

Citrus disease detection and classification using end-to-end anchor-based deep learning model

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Accepted: 20 April 2021

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Abstract

Plant diseases are the primary issue that reduces agricultural yield and production, causing significant economic losses and instability in the food supply. In plants, citrus is a fruit crop of great economic importance, produced and typically grown in about 140 countries. However, citrus cultivation is widely affected by various factors, including pests and diseases, resulted in significant yield and quality losses. In recent years, computer vision and machine learning have been widely used in plant disease detection and classification, which present opportunities for early disease detection and bring improvements in the field of agriculture. Early and accurate detection of plant diseases is crucial to reducing the disease's spread and damage to the crop. Therefore, this paper employs a two-stage deep CNN model for plant disease detection and citrus diseases classification using leaf images. The proposed model consists of two main stages; (a) proposing the potential target diseased areas using a region proposal network; (b) classification of the most likely target area to the corresponding disease class using a classifier. The proposed model delivers 94.37% accuracy in detection and an average precision of 95.8%. The findings demonstrate that the proposed model identifies and distinguishes between the three different citrus diseases, namely citrus black spot, citrus bacterial canker and Huanglongbing. The proposed model serves as a useful decision support tool for growers and farmers to recognize and classify citrus diseases.

 $\textbf{Keywords} \ \ Agriculture \cdot Citrus \ diseases \cdot CNNs \cdot Deep \ learning \cdot Disease \ recognition \ and \ classification \cdot Machine \ learning$

1 Introduction

1.1 Background and motivation

Agricultural production plays a pivotal role in the world economy and crucial to economic growth. Factors like climate change [28], arable land, access to technology, insect pests [15] and new diseases [31] are the main hurdle for food production. Plant diseases pose a significant risk to crop health and global food security, crop production

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Published online: 13 May 2021

and world economy and affect the yield and quality of crops worldwide [49, 56]. It is estimated that crops suffer losses due to plant pathogens of nearly 16% globally [41]. Fruit crops are a significant component of agricultural production, with citrus as one of the essential fruit crop cultivated in the world and the most consumed and traded agricultural commodity worldwide [18, 39]. Citrus production and cultivation are threatened continuously by many challenges such as pathogens, pests and diseases that lead to considerable economic losses and social impacts in all growing areas worldwide [31]. Breeding disease-resistant cultivars have been suggested as the best sustainable method for plant disease control [27]. Many signs of progress have been made to advance and improve the breeding program through the employment of biotechnological tools and genome sequence for citrus disease resistance [11]. However, there are still challenges, and limitations in developing new citrus varieties resistant to diseases [55] such as different experimental condition in the lab and real field [40]. The agricultural diseases that infect citrus plants are citrus bacterial canker (CBC) and citrus



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black spot (CBS), which occur in major citrus growing regions [13, 57]. Citrus huanglongbing (HLB), also known as yellow dragon disease, is considered as one of the most devastating citrus diseases in the world [7, 19] due to its complexity and destructiveness that affect fruit production and quality. All commercial citrus varieties are prone and susceptible to these diseases.

Xanthomonas citri subsp. citri (XCC) bacterial pathogen is the causal agent of CBC that affects many commercial varieties of citrus, including grapefruit, lemons, limes and sweet oranges, which resulted in considerable losses to citrus industries across the globe [13]. This disease is more prevalent in humid-wet climates such as high temperature, rainfall and windy conditions [29, 38]. The disease's symptoms include premature leaf and fruit drop, twig dieback, brown spots and blister-like lesions on leaves, fruit, and stems that start small and enlarge as the disease progress [10, 22] and eventually, the plant can die. CBC can be treated with copper and more effective on new seedlings when applied before infection. However, the frequent application is essential to achieve adequate control of the disease during the most susceptible growth stages of leaf and fruit [23]. CBS caused by fungal pathogen Phyllosticta citricarpa affects citrus production in citrus-producing areas on a global level [4, 37]. CBS's occurrence is more evident in citrus growing regions with warmer summer rainfall than areas with cooler temperature, and winter rainfall [37]. Infected citrus usually produces lesion spots on leaves and twigs, freckle spots and false melanose on the fruits that affect both quality and yields [24, 33]. In Australia, it was estimated that the growers lost \$80 million annually for fungicide application, yield loss due to fruit damage and export restrictions [17]. The majority of the losses is due to external blemishes that affect external fruit quality, which make the fruit unsuitable for fresh marketing [37] and consumption.

HLB is listed as the most severe disease of citrus trees due to the devastating effects and severe threats for the citrus industry worldwide [5, 7, 59]. This disease is caused by a vector-transmitted pathogen Asian citrus psyllid (ACP) ((Diaphorina citri), and the causative agent is Candidatus liberibacter spp. [7]. There is no cure for HLB, and the only way to stop the spread is the rapid removal of all the infected trees [50]. HLB is spread by insect vector or through propagating material across the tree canopy that affects the vascular system, causes decline and death of the infected tree [60]. It is vital to manage the insect vector to stop the spread and attenuate symptoms in infected plants [43]. Various control measures have been introduced to control HLB, including contact insecticides [6]; however, frequent application is required for effective results since the spread of the disease can quickly be done by only a few adult psyllids [8].



1.2 Problem statement

Generally, the eradication program is difficult and costly, as it requires lots of labour and resources but provides economic benefit in returns. The eradication cost of citrus canker in Florida, from 1995 to 2005 was estimated to be nearly US\$1 billion [21] and AU\$18.5 million in Queensland, Australia. Up to now, there is no successful approach to eradicate citrus diseases, and the only fundamental approach to prevent the spread and lessen the impact of infection is through the removal of infected plants. To date, numerous efforts have been made to develop strategies to address challenges concerning plant pests and diseases and prevent crop losses. Although various methods have been applied and introduced to control plant diseases, the early identification and accurate diagnosis of diseases are the keys to tackle this issue to reduce the spread of disease and the damage to the crop. Nevertheless, disease detection remains challenging due to the lack of necessary infrastructure and many computing resources and datasets. Predicting and detecting diseases at an early stage, monitoring plant health and consequent application of control measures are critical for sustainable agriculture. It is a constant battle for the researchers to stay ahead of these pests and diseases and continue fighting and providing the farmers and agricultural industry with the latest tools to combat plant diseases. The advancement in computational systems in recent years has resulted in the extensive application of image recognition in plant disease recognition and plant severity studies [2, 3, 30, 45, 53]. Significant progress has been made in plant diseases recognition (based on computer vision technology) using artificial neural network and digital image processing [16]. Deep learning approaches have been introduced into agriculture and plant protection, particularly for plant disease diagnosis, detection and classification [35, 48]. Conventional machine learning and artificial intelligence approaches require a step called feature extraction for image classification [42], which is not required in deep learning techniques. The essential advantage of deep learning in computer vision is delivering higher accuracy with the ability to perform an automatic image feature extraction from raw images/data [58] and solve the feature extraction problem.

1.3 Contribution

Deep learning classifiers are end-to-end systems that directly exploit image without any human-crafted features and provides higher accuracy for object detection, image classification, and semantic segmentation [34]. Various approaches have been used, and the most common and extensively studied are Convolutional Neural Networks

(CNNs), a class of deep neural networks [20, 36]. The objective of this paper is to develop a convolutional neural network with the ability to classify the diseases according to the symptoms and detect the infected regions in citrus leaves. The proposed model's application serves as an early warning tool for accurate identification and classification of citrus diseases. It is a useful strategy for automatically diagnosing citrus plant diseases and further expanding to support an integrated plant disease identification system for the application in real field conditions. The developed tool will help prevent crop diseases at an early stage and reduce the cost of pesticides while protecting the environment.

1.4 Paper organization

The rest of the paper is organised as follows. Section 2 discusses the related work and it's findings. Section 3 presents the proposed methodology, Section 4 dicusses the achieved experimental results and finally conclusion is drawn in Section 5.

2 Related work

The main reason limiting the timely and broad identification of the disease is the lack of experts in plant pathology. Misjudgement of disease diagnosis and identification reduces the possibility to stop the spread of the disease. Automatic recognition of plant diseases through image processing techniques and machine learning has transformed the agriculture field and potentially be integrated as a promising solution to overcome the challenges. Several studies have been carried out, and some of the DL-based approaches that focus on the diagnosis of citrus diseases are discussed. In general, considering citrus diseases, the detection process involves major steps like pre-processing, feature extraction, classification and segmentation [26].

Rauf et al. [46] provided a dataset of citrus plant images of different diseases (black spot, canker scab, greening and melanose)that is accessible for researchers at Mendeley data. The dataset contains 759 images of healthy and diseased fruits, and leaves may serve as a reference for comparing and detecting citrus diseases. Xing et al. proposed a lightweight CNN model called Weakly DenseNet for diagnosis and identification of citrus pests and diseases [63]. A total of 9051 images of 17 citrus pests' species and 3510 images of seven group of citrus diseases (anthracnose, canker, melanose, scab, sooty mold, leaf miner, and pest holes) were included in their dataset. They employed a feature reuse method and data augmentation algorithm to reduce the similarity between generated images. Their algorithm improved the parameter efficiency and achieved an accuracy of 93.3%. The model can be utilized in mobile application due to its lightweight feature. Chen et al. employed deep CNN models to perform citrus leaf diseases recognition [12]. A dataset used in the study consists of 3171 images of citrus canker, scab and anthracnose to train and test the model. Their model achieved an accuracy of 98.6%, 93.25% and 95.12% for CBC, scab and anthracnose, respectively. Sharif et al. detected lesion spot on citrus fruits and leaves and classified citrus diseases using a hybrid method by extracting the best features of color, texture and geometric using PCA score, entropy and skewness-based covariance factor to select the best feature [52].

Multiclass Support Vector Machine (M-SVM) classifier was used to classify citrus diseases, namely anthracnose, black spot, canker, scab, greening and melanose in conjunction with four stages comprising of (a) image segmentation, (b) lesion segmentation to identify the infected area, (c) feature extraction using codebook, (d) feature selection and classification. They used citrus diseases images from a public dataset (PlantVillage and Citrus Disease Image Gallery) (570 images), a combined dataset (previous studies) (5632 images) and own dataset (440 images). Their model employed an optimized weighted segmentation and feature selection and achieved an average of 92.44% of accuracy on all datasets used.

Senthilkumar et al. presented a model called HT-RFANN (Hough Transform-rough fuzzy artificial neural network) as a classification model for citrus diseases (CBS, CBC, HLB and scab) using images obtained from Citrus Image Gallery [51]. Their model achieved an accuracy of 96.93% with superior classification. However, the proposed model is not a deep learning-based model. Wetterich et al. presented a new technique for identifying citrus canker that used the combination of fluorescence imaging spectroscopy (FIS) and SVM [61]. The introduced approach was able to detect and distinguish citrus scab and CBC with an accuracy of 97.8%. A novel technique for HLB classification using an SVM classifier based on C-SVC (cost-support vector classification), visible spectrum image processing detection and PCA (principal component analysis) for reduction of extracted features was used by Deng et al. [14]. The lowcost proposed technique achieved 91.93% of accuracy and required minimum computational complexity.

Qadri et al. used an optimized fused multi-features leaf dataset [44]. They tested on several classifiers, namely Multilayer Perceptron (MLP), J48, Random Forest (RF) and Naïve Bayes, using citrus leaf images of eight cultivars. Among all the tested machine learning classifiers, MLP presented the best overall accuracy of 98.14%. In another study, Partel et al. developed and evaluated an automated vision-based system by employing computer vision and machine learning approaches to scrutinize ACP, the insect vector responsible for transmitting HLB [43]. The proposed



Table 1 Summary of related work presented in this study

Summary					
Reference	Diseases	Method			
Rauf et al [46]	black spot, canker scab, HLB, melanose	Hyperspectral sequence of citrus disease images			
Xing et al [63]	anthracnose, canker, melanose, scab, sooty mold ,leaf miner, and pest holes	Weakly DenseNet			
Chen et al [12]	CBC, scab, anthracnose	CNN models			
Sharif et al [52]	anthracnose, CBS, CBC, scab, HLB, melanose	M-SVM			
Senthilkumar et al [51]	CBS, CBC, HLB, scab	HT-RFANN			
Wetterich et al [61]	canker, scab, CBC	SVM			
Deng et al [14]	HLB	SVM			
Partel et al [43]	Aphids (pest)	Automated vision-based system			
Abdulridha et al [1]	black spot, canker scab, HLB, melanose	Hypersectral imaging and Machine learning			

system comprises a tapping mechanism to scout and collects ACP from citrus tree branches and a grid of image acquisition cameras. The software and hardware components in the proposed technology were integrated using an NVIDIA TX2. The system obtained a precision of 80% for detection on 90 young citrus plants.

Finally, the authors of [1] developed a UAV (unmanned aerial vehicle) equipped with a multispectral imaging system for detection of CBC under both laboratory and field conditions. In laboratory condition, the proposed model positively identified immature citrus fruits infected with CBC and differentiated them from healthy fruit. While in the field, the UAV-based proposed technique using Neural Network Radial Basis Function (RBF) method achieved 96% and 100% of accuracy for healthy vs early-stage and healthy vs late stage, respectively, for both leaf and fruit. Table1 is summarizing the the methods and the type citrus disease that above-mentioned studies were focusing on.

This paper proposes a citrus disease detection and classification model to analyze the leaf images of healthy and infected with CBC, CBS, and HLB using deep CNNs.

3 Proposed methods

3.1 Data

The data which is used for this study is a publicly available citrus dataset from the Kaggle website¹ for the experiment, which includes samples of three types of citrus disease (black spot, canker and Huanglongbing) and a healthy control class. All these three types of diseases have some effects on the citrus leaves. This dataset has collected images of the citrus leaves with visible disease patterns. To visualize some sample of disease refer to Fig. 1. All the

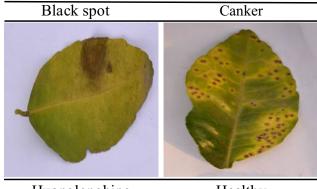
¹https://www.kaggle.com/dtrilsbeek/citrus-leaves-prepared? select=citrus_leaves_prepared



samples in the dataset were in png format with the image size of 256 x 256. The dataset has separate sets of samples for training and testing. Table 2 summarizes the information of the dataset.

3.2 Data preparation

Several steps of data pre-processing were done to prepare the data for the training. First, all images are converted to grayscale images. During the pre-processing, it is noticed that images have different intensity level; therefore, a



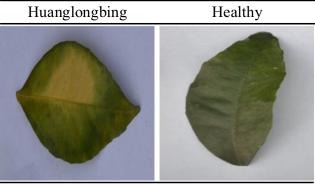


Fig. 1 Samples of citrus leaf images infected with **a** canker, **b** black spot, **c** Huanglongbing used in this study and their visual impacts on the citrus leafs compared with a healthy leaf

Table 2 Summary of the dataset information

Disease type	No. of training sample	No. of test sample	Image size
Black spot	138	35	256x256
Canker	130	33	256x256
Huanglongbing	163	41	256x256
Healthy	46	12	256x256
Total	477	121	_

Bold signifies total number

histogram equalization technique is performed to bring all the images into the same intensity range. It is a crucial step to standardize the image intensity before converting to a binary image. In the next step of pre-processing, the grayscale images are converted to binary images using a thresholding function. Since all samples' intensity is mapped to a standard range, the application of the thresholding function provides uniform output across the dataset samples.

The binary masks are used to define the bounding box around the original leaf and separate them from the background. After that, the bounding box information is applied to the original image to extract the leaf image from the background. Figure 2 shows the step by step process of leaf extraction and bounding box definition. The first column shows the original image over three main categories of citrus diseases. The binary image is used

as the mask for any segmentation purpose. In the third column, the pink bounding box determines the leaf's area in the input sample. The same bounding box is applied to the original image for visualization purposes in the last column.

Each of the input samples is associated with a label to determine its class. The labels could be any of black spot, canker, Huanglongbing or healthy class. The labels are defined by the numbers from 0 to 3 respectively and stored in a text file format.

In the process of data preparation, we performed very basic data augmentation such as rotation to balance the number of samples in all classes. This is done to deal with unbalance number of samples per classes by oversampling the minority classes. With this basic data augmentation, the proposed model can provide competitive classification accuracy using a medium size of the dataset.

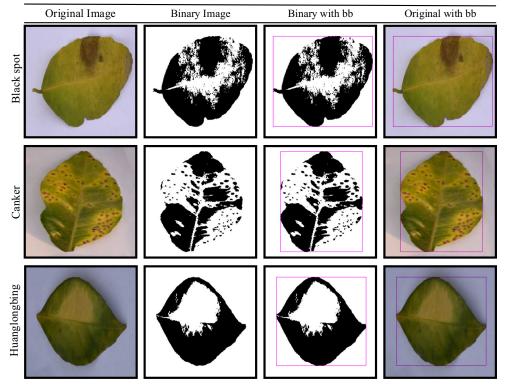


Fig. 2 Preprocessing of input samples

3.3 Network structure

The proposed network structure for this study is a twostage deep convolutional neural network based on Faster R-CNN [47]. The network structure consists of four components of feature extractor, Region Proposal Network (RPN), Region of Interest (ROI) pooling and classifier. Figure 3 shows a block diagram of the proposed model in a high-level view.

The feature extractor is the first component of the proposed model, which extracts the image features. These extracted features are shared between the following components of Region Proposal Network and classifier. Sharing features speed up the training process and also significantly save memory. The proposed model uses ResNet101 as the feature extractor where residual connections enable the model to go deeper and provide better accuracy without facing the gradient vanishing problems [25]. The feature extractor consists of several residual blocks, each using 3×3 filters and performs downsampling by employing convolutional layers with the stride of 2. These residual blocks are stacked on top of each other and then followed by a global average pooling layer and a fully connected layer with a softmax at the end.

The region proposal network is the second component of the proposed model, which extracts potential anchors containing the target object within the given image. To generate the regions, a small sliding window covers the feature maps shared by the feature extractor. The RPN network structure is implemented with an $n \times n$ convolutional layer followed by two siblings 1×1 convolutional layers. For more details on the implementation of RPN, we refer the reader to [47]. Each potential region comes with an objectness score,

determining how close is the proposed region to the target object. We have limited the number of proposed anchors to 300 with an Intersection over Union of above 0.5. This means only 300 proposed regions with more than 50% intersection with the target object are passed to the next stage. The target objects are marked with the bounding box, as shown in Fig. 2. In the case of no region passing the condition, the input sample considers as a missing-target class.

ROI pooling is the third component of the proposed model, where the top 50 ROIs with the highest objectness score are selected and passed to the classifier. The ROI pooling will limit the number of potential regions, reducing the chance of false-positive and miss-classification.

The classifier is the fourths component of the model. After extracting the potential target regions, all these regions will be passed to the classifier, in which the final classification will be done. The classifier will use the features extracted by the feature extractor to perform the classification. The sharing of the features between classifier and RPN helps to increase the entire processing time during the model training.

For the network training, we performed a transfer learning approach in which weights are transferred from a pre-trained model. Transfer learning is proven to improve the performance of the network [25]. In this study, we trained the model in two stages; First, the weights are loaded from a pre-trained model on the COCO dataset. In the first stage of training, only the feature extractor is trained for some epochs. All the rest of the weights for other components of the network were kept frozen. Then in the second stage, the rest of the weights are injected in, and the entire model trained together.

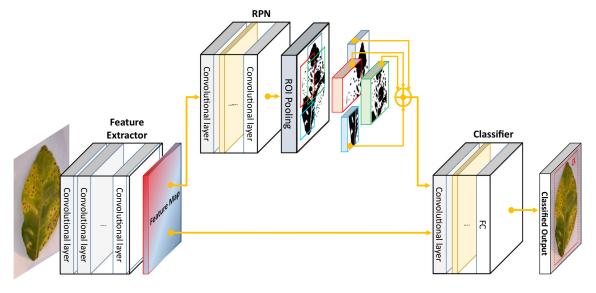


Fig. 3 Block diagram of the proposed model structure



One of the critical tasks in this experiment was monitoring the loss function of the model. Since our model has a couple of components, and each can provide a different loss value, we decided to define separated losses and combine them to generate the model's final loss.

In the ROI network, the regions with an IoU of greater than 0.5 received a label, the class number of the ground truth. Then their loss is compared against the actual class label and called RPN class loss. Similarly, the loss is calculated at the classifier and called classifier class loss. The total loss of the network is the average of the above losses as per (1)

$$L(S) = \frac{1}{2} \left(\sum_{class=c}^{C} loss_{c}(RPN) + \sum_{class=c}^{C} loss_{c}(Classifier) \right) \tag{1}$$

where L(S) is the loss for the given sample of S and C is the total number of target classes.

In the next section, we will look at the achieved results and discuss them.

4 Experiments and discussion

4.1 Results and discussion

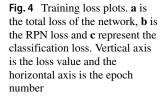
Experiment setup The proposed model is implemented in Keras on a Linux (REH7.5) machine with an Nvidia Quadro P5000 with 16 GB of memory and CUDA version of 10.0.

model is implemented in ne with an Nvidia Quadro of the lad CUDA version of 10.0. process

During the training of the model we performed a twostage training. In the first stage, the feature extractor was trained individually with the weights loaded from a pretrained model on the COCO dataset. For this stage, model were trained for 35 epochs and after that, the rest of the network components were added to the model and trained together for another 370 epochs. Figure 4 shows how the loss functions of each component are reduced throughout the training process and comparing it with the total loss function of the entire model.

By looking at the RPN loss function over training epochs, as shown in Fig. 4b, there is fluctuation due to the non-target regions picked by the model. The majority of the proposed regions are then filtered by the ROI pooling component. Therefore, the classification loss shows smoother reduction during the training, which we believe is because the classifier receives uniform inputs containing the target object.

During the experiment, it is noticed that training the model with more than 400 epochs did not have significant positive effects on the outputs' accuracy. Yet, it might put the model at the risk of over-fitting. To avoid overfitting training, we have set two early stopping criteria. First, the maximum number of epochs for training is limit to 500. Second, a monitoring mechanism defined to check the improvement of validation accuracy over the last ten consecutive epochs. If the average accuracy improvement of the last ten epochs is lesser than 1%, then the training process will be terminated.



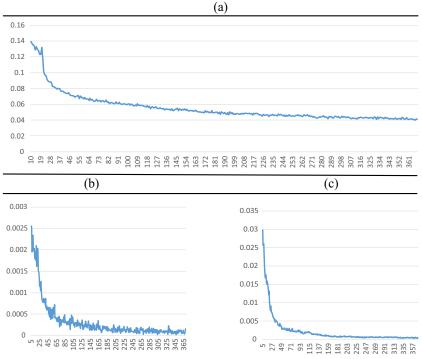




Fig. 5 Qualitative results of the detection of diseases on citrus leaf images

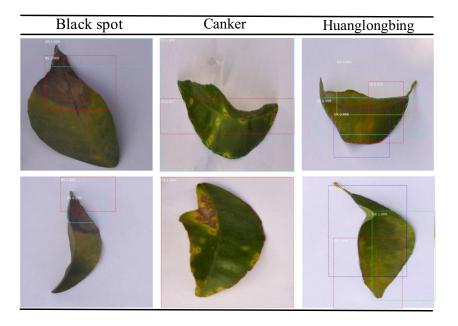


Figure 5 shows some sample images from the test set with their corresponding classification outcomes. For visualization purposes, we chose to show some of the proposed regions with the highest objectness score, classified by the model. We observed that the proposed model is capable of recognizing the target class precisely accurate.

To validate the proposed model's achieved results, we performed a 5- fold cross-validation strategy and average the accuracy over five folds. We also presented the standard deviation together with each parameter. Table 3 summarizes the detection results of all 5-folds. The achieved accuracy on the detection of the disease can highlight the performance of our proposed model in the detection section.

To have a clearer insight into our model's classification results, the confusion matrix of each fold is calculated and accordingly, other evaluation measures are extracted. Figure 6 shows the confusion matrix for classification. The missing column added because the model could not generate any output for some of the samples. Therefore we called them missing samples and added them in the missed column.

Table 3 Detection accuracy of individual folds in the 5-fold cross validation process

Fold no.	No. of samples	Detected	Missed	Acc (%)
Fold 1	86	83	3	96.51
Fold 2	86	79	7	91.86
Fold 3	84	78	6	92.85
Fold 4	86	82	4	95.35
Fold 5	85	81	4	95.29
Overall	427	403	24	94.37

For further evaluation of the model, some of the most frequently used accuracy measures like F1-score, precision and recall are recorded. Table 4 compares the achieved results of our model with some of the state-of-the-art methods. As can be seen in the table, our model was able to outperform the competitors. Moreover, our model produced a very low standard deviation, which represents the robustness of the model. The smaller number of samples we employed for training compared with other states of the art methods highlights the efficiency of the proposed model. Especially when it comes to the tedious and costly task of data collections and annotation, our model's capability considers as a significant advantage over the state of the arts.

By looking at Table 4 and comparing all confusion matrix, we can see the CBS class is a more challenging

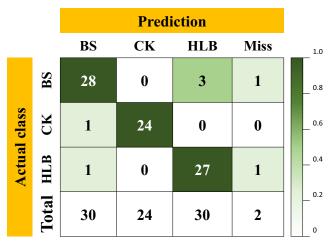


Fig. 6 Confusion matrix of fold 3 as a sample of the confusion matrices



Table 4 Comparison of results

Disease Type	Ref	No. of samples	F1-score (%)	Precision (%)	Recall (%)	Accuracy %)
Black spot	[9]	200	_	_	_	92.0
	[32]	135	_	_	_	88.65
	Our Method	86	90.0 ± 2.91	93.8 ± 7.79	87 ± 1.87	86.18 ± 2.08
Canker	[64]	1000	_	_	_	89.5
	[63]	598	_	_	_	93.3
	Our Method	86	97.9 ± 3.34	99.0 ± 7.79	95.8±4.38	97.2 ± 4.38
Huanglongbing	[62]	100	_	_	_	92.0
	[54]	100	_	_	_	93.3
	Our Method	86	93.0 ± 2.12	91.0 ± 3.46	94.6 ± 5.12	94.64 ± 5.1

class to be classified. This is due to drastic changes in the disease's spot size on the leaf. The spot size may vary from a small dot to a big spot covering up to half of the leaf. This considerable variation in the lesion's size can be interpreted as the main reason for the accuracy deterioration. Yet, the model could deliver a reasonable classification accuracy in many measures and stands on top of the state-of-the-arts.

The main reason behind the solid performance of our model is that by adding RPN to the model, the classifier can focus on the classification of a manageable number of target-like candidates. This property leads to a reduction of false positives caused by other areas of the image that are not contributing to the target class. Overall, the RPN network has a significant impact of between 10% to 50% in the final classification accuracy.

Since the feature maps are being shared between the RPN and classifier, RPN has almost no training cost for the entire model, which is a great advantage in terms of the training cost.

The false-positive rate is a crucial evaluation metric in all detection problems. The high precision rate achieved by the proposed model shows that there is a deficient number of false positives in the detection outputs. As mentioned before, this is the positive impacts of the region proposal network.

Another contributing factor is the application of a deep feature extractor. The deeper networks tend to provide better results; therefore, by using a residual network structure, the proposed model increases the depth of the network significantly and generates more meaningful features for other components.

Moreover, with the application of two-level networks, the proposed model doesn't require to extract the object from the background for achieving higher accuracies. Note that in our experiment, we performed thresholding only to draw the bounding box around the object and create the ground truths. But, all our input images are passed as a

whole image, and there was no necessary to segment the foreground from the background.

Lastly, to highlight the advantage of our model over conventional Faster RCNN we need to point to the modification in the loss function. In Faster- RCNN, all the proposed regions by RPN are treated equally in the classifier and, consequently, contribute equally to the classifier's final decision-making. While in our proposed loss function, the regions with lesser RPN loss(the regions with higher potential of containing the target pattern) have a higher impact on the classifier's final decision-making. In other words, by using the proposed loss function, the proposed regions are not treated equally. The regions with a lower possibility of containing the disease pattern contribute less to the final decision of the model.

5 Conclusion

This paper proposes an advanced detection and classification method based on deep learning models to perform the task of disease detection on three common citrus diseases of black spot, canker and Huanglongbing. The proposed two-stage classification model contains a feature extractor and a region proposal network which proposes the potential regions to the classifier. The features are shared between RPN and classifier to reduces the training overhead. This paper introduces a new loss function that averages the loss from the RPN model and the classifier. Therefore, all the proposed regions by the RPN network are not treated equally, and their contribution in the final decision of the model is based on their loss from the RPN network. In this way, the regions with a higher chance of containing the disease pattern will contribute more to the final decision of the model. Moreover, our model can perform the detection and classification task with high accuracy of 86.2%, 97.2%



and 94.6% for black spot, citrus canker and Huanglongbing, respectively by conducting the training on a very minimal number of samples.

6 Future studies

Authors are aware that applying the proposed method on real field-collected data may result in a drop in the accuracy. Therefore, we plan to have an extended experiment of the proposed method on those data once the data collection process is completed. The challenges of such an experiment and the necessary changes in the model are the subject of our future study. Moreover, to further improve the robustness of the model and reduce the standard deviation, we are planning to perform extended data augmentation.

Author Contributions Conceptualization, SFSAR and MHH; methodology, SFSAR and MHH; software, SFSAR and MHH; validation, MHH; formal analysis SFSAR and MHH; investigation, SFSAR and MHH; resources, SFSAR and MHH; data curation, SFSAR and MHH; writing—original draft preparation, SFSAR; writing—review and editing SFSAR, MHH and MP; visualization, SFSAR and MHH; supervision, MP; project administration, SFSAR, MHH and MP; All authors have read and agreed to the published version of the manuscript.

Declarations

Conflict of Interests The authors declare that they have no conflict of interest.

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