other things, the proposed approach solves the class imbalance, inter-class similarity, light variation and leaf orientation and other problems. Accuracy, confusion matrices, precision and recall were used in order to evaluate performance. Results from experimental study revealed high classification ability and good learning performance of features. Accordingly, this study offers a reproducible deep learning model for plant disease detection and brings practical implications to future agricultural applications.

II. LITERATURE REVIEW

Nowadays, in light of the emergence of substantial labeled image datasets as well as deep learning approaches in automation, plant disease diagnosis works wonders. Studies conducted early on have proven that deep convolutional neural networks (CNNs) have been excellent for image-based plant disease diagnosis. Hughes and Salathé published a representative image dataset of plant diseases used by the agriculture industry, which further supports the search for AI supervised classification of various crops and diseases [1]. Mohanty et al. demonstrated greater accuracy of transfer learning using pretrained CNN models than traditional image processing methodologies [2]. Further studies highlighted the importance of appropriate evaluation processes, higher quality of data, and augmentation approaches for reliable disease identification [3]. The Inception architecture used multi-scale convolutional filters (i.e., kernel size = 1×1, 3×3, 5×5) to effectively model different lesion characteristics in this paper [4]. Further work, such as EfficientNet, underlined trade-off between prediction accuracy and computation efficiency when considering small device utilization [5]. They also emphasized augmentation, class imbalance management, and interpretability techniques, e.g., confusion matrices, Grad-CAM, to help enhance robustness and reliability [3], [6]. Recent literature review also shows that multimodal CNN architectures with augmentation and analytical estimation can provide extremely accurate and transferable plant disease classification systems [3], [7].

III. METHODOLOGY

The study is based on a complete New Plant Dataset of 38 healthy and diseased plant leaves of a range of crops sourced from Kaggle database. There were extensive preprocessing operations before training the model to maximise data quality and to validate results. We used perceptual hashing and metadata analysis to create duplicate and quasi duplicates of images. This data was removed or unified among the same datasets, so that no data will leak. A stratified splitting of the data was used to ensure equal class distribution in the training, validating, and test datasets. Train—validation split of 80/20 was utilised, and class frequency analysis was analysed to identify instances of imbalance in class size, which were handled with oversampling and class weight loss functions. Image preprocessing and augmentation methods were also explored to help improve model generalization for realistic environmental analysis. The images were scaled to 224 × 224 pixels and normalized using ImageNet mean and standard deviation. The training augmentations were random crop, horizontal and vertical flip, slight rotation, color jittering, Gaussian blur, random erase and additive noise. These enhancements improved performance in the face of changes in light, angle, occlusion, field-based image dispersion, etc. Deterministic preprocesses for validation and testing were applied to ensure evaluation consistency and validity of validation and testing. We train this model on a small scale Inception style CNN, which is based on a neural network with a high dimensional convolutional neural network written in PyTorch. It begins with low-level feature extraction by a CNN-style stem layer which first relies on convolutional stem, then pooling operations. Model features: Three sequential Inception modules with parallel 1×1, 3×3, and 5×5 convolutional branches, pooling projections. These multi-scale branches enable the simultaneous extraction of fine lesion textures and large-scale disease patterns. Finally, to classify by 38 disease factors, we use adaptive average pooling, dropout regularization and fully connected layer. This has the virtue of reconciling computation efficiency and accuracy of classifications for plant disease detection.

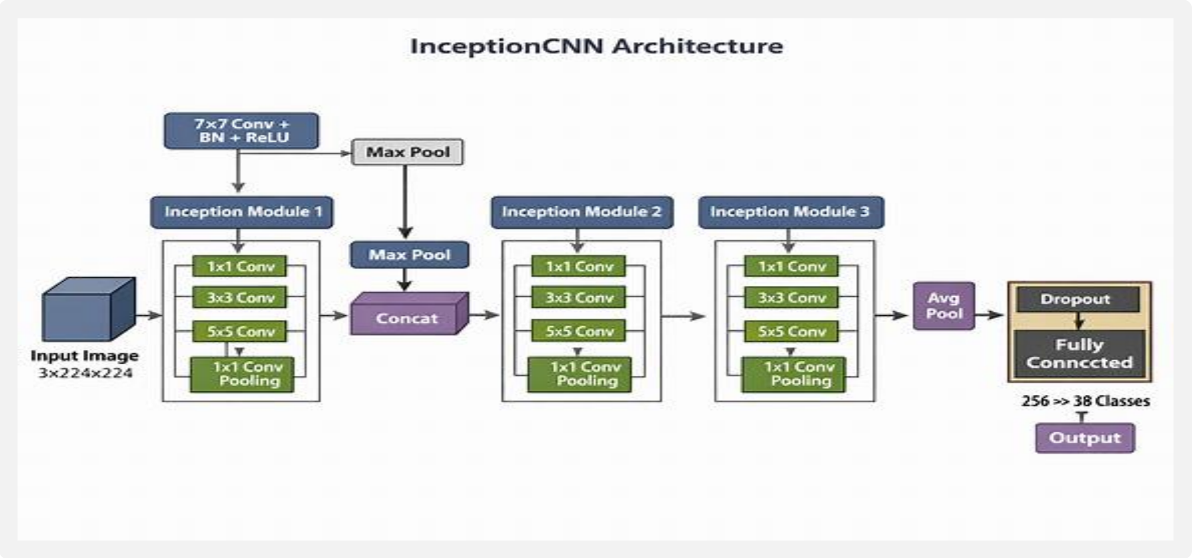

Fig.1 Model Architechture

Algorithm:

1) Load an RGB image of a plant leaf.Load an RGB plant leaf image.
2) Apply Conv2D (7×7, 64 filters)
3) Apply BatchNorm + ReLU
4) Perform MaxPooling
5) Passed features into Inception Module 1

6) Apply MaxPooling
7) Go through Inception Module 2
8) In the 8th module, Pass through Inception Module 3.
9) Use Adaptive Average Pooling (9.14% of the time).
10) Apply Dropout (0.3)
11) Send Features to Fully Connected Layer (256→38)
12) Apply Softmax activation
13) Next, return the predicted disease class.
14) Then return the predicted disease class.

Training was carried out following a transparent and systematic approach to achieve good convergence of the model. Cross-entropy loss was used as the primary loss function and the class imbalance was optimized with inverse frequency class weights and oversampling for the minority classes. The Adam optimiser which had defaults for beta values and an initial learning rate of 1×10^{-3} was set for model optimization. In the transfer learning work, low rates for pre-trained layers were selected and high rates for the freshly initialized classifier layers. Learning rate scheduling methods such as ReduceLROnPlateau and cosine annealing were used, in which the convergence is improved. Batch sizes (as per GPU memory availability) were 32–128, and dropout and L2 weight decay regularization was applied in order to minimize overfitting. All the models were trained for 15 epochs and checkpoint saving was performed according to the maximal validation accuracy. For reproducibility we fixed the random seed in Python, Numpy and PyTorch. Environment configuration files were retained. Moreover, the evaluation process also utilized both overall indexes and performance indices for individual groups of classes. The overall prediction of classification accuracy, precision, recall, F1-score, confusion matrices, ROC curves and AUC were found by calculating top-1 accuracy, precision, recall, F1-score, confusion matrices, ROC curves and AUC. Random seed experiments were then conducted through a sequence of analyses of such as reliability and quality. Calibration metrics, including ECE, were also validated for probability validity. Interpreting techniques such as Grad-CAM, saliency maps, and occlusion sensitivity analysis have been applied to represent essential areas of the lesion and verify the model attention response performance. The misclassified samples were then critically reviewed for evidence of issues ranging from unclear symptoms, label discrepancies and the lack of diversity in training. This was also done by isolating the implementation on dataset, models, training and evaluation files, TensorBoard logging, managing checkpoints and all hardware configurations in the document to provide reproducibility and scalability of the experimental infrastructure.

IV. RESULT

InceptionCNN model training results for plant disease classification demonstrate very powerful learning process which is reflected by rapid convergence rates, very good generalization and almost perfect performance in several classes. The 15 epochs of model evolution, however, strongly indicate a growing trend toward improvement in training and validation metrics to better accuracy and lower loss. In addition, the graphs and confusion matrix reveal the framework to be robust and reliable and the classification report clearly illustrates the uniformity and high accuracy of the architecture against all 38 plant disease types. This early performance has shown us that from the outset, this method appears to offer a promising means of learning features from the data. Both the training loss of 0.9173 and validation loss of 0.3985 are considered significant enough to convince us that, in order for a model to be able to generalize well (by design) it must not be too error-prone.

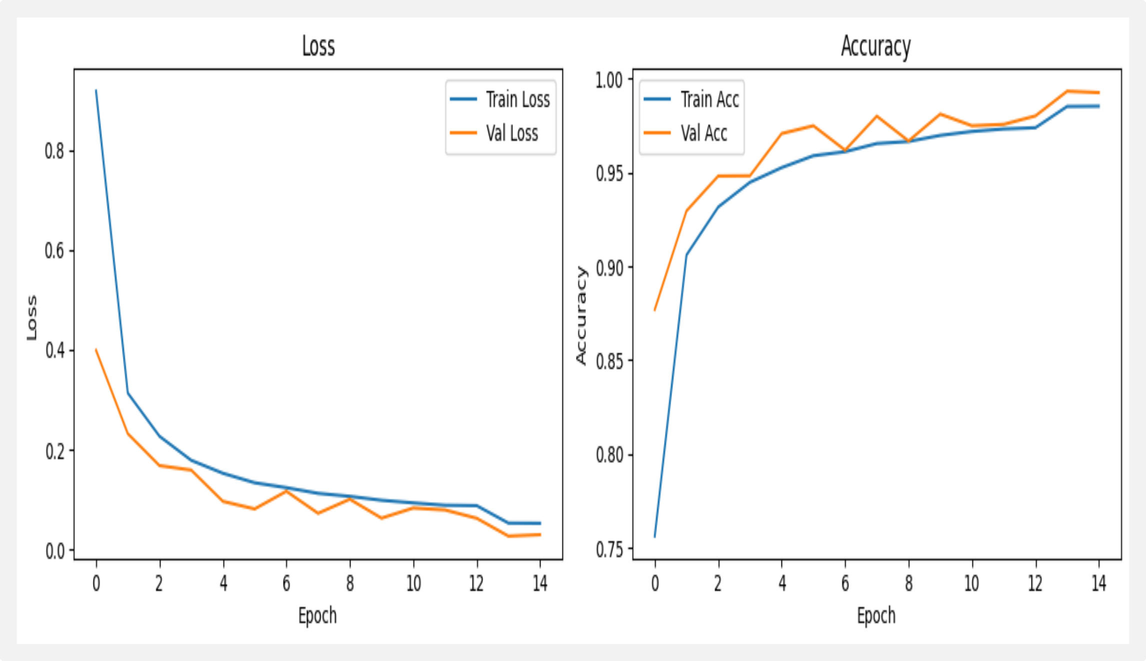

Fig. 2 Model Loss and Accuracy Graph

Both metrics make tremendous gains throughout training:

1) The validation accuracy level at Epoch 5 is up to 97.06% and validation loss is 0.0961, indicating that the model is performing much better than it was as well.
2) Stabilize the model between Epochs 6 and 10, ensuring that the validation accuracy remains between 97-98%, with small fluctuations introduced by regularization and dropout.
3) Finally, epoch 15 holds the training accuracy of 98.51% and validation accuracy at 99.24% with 0.0523 and 0.0294 losses, respectively.

TABLE I: MODEL TRAINING AND VALIDATION PERFORMANCE

Epoch	Train Loss	Train Accuracy	Validation Loss	Validation Accuracy
1	0.9173	0.7564	0.3985	0.877
2	0.3131	0.906	0.2317	0.9294
3	0.2265	0.9315	0.1677	0.948
4	0.1784	0.9446	0.1588	0.9481
5	0.1524	0.9525	0.0961	0.9706
6	0.1334	0.9588	0.081	0.9747
7	0.1236	0.9609	0.1163	0.9618
8	0.1122	0.9653	0.0722	0.9799
9	0.1062	0.9664	0.1004	0.9667
10	0.0983	0.9696	0.0626	0.9809
11	0.0931	0.9717	0.0828	0.9747
12	0.0884	0.973	0.0789	0.9755
13	0.0876	0.9737	0.0623	0.98
14	0.0526	0.985	0.0266	0.9931
15	0.0523	0.9851	0.0294	0.9924

This gradual increase is due to a well-balanced training regime, in which the model is not in overfitting condition even with high capacity. Batch Normalization, Dropout (p=0.3) and Adaptive Average Pooling are employed to normalize activations, avoid co-adaptation and maintain spatial invariance. The accuracy graph exhibits two upward curves, training and validation, which rise gradually from the first epoch to the fifteenth. The validation curve is frequently close to the training curve, indicating good generalization and little overfitting. Nearly 99% accuracy close to the convergence point would signal success to learn the discriminative features of plant disease image by the model. However, there are two downward curves in the loss graph where the training and validation drop down step by step. The validation loss is still a bit lower than the training after epoch 5, hence suggesting the model's normalization techniques are performing its best work. Final loss values around 0.03 indicate that the predictions of the network are both accurate and confident. Individually, however, these graphs demonstrate very well the classical models of success achieved by training deep learning with very high accuracy / low loss / parallel convergence with rapidly converging metrics of training and validation.

V. CONFUSION MATRIX

The confusion matrix allows us to conduct a full assessment regarding the performance of the model in predicting all 38 plant diseases. Correct predictions are the dark diagonal line and the relatively small off diagonal points suggest that the probability for misclassification is low on the data. The visual evidence provided aligns well with and correlates with the quantitative metrics presenting the model as accurately predicting the diseases.

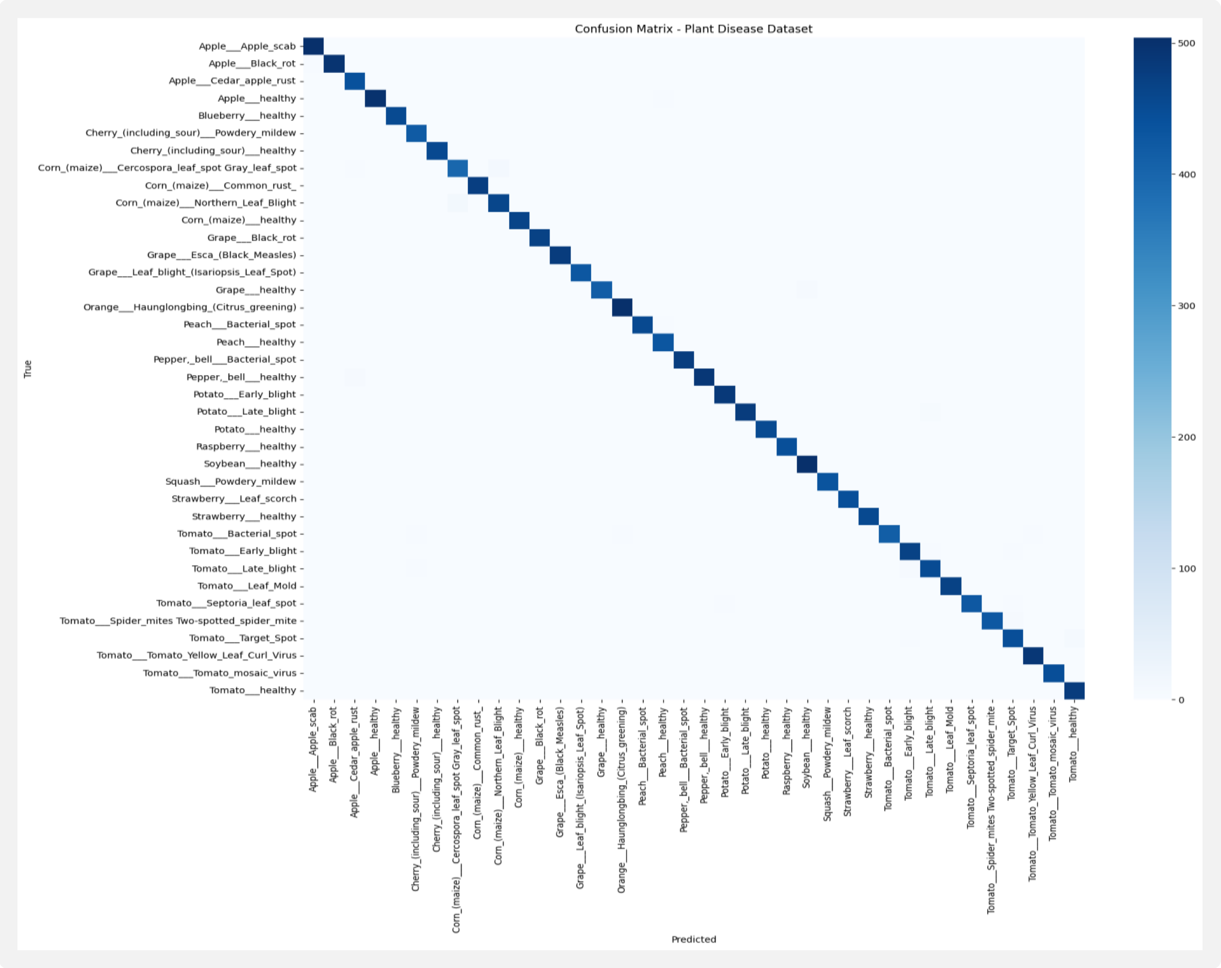

Fig. 3 Confusion Matrix Model

The confusion matrix thus verifies the model performance for picking up the subtle visual variations between disease patterns, leaf textures and color changes which are very important in real-life agricultural diagnostics.

a. Classification Report

A classification report shows how a model performs on precision, recall and F1 score in different groups. There is consistent performance for each category with a macro and weighted average equal to 0.99. Key Observations include:

1) Precision (0.99) Few false positives happen from the model's prediction. When it predicts disease, it almost always does.

2) Recall (0.99) The model can pick up most true cases for each and every single disease. This means that there are hardly any false negatives.
3) F1-score (0.99), the harmonic mean of precision and recall is well tuned, without loss in sensitivity and specificity.

TABLE II: CLASSIFICATION TABLE

Disease Class	**Precision**	**Recall**	**F1-Score**	**Support**
Apple___Apple_scab	1	1	1	504
Apple___Black_rot	1	1	1	497
Apple___Cedar_apple_rust	0.97	1	0.99	440
Apple___healthy	1	1	1	502
Blueberry___healthy	1	1	1	454
Cherry_(including_sour)___Powdery_mildew	0.99	1	0.99	421
Cherry_(including_sour)___healthy	1	1	1	456
Corn_(maize)___Cercospora_leaf_spot Gray_leaf_spot	0.97	0.97	0.97	410
Corn_(maize)__*Common_rust*	1	1	1	477
Corn_(maize)___Northern_Leaf_Blight	0.98	0.97	0.97	477
Corn_(maize)___healthy	1	1	1	465
Grape___Black_rot	1	0.99	1	472
Grape___Esca_(Black_Measles)	1	1	1	480
Grape___Leaf_blight_(Isariopsis_Leaf_Spot)	1	1	1	430
Grape___healthy	1	0.98	0.99	423
Orange___Haunglongbing_(Citrus_greening)	0.99	1	1	503
Peach___Bacterial_spot	1	0.99	1	459
Peach___healthy	0.98	1	0.99	432
Pepper,_bell___Bacterial_spot	0.99	1	1	478
Pepper,_bell___healthy	1	0.98	0.99	497
Potato___Early_blight	0.99	1	1	485
Potato___Late_blight	1	0.99	0.99	485
Potato___healthy	1	1	1	456
Raspberry___healthy	1	1	1	445
Soybean___healthy	0.99	1	0.99	505
Squash___Powdery_mildew	1	1	1	434
Strawberry___Leaf_scorch	1	1	1	444
Strawberry___healthy	1	1	1	456
Tomato___Bacterial_spot	1	0.97	0.99	425
Tomato___Early_blight	0.97	0.98	0.98	480
Tomato___Late_blight	0.98	0.98	0.98	463
Tomato___Leaf_Mold	1	1	1	470
Tomato___Septoria_leaf_spot	1	0.98	0.99	436
Tomato___Spider_mites Two-spotted_spider_mite	1	0.98	0.99	435
Tomato___Target_Spot	0.97	0.97	0.97	457
Tomato___Tomato_Yellow_Leaf_Curl_Virus	0.99	1	0.99	490
Tomato___Tomato_mosaic_virus	1	1	1	448
Tomato___healthy	0.98	1	0.99	481

VI. CONCLUSION

This shows that training the InceptionCNN model on the data yields a very good learning behavior and great predictive accuracy in plant disease classifying. It develops from intermediate performance to near-perfect classification in 15 epochs, with a validation accuracy of 99.24% and a validation loss of 0.0294. The convergence with the accuracy &

loss graphs are stable and confirm the long-term convergence and with the confusion matrix & classification report the model's validity for all the 38 classifications of disease. The model’s own merits (proven) can be attributed to a multi-branch convolutional architecture, good regularization, and balanced training. Its ability to generalize between plants, as well as with the phenom forms of diseases — and its generalization — makes it a powerful tool in precision agriculture. This work is the first step in AI based crop health monitoring, which not only has academic usefulness but also can be revolutionized through technology which automate, scale and analyze data real-time process of plant health monitoring in agricultural diagnostics. Finally, the InceptionCNN successfully performed its task and its performance proved that deep learning can bring together high-level computational vision and biological perspective – which will be helpful for farmers, researchers and policymakers, who can employ deep learning to promote the production of healthy vegetation and sustainable agricultural eco farmer’s friendly system.

REFERENCES

[1]. Hughes, David, and Marcel Salathé. "An open access repository of images on plant health to enable the development of mobile disease diagnostics." arXiv preprint arXiv:1511.08060 (2015).

[2]. Mohanty SP, Hughes DP and Salathé M (2016) Using Deep Learning for Image-Based Plant Disease Detection. Front. Plant Sci. 7:1419. doi: 10.3389/fpls.2016.01419

[3]. Zhihong Zhang, Heping Zhu, Huseyin Guler, Yue Shen, Improved premixing in-line injection system for variable-rate orchard sprayers with Arduino platform, Computers and Electronics in Agriculture, Volume 162, 2019, Pages 389-396,ISSN 0168-1699, https://doi.org/10.1016/j.compag.2019.04.023.

[4]. Szegedy, Christian, et al. "Going deeper with convolutions." Proceedings of the IEEE conference on computer vision and pattern recognition. 2015.

[5]. Tan, Mingxing, and Quoc Le. "Efficientnet: Rethinking model scaling for convolutional neural networks." International conference on machine learning. PMLR, 2019.

[6]. Selvaraju, Ramprasaath R., et al. "Grad-CAM: visual explanations from deep networks via gradient-based localization." International journal of computer vision 128.2 (2020): 336-359.

[7]. Andreas Kamilaris, Francesc X. Prenafeta-Boldú, Deep learning in agriculture: A survey,Computers and Electronics in Agriculture, Volume 147, 2018,Pages 70-90,ISSN 0168-1699, https://doi.org/10.1016/j.compag.2018.02.016.