

ResNet-Driven Automated Identification of Custard Apple Diseases for Sustainable Smart Agriculture

Sürdürülebilir Akıllı Tarım için Muhallebi Elması Hastalıklarının ResNet Odaklı Otomatik Tanımlanması

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Abstract

The development of an automated fruit disease detection system is critical to improve agricultural productivity. This study specifically addressed disease detection in custard apple plants by using a deep learning-based classification approach. Using an extensive image database from different regions, including India, Portugal, Thailand, Cuba and the West Indies, the system successfully classified 8226 images of fruit and leaf diseases of custard apple into six different categories: anthracnose, black canker, diplodia rot, leaf spot on fruit, leaf spot on leaf, and mealy bug. Using transfer learning, the system demonstrated strong classification performance, even with images taken in natural environments with complex backgrounds. By analyzing the unique features of the images, the proposed model accurately identified disease symptoms. In addition, evaluation metrics such as classification accuracy (CA), recall, precision, F1 score and confusion matrix underscored the model's effectiveness, with ResNet standing out as the most efficient architecture, achieving an impressive 99.77% CA. This study demonstrated the potential of the system to significantly improve disease detection in custard apple crops, and offers a promising tool for improving agricultural management.

Keywords: Smart Agriculture, Custard Apple, Deep Learning, Disease Classification, Multi-class Classification, Transfer Learning.

Öz

Otomatik bir meyve hastalığı tespit sisteminin geliştirilmesi, tarımsal verimliliğin artırılması açısından kritik öneme sahiptir. Bu çalışma, özellikle derin öğrenmeye dayalı sınıflandırma yaklaşımı kullanarak ekşi elma (custard apple) bitkilerinde hastalık tespitini ele almıştır. Hindistan, Portekiz, Tayland, Küba ve Batı Hint Adaları gibi farklı bölgelerden geniş bir görüntü veri tabanı kullanılarak, sistem 8226 meyve ve yaprak hastalığı görüntüsünü altı farklı kategoriye başarıyla sınıflandırmıştır: antraknoz, kara kanser, diplodia çürüklüğü, meyvedeki yaprak lekesi, yapraktaki yaprak lekesi ve unlu bit. Transfer öğrenme kullanılarak, sistem karmaşık arka planlara sahip doğal ortamlarda çekilmiş görüntülerle bile güçlü bir sınıflandırma performansı sergilemiştir. Görüntülerin özgün özellikleri analiz edilerek, önerilen model hastalık belirtilerini doğru bir şekilde tanımlamıştır. Ayrıca, sınıflandırma doğruluğu (CA), duyarlılık, keskinlik, F1 skoru ve hata matrisi gibi değerlendirme metrikleri, modelin etkinliğini ortaya koymuş; ResNet, en verimli mimari olarak öne çıkarak etkileyici bir %99,77 CA elde etmiştir. Bu çalışma, sistemin ekşi elma ürünlerinde hastalık tespitini önemli ölçüde iyileştirme potansiyelini göstermiş ve tarımsal yönetim ile üretim verimliliğini artırmak için umut verici bir araç sunmaktadır.

Anahtar Kelimeler: Akıllı Tarım, Muhallebi Elması, Derin Öğrenme, Hastalık Sınıflandırması, Çok Sınıflı Sınıflandırma, Transfer Öğrenme.

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1. Introduction

Agriculture is a fundamental sector encompassing diverse activities related to plant and animal production, including crop cultivation, animal husbandry, and fisheries (Ergün 2024a; Ergün 2025). It plays a crucial role in meeting human needs by facilitating the cultivation, processing, and commercialization of agricultural products for food, feed, textiles, and energy. Within this domain, fruit cultivation holds significant importance due to its multifaceted benefits. Primarily, fruits contribute to food security and nutrition by serving as rich sources of vitamins, minerals, and dietary fiber, essential for maintaining a balanced diet. Additionally, the inclusion of diverse fruits enhances dietary variety, promoting overall health benefits. Economically, fruit cultivation is a vital industry, generating substantial revenue in both local and global markets (Tianjing et al., 2024). It also serves as a key employment sector, offering job opportunities to numerous individuals. Furthermore, fruit farming enhances agricultural diversity, enabling farmers to mitigate risks associated with monocropping and ensuring stable income sources. Beyond economic aspects, orchards play a pivotal role in ecological sustainability by preventing soil erosion, regulating the water cycle, and fostering biodiversity. Sustainable orchard management contributes to ecosystem conservation by supporting agroecological balance. Moreover, the expansion of agritourism, including farm visits and fruit harvesting activities, fosters rural tourism development. Environmentally, fruit farming encourages sustainable agricultural practices by reducing dependency on synthetic fertilizers and pesticides. From a public health perspective, the consumption of fresh fruits aligns with healthier lifestyles, reinforcing the broader significance of fruit cultivation in ensuring agricultural sustainability, economic resilience, and societal well-being.

Among various fruit species, the custard apple (*Annona squamosa*), commonly referred to as the sugar apple or sweetsop, is a tropical fruit cultivated predominantly in temperate regions. Characterized by its soft, creamy texture and sweet flavor, this fruit holds substantial nutritional and economic value (Tianjing et al., 2024; Chaitanya et al., 2024). Custard apples are rich in essential nutrients such as vitamin C, potassium, magnesium, and fiber, which contribute to overall health and wellness. Their market potential extends beyond fresh consumption, as they serve as key ingredients in processed products like juices, purees, ice creams, and desserts, making them commercially significant. The adaptability of custard apples to tropical and subtropical climates facilitates their widespread cultivation, providing an alternative income source for farmers across various regions. Moreover, their contribution to biodiversity enhances agricultural ecosystems, as different fruit species acclimate to diverse soil compositions and climatic conditions, thereby enriching agricultural landscapes. Additionally, custard apple cultivation supports local economies by ensuring sustainable

income opportunities for farmers. Given its nutritional and commercial advantages, custard apple farming holds considerable value in enhancing both the agricultural sector and rural livelihoods.

Despite its numerous benefits, custard apple cultivation is susceptible to various plant diseases that threaten fruit yield and quality. Common afflictions such as anthracnose, fungal infections, bacterial spot, root rot, and viral pathogens pose significant challenges to growers, leading to economic losses and reduced productivity (Cheng et al. 2024). These diseases not only compromise fruit quality but also adversely impact tree longevity and overall orchard sustainability. Consequently, early detection and effective disease management strategies are imperative for safeguarding production. Recent advancements in technology offer promising solutions for automating disease detection in custard apples. The integration of image processing, artificial intelligence (AI)-based analysis, and sensor technologies facilitates early disease diagnosis, enabling growers to implement timely interventions (Chen et al. 2024). AI-driven image analysis, in particular, provides a precise mechanism for identifying disease symptoms by analyzing color, texture, and morphological changes in leaves and fruits. These intelligent systems enhance agricultural decision-making by enabling proactive disease management, minimizing economic losses, and extending orchard lifespan. Furthermore, AI-based diagnostic tools optimize pesticide usage, reducing environmental impact and promoting sustainable farming practices (Vallabhajosyula et al. 2022). The application of these advanced technologies not only revolutionizes disease management in custard apple farming but also fosters a transition toward more resilient and eco-friendly agricultural methodologies. The primary scientific contributions of this study are as follows:

- A deep learning (DL)-based system was developed for the automated classification of diseases in custard apple plants. Leveraging advanced architectures such as ResNet, the proposed approach achieved high accuracy in detecting multiple disease classes, thereby improving early diagnosis and management.
- A comprehensive dataset comprising images of custard apple fruits and leaves affected by six different disease types was utilized. This extensive dataset enhanced the robustness of the DL model, ensuring precise and reliable disease identification.
- The proposed method contributed to maintaining custard apple plant health and productivity while supporting global food security by mitigating potential crop losses and fostering sustainable agricultural practices.

Following this introduction to automated disease detection in custard apples, the remainder of this paper is structured as follows: The “Related Work” section reviews relevant literature, while the “Materials and Methods” section details the dataset and methodological approach. The “Results and Evaluation” section presents the experimental findings and analysis, and the “Conclusion” section summarizes the study’s key contributions.

2. Related Work

Recently, several research groups have begun to apply machine learning, DL and transfer learning (TL) methods to address practical challenges in agriculture. As shown in Table 1, these groups have focused on identifying various diseases that affect both apple trees and their leaves. Diseases studied include cedar rust, scab, black rot, mosaic, grey spot, as well as broader categories of apple diseases such as scab, normal, blotch and rot, bitter rot, black rot, anthracnose and ring rot. In particular, the researchers used image datasets ranging from 110 to 50000 and extensively adapted ResNet, convolutional neural network (CNN) and VggNet to detect apples or apple-related diseases. Classification accuracy (CA) values, calculated on the basis of different class numbers, ranged from 73.70% to 99.50%.

Table 1. Related work on classification of various apple and apple leaf diseases

References	Procedure					
	Class Name	Type	Number of Classes	Number of Images	Model	CA(%)
(Chen et al. 2023)	Cedar rust, scab and healthy	Apple leaf	3	1977	ResNet	97.78
(Sulistyowati et al. 2023)	Scab, multiple disease, rust and healthy	Apple leaf	4	1821	VggNet	92.94
(Chuanlei et al. 2017)	Powdery mildew, mosaic and rust	Apple leaf	3	90	Genetic Algorithm	94.22
(Upadhyay et al. 2024)	Black rot, rust, scab and healthy	Apple leaf	4	9395	ResNet	98.94
(Zhu et al. 2022)	Alternaria blotch, brown spot, gray spot, mosaic and rust	Apple leaf	5	10000	AppleNet	95.90
(Dubey et al. 2016)	Scab, normal, blotch and rot	Apple	4	320	Multi-SVM	95.94
(Zhong et al. 2020)	Serious cedar rust, serious scab, general scab, gray spot, general cedar rust and healthy	Apple	6	2462	DenseNet	93.71
(Yu et al. 2022)	Rust, scab, alternaria leaf spot, alternaria leaf spot and powdery mildew	Apple leaf	5	2516	ResNet50	95.70
(Azgomi et al. 2023)	Scab, bitter rot, black rot, and healthy	Apple	4	110	Artificial Neural Network	73.70
(Singh et al. 2022)	Marsonina coronaria, scab	Apple leaf	2	50000	CNN	99.20
(Zhang et al. 2022)	Healthy, anthrax, ring rot	Apple	3	3336	Multi-scale dual-channel CNN	99.50

(Li et al. 2022)	Alternaria leaf spot, mosaic and rust	Apple leaf	3	450	Modified CNN	94.22
(Hasan et al. 2022)	Scab, black rot and cedar rust	Apple leaf	3	1901	Random Forest	98.63

While the existing literature includes various studies on apples and their leaves, research specifically focused on the detection of custard apple diseases remains relatively limited. In this context, machine learning and DL techniques have been proposed as viable approaches for automated disease detection (Chen et al. 2022; Thangaraj et al. 2001). However, a comprehensive review of the studies conducted shows that there is still room for improvement in this area. Looking at the studies based on custard apples, Wakchaure et al. presented a pioneering prototype device for fruit classification in custard apples using an image processing based approach to detect maturity stages. This device is designed to assess changes in the physical, chemical and imaging characteristics of custard apple fruits. The methodology involves image pre-processing and segmentation, followed by extraction of imaging features, including the relative R, G and B components. The relationship between these imaging features and chemical properties such as Total Soluble Solids (TSS) is also established. The authors used k-means clustering and support vector machine (SVM) algorithms for image classification, implementing model training and classifier codes in Python to achieve the desired results. The results of their study showed a significant correlation between the maturity levels and the values of R, G and TSS. The statistical analysis performed by Wakchaure et al. showed a clear distinction between different maturity levels based on these parameters. The authors achieved 100.00% CA in the classification of custard apple fruit at different stages of maturity (Wakchaure et al. 2024).

Gaikwad et al. approached the task of fruit leaf disease classification by implementing a deep CNN architecture. The focus of their study was on three predominant fruits in the Hyderabad and Karnataka region of Karnataka, India, namely apple, custard apple and guava. In an effort to increase the relevance of their findings to the local agricultural context, they meticulously collected an extensive dataset of 14181 images, including 10 different class labels. To ensure the robustness of their approach, the researchers used three different versions of the dataset, including color, black and white and grey images for experimental purposes. They trained two well-established CNN models, AlexNet and SqueezeNet, on the dataset using identical hyper-parameters. They achieved almost identical recognition CA of 86.80% and 86.60% for color images. This consistency in performance highlights the effectiveness of color images in the classification process and emphasizes their importance in the accurate identification of fruit leaf diseases (Gaikwad et al. 2021). Renugadevi et al. presented an innovative and accurate predictive method for the classification of custard apple leaves using deep CNNs. In their study, an image dataset specifically curated for custard apple leaves

was created and a customized CNN architecture was used for the classification task. The researchers reported a CA of 85.00% in predicting the health status of custard apple leaves, distinguishing between healthy and diseased conditions (Renugadevi et al. 2021). Shilaskar et al. focused on the early detection of mealybugs in custard apples, a critical issue due to the damaging effect these cotton-like insects have on the outer surface of the fruit. In their approach, the researchers used various models, including CNN, Random Forest, Xgboost and SVM, using a carefully collected data set. The system they developed demonstrated the ability to detect mealybugs on green custard apples and effectively classify them as either infected or uninfected (Shilaskar et al. 2023).

In addition to custard apple disease identification, recent studies have emphasized the increasing importance of DL for detecting various plant diseases. Altan et al. investigated the application of capsule networks for bell pepper leaf disease classification, demonstrating that this architecture effectively preserved spatial information and achieved strong accuracy by identifying even small lesions (Altan 2020). Varma et al. performed a comparative evaluation of multiple pre-trained CNN models for mango leaf disease detection, showing that InceptionV3 achieved the highest performance with nearly perfect accuracy, thereby underscoring the effectiveness of transfer learning in plant pathology (Varma et al. 2025). Complementing these findings, Hossen et al. presented a comprehensive review of transfer learning in agriculture, addressing model selection, dataset limitations, implementation challenges, and future research opportunities (Hossen et al. 2025). Collectively, these studies highlight the capability of advanced DL methods for reliable plant disease classification and the crucial role of transfer learning in overcoming data scarcity across agricultural applications.

The study of fruit disease classification addresses major challenges in the agricultural sector. Improving the efficiency of agricultural treatments relies heavily on solutions capable of detecting diseases at an early stage. In this context, the present study presents a novel approach using DL algorithms specifically designed to analyze images and identify plant diseases. The proposed system aims to automatically detect diseases in custard apple plants, a vital source of food for many countries. The use of a comprehensive image dataset (Thite et al. 2024), which includes color images of custard apples and custard apple leaves affected by various diseases, enhances the effectiveness of disease detection. The dataset includes six different classes, namely athracnose, black canker, diplodia rot, leaf spot on fruit, leaf spot on leaf and mealy bug. By using advanced technologies such as DL, this method not only contributes to the early detection of diseases, but also promises to revolutionize the way we approach agricultural challenges, ultimately contributing to global food security.

3. Materials and Methods

3.1. Introduction of the Dataset

This study utilized an image dataset compiled by Thite et al. (2024) from the Nimgaon-Bhogi region of Taluka-Shirur in the Pune district of Maharashtra, India. To ensure dataset diversity and representativeness, images were collected from various custard apple fields, accounting for different growth stages, environmental conditions, and disease symptoms. The dataset encompasses images of custard apple fruits and leaves affected by six distinct diseases: anthracnose, black canker, diplodia rot, leaf spot on fruit, leaf spot on leaf, and mealybug infestation. The dataset acquisition process is illustrated in Figure 1.

Images were captured using the rear camera of a Samsung F23 5G and stored in JPG format, subsequently resized to a resolution of 1024×768 pixels. High-resolution images of custard apple leaves were taken from multiple angles using high-quality cameras, ensuring comprehensive coverage of both fruit and leaf surfaces. The dataset collection process, outlined in Figure 2, consisted of three stages. First, field visits were conducted to capture images of custard apple diseases under natural daylight conditions. In the second stage, image preprocessing was performed to filter, enhance, and standardize the collected images, ensuring consistency in the dataset. Finally, in the third stage, disease classification was carried out, where images were systematically labeled with unique identifiers corresponding to specific disease categories.

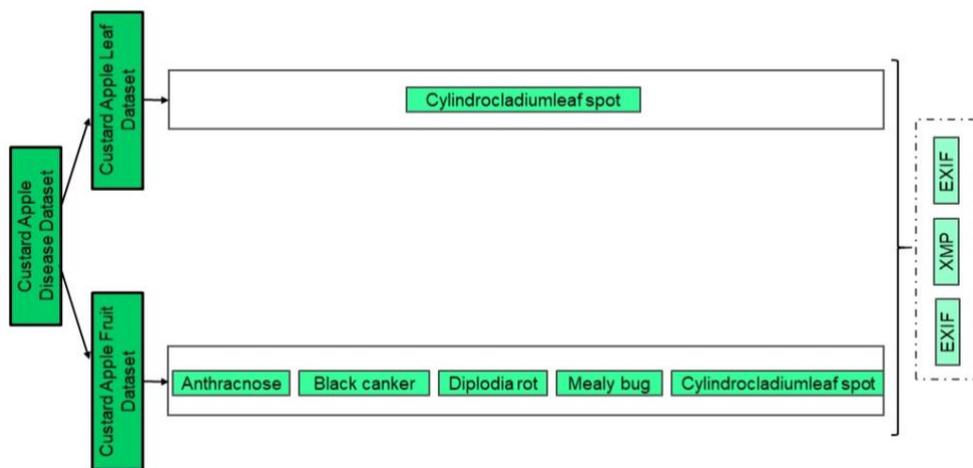


Figure 1. The dataset flowchart of custard apple disease (Thite et al. 2024)

India's apple orchards provided the dataset. As shown in Table 2, it contains 8226 color photographs. The dataset contains six classes of apple diseases, including classes for *Cylindrocladium* leaf spot, black canker, mealy bug, diplodia rot and anthracnose. In addition, Figure 2 shows

illustrative examples of the texture and color patterns associated with each apple disease. The photographs in Figure 2 were randomly selected from each class.

Table 2. Corresponding relationship between disease category and label

Class Name	Custard apple disease dataset		
	Abnormality type	Total images	Classes Name
Diplodia rot	Fruit	1645	3
Black canker	Fruit	1780	2
Mealy bug	Fruit	1604	6
Anthracnose	Fruit	1075	1
Cylindrocladium leaf spot	Fruit	867	4
Cylindrocladium leaf spot	Leaf	1255	5
Total image		8226	

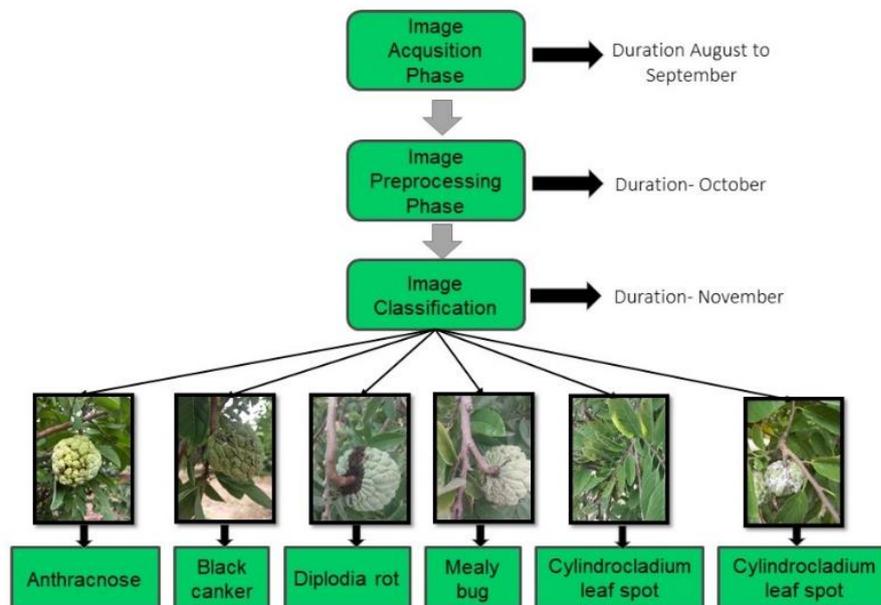


Figure 2. Custard apple phase of data collecting (Thite et al. 2024)

3.2. Methods

The structural configuration of CNN is based on DL data. CNNs have shown robust performance in tasks such as image classification and object detection (Liu et al. 2024; Gürsoy et al. 2022). DL encompasses several subfields, including recurrent neural networks such as long short-term memory and convolutional neural networks. Using training data, these neural networks have the ability to classify photographs into different classes. Neural networks with layers of max-pooling, activation units, convolutional layers and fully connected layers undergo a learning process based on the data within their respective layers (Ahila Priyadarshini et al. 2019; Korkut et al. 2024). Training

deep neural networks on large datasets can take many days to weeks. To mitigate this, pre-trained models are used to reduce errors and training time. The use of pre-trained models involves the recycling of weights between layers, allowing adaptation to the specific task at hand. These pre-trained models can be used in whole or in part to build a new neural network model. The conservation of pre-trained model weights can be ensured by freezing them. In our study, ResNet is used as a pre-trained model. Figure 3 illustrates the overall architecture of the CNNs using the proposed method, trained by ResNet on images representing six classes of apple diseases.

The computational complexity of the proposed framework was evaluated to assess its efficiency. Feature extraction and classification using ResNet with transfer learning has a complexity of $O(n \cdot d)$, where n denotes the number of images and d represents the dimensionality of extracted features. For the current dataset of 8226 images and feature dimensionality of 2048, the approximate number of operations per epoch is $n \cdot d \approx 16.8$ million, confirming that the model is computationally feasible. For 5-fold CVM, the ResNet weights were re-initialized at the beginning of each fold to ensure independent training. Considering both the Big-O notation and the dataset specifics, the ResNet-based system maintained practical efficiency and completed all experiments successfully on a 16 GB, 2.92 GHz Intel Core i7 workstation within reasonable time limits. All implementations of the ResNet model were carried out using the MATLAB DL Toolbox and associated pretrained model libraries, ensuring reliable integration of residual network architectures for transfer learning.

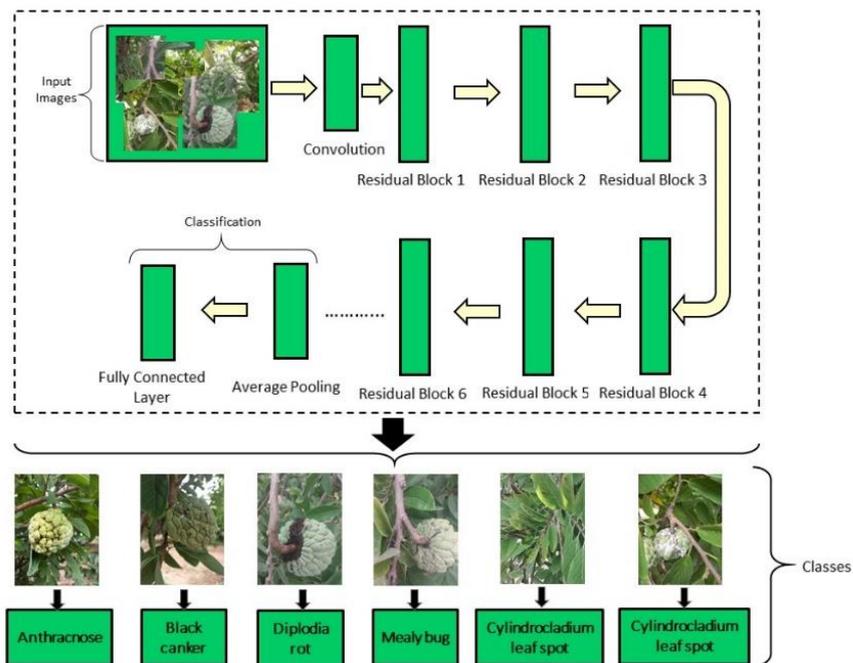


Figure 3. Overview of the proposed algorithm used to classify custard apple diseases

3.2.1. ResNet

ResNet was developed as a solution to the challenges posed by increasing network depth, which tends to reduce system performance due to network complexity (Tanwar et al. 2023). ResNet consists of multiple residual blocks with interconnections between layers. The model is available in variations of 50, 101 and 152 layers and was introduced by He et al. under the name ResNet or deep residual network (Sun et al. 2023). This innovative design aimed to overcome the time-consuming nature and layer limitations associated with DL training. Skip connections increase network depth without degrading performance. However, despite this complexity, the ResNet model maintains a performance advantage over other architectural models as its design becomes more complex. There is also a reduction in computational requirements and an improvement in network training capabilities. The ResNet model uses skip connections at two to three levels and incorporates ReLU and batch normalization between designs. He and colleagues demonstrated that the ResNet model outperformed other models in image classification, demonstrating its effectiveness in extracting valuable image information. Residual learning is applied across multiple levels, and Equation 1 defines a residual block within the ResNet framework. In Equation 1, the residual map represents the f function, a is the input layer and b is the output layer. If the dimensions of the input and output data are the same, a residual block can be completed on ResNet. Additionally, the ResNet architecture used in this study consists of five layers, including the fully connected layer, convolutional layers, max-pooling layers, dropouts and data augmentation.

$$b = f(a, W + a) \quad (1)$$

3.2.2. Evaluation Metrics

Classification is the process of grouping data according to certain criteria and is widely used in fields such as machine learning (Vijayaganth et al. 2024). The accuracy measure, which is often used in research, is widely used to calculate the classification accuracy of classifiers. In this study, metrics such as CA, F1 score, recall and precision values, which are commonly used to measure and analyze the performance of classifiers, were used by obtaining them from the confusion matrix. The F1 score provides a balance between precision and sensitivity and is calculated as the ratio of true positives to false positives and false negatives (Ergün et al. 2020). Precision refers to the ratio of true positives to total positive predictions, while sensitivity refers to the ratio of true positives to total true positives. These metrics play an important role in evaluating performance metrics such as model accuracy, reducing false positives while increasing true positives. Confusion matrices are an important tool for

visualizing and improving model performance (Ergün 2024b). An example of a multi-class confusion matrix is shown in Table 3. This confusion matrix shows the correct predictions of the model on the diagonal and places incorrect predictions in the appropriate cells. For example, the values in the upper left corner of the matrix indicate that images belonging to class N_1 were correctly classified, while the values in the upper left corner of the matrix indicate the number of images that belonged to class N_1 but were misclassified as N_2 , N_3 or N_4 . The formulas for the CA, recall, precision and F1 scores calculated from the table are given in Equations 2, 3, 4 and 5 (Ergün 2025), respectively.

Table 3. A confusion matrix for many classes

Confusion Matrix		Predicted Classes			
		N_1	N_2	...	N_i
Actual Classes	N_1	$N_{1,1}$	BK	...	$N_{1,i}$
	N_2	BC	AT	...	BC

	N_i	$N_{i,1}$	BK	...	$N_{i,i}$

$$CA = \frac{\sum_{j=1}^i AT(N_j)}{\sum_{j=1}^i \sum_{n=1}^i N_{j,n}} \times 100 \quad (2)$$

$$\text{Recall} = \frac{\sum_{j=1}^i AT(N_j)}{\sum_{j=1}^i BC(N_j)} \times 100 \quad (3)$$

$$\text{Precision} = \frac{\sum_{j=1}^i AT(N_j)}{\sum_{j=1}^i BK(N_j)} \times 100 \quad (4)$$

$$F1 = 2x \frac{\text{Recall} \times \text{Precision}}{\text{Recall} + \text{Precision}} \quad (5)$$

To evaluate the proposed technique, we used the k-fold cross validation method (CVM). In n iterations, CVM was used to select a model for training the learning problem. Our study focuses on the 5-fold CVM. An advantage of using multiple k-fold approaches in our studies is that we avoid bias and overfitting problems. CVM reduces the generalization of errors (Luque et al. 2019). CVM examines model performance on different data sets to achieve a fair evaluation. For the 5-fold CVM, the data is randomly divided into k subgroups. k-1 is used for training, while the other subset is used for testing. This process continued until all samples had been tested.

4. Results of Evaluation

TL is an important technique that allows a pre-trained CNN model to be used in a new visual task. In this way, general features and patterns learned by models trained on large datasets can be evaluated in different tasks. A pre-trained CNN model is typically trained on a large and diverse dataset and learns general features (Ma et al. 2020). ResNet, one of these DL models trained on large

datasets, was used in this study. ResNet is known for its multi-layer structure and depth features and performs well on large datasets. In order to use the model, the size of the images was converted to a format of 224×224 pixels. This size reduces processing time and is also a standardized practical size for training deep neural networks. In addition, a 5-fold CVM was performed to evaluate the performance of the model. During this validation process, the data was run through the verification phase and then all images were resized and processed to 224×224 . This allowed the overall performance of the model to be evaluated more reliably, as every data point in the dataset was used in both the training and validation phases. In this study, the use of GoogleNet DL models with TL and their performance evaluation were provided to compare ResNet and its performance.

4.1. Evaluation of the hyper parameters in comparison

The dataset in this study was initially evaluated using both ResNet and GoogleNet to identify the optimal recognition model, with hyperparameter values determined based on the average accuracy obtained on the test set. The learning rate controlled the speed at which network weights were updated, and appropriate tuning ensured rapid convergence of the objective function to a local minimum. For the 5-fold CVM approach, the ResNet model weights were re-initialized at the start of each fold, guaranteeing that each fold was trained independently without influence from the previous folds, thereby providing an unbiased assessment of model performance.

In this article, ResNet and GoogleNet are trained with learning rates of 0.0001 and 0.00001 respectively. The speed and performance of the model is also affected by the batch size. In this work, comparative tests were carried out using batch sizes of 8 and 16. The Adam optimization technique was selected for this study after a thorough evaluation of training time and hardware performance. Its minimal memory requirements and good computational efficiency made it the preferred choice. In addition, the number of epochs is a crucial parameter for the training phase. The optimal weight values of the model are determined by repeating the epoch at each training step; in this case, a value of 20 was found to be favored. The dataset is of two types: 80% of the photos are training images and 20% are test images. The statistics from the custard apple dataset are also shown in Table 4.

Table 4. Summary of the custard apple dataset training image and test image

Class Name	Custard apple disease dataset		
	Total images	Image of training	Image of testing
Anthraco nose	1075	860	215
Black canker	1780	1424	356
Diplodia rot	1645	1316	329
Leaf spot fruit	867	693	174
Leaf spot leaf	1255	1004	251
Mealy bug	1604	1283	321
Total image	8226	6580	1646

4.2. Comparative analysis of performance of different models

We generated and examined the confusion matrix for each fold in our study to do a thorough analysis and assess the classification performance of our model. This made it possible for us to extract more assessment measures that offer a more complex picture of the model's effectiveness. A thorough examination procedure produced the confusion matrix data, which show the true positives, false positives, true negatives, and false negatives for each class.

In particular, we used the ResNet architecture, a well-known DL framework renowned for its reliable performance in image classification tasks, in a 5-fold CVM. Two distinct batch sizes, 8 and 16, were used in the experimental setting to evaluate the model's sensitivity to changes in the processing of training data. A detailed analysis of the results of the confusion matrix for different batch sizes is given in Figures 4 and 5. Table 5 presents a summary of the detection results obtained from all five folds. The high accuracy values in the detection of custard apple diseases demonstrate the effectiveness of the proposed model during the detection phase. Specifically, for batch size 16, a CA of 99.94% was obtained for Fold 1, while Folds 2, 3, and 4 achieved CA values of 99.76%, 99.70%, and 99.70%, respectively. Fold 5 yielded a CA of 99.57%. Overall, the 5-fold CVM approach achieved an overall CA of 99.73% for batch size 16. Similarly, for batch size 8, Fold 1 achieved a CA of 99.94%, while Folds 2 and 4 yielded 99.76%. In addition, Folds 3 and 5 achieved CA values of 99.70%. The overall CA obtained with batch size 8 was 99.77%, confirming the stability and robustness of the proposed model across different batch configurations.

Confusion Matrix		Predicted Classes					
		Anthracnose	Black canker	Diplodia rot	Leaf spot fruit	Leaf spot leaf	Mealy bug
Actual Classes	Anthracnose	214	0	0	0	0	1
	Black canker	0	356	0	0	0	0
	Diplodia rot	0	0	329	0	0	0
	Leaf spot fruit	0	0	0	174	0	0
	Leaf spot leaf	0	0	0	0	251	0
	Mealy bug	0	0	0	0	0	321

a)

Confusion Matrix		Predicted Classes					
		Anthracnose	Black canker	Diplodia rot	Leaf spot fruit	Leaf spot leaf	Mealy bug
Actual Classes	Anthracnose	215	0	0	0	0	0
	Black canker	0	356	0	0	0	0
	Diplodia rot	0	1	328	0	0	0
	Leaf spot fruit	0	1	0	173	0	0
	Leaf spot leaf	0	1	0	0	250	0
	Mealy bug	0	0	0	1	0	319

b)

Confusion Matrix		Predicted Classes					
		Anthracnose	Black canker	Diplodia rot	Leaf spot fruit	Leaf spot leaf	Mealy bug
Actual Classes	Anthracnose	214	0	0	0	0	1
	Black canker	0	354	0	1	0	1
	Diplodia rot	0	0	329	0	0	0
	Leaf spot fruit	0	0	0	172	0	1
	Leaf spot leaf	0	0	0	0	251	0
	Mealy bug	0	1	0	0	0	320

c)

Confusion Matrix		Predicted Classes					
		Anthracnose	Black canker	Diplodia rot	Leaf spot fruit	Leaf spot leaf	Mealy bug
Actual Classes	Anthracnose	213	0	0	0	0	2
	Black canker	0	356	0	0	0	0
	Diplodia rot	0	0	329	0	0	0
	Leaf spot fruit	0	0	0	173	0	0
	Leaf spot leaf	0	0	0	0	251	0
	Mealy bug	0	0	1	0	1	319

d)

Confusion Matrix		Predicted Classes					
		Anthracnose	Black canker	Diplodia rot	Leaf spot fruit	Leaf spot leaf	Mealy bug
Actual Classes	Anthracnose	214	0	0	0	0	1
	Black canker	1	355	0	0	0	0
	Diplodia rot	0	0	329	0	0	0
	Leaf spot fruit	0	1	0	172	0	1
	Leaf spot leaf	0	0	0	0	251	0
	Mealy bug	0	1	0	0	0	320

e)

Figure 4. Confusion matrix result of a) 1st, b) 2nd, c) 3rd, d) 4th and e) 5th fold for ResNet for batch sizes for 8

Confusion Matrix		Predicted Classes					
		Anthracnose	Black canker	Diplodia rot	Leaf spot fruit	Leaf spot leaf	Mealy bug
Actual Classes	Anthracnose	214	0	0	0	0	1
	Black canker	0	356	0	0	0	0
	Diplodia rot	0	0	329	0	0	0
	Leaf spot fruit	0	0	0	174	0	0
	Leaf spot leaf	0	0	0	0	251	0
	Mealy bug	0	0	0	0	0	321

a)

Confusion Matrix		Predicted Classes					
		Anthracnose	Black canker	Diplodia rot	Leaf spot fruit	Leaf spot leaf	Mealy bug
Actual Classes	Anthracnose	214	0	0	1	0	0
	Black canker	0	356	0	0	0	0
	Diplodia rot	0	0	328	0	0	1
	Leaf spot fruit	0	1	0	173	0	0
	Leaf spot leaf	0	0	0	0	251	0
	Mealy bug	0	0	0	1	0	319

b)

Confusion Matrix		Predicted Classes					
		Anthracnose	Black canker	Diplodia rot	Leaf spot fruit	Leaf spot leaf	Mealy bug
Actual Classes	Anthracnose	213	0	0	0	0	2
	Black canker	0	355	0	1	0	0
	Diplodia rot	0	0	329	0	0	0
	Leaf spot fruit	0	0	0	172	0	1
	Leaf spot leaf	0	0	0	0	251	0
	Mealy bug	0	1	0	0	0	320

c)

Confusion Matrix		Predicted Classes					
		Anthracnose	Black canker	Diplodia rot	Leaf spot fruit	Leaf spot leaf	Mealy bug
Actual Classes	Anthracnose	212	0	0	0	0	3
	Black canker	0	356	0	0	0	0
	Diplodia rot	0	0	329	0	0	0
	Leaf spot fruit	0	0	0	173	0	0
	Leaf spot leaf	0	0	0	0	251	0
	Mealy bug	0	1	0	0	1	319

d)

Confusion Matrix		Predicted Classes					
		Anthracnose	Black canker	Diplodia rot	Leaf spot fruit	Leaf spot leaf	Mealy bug
Actual Classes	Anthracnose	214	0	0	0	0	1
	Black canker	1	355	0	0	0	0
	Diplodia rot	0	0	327	2	0	0
	Leaf spot fruit	0	1	0	171	0	2
	Leaf spot leaf	0	0	0	0	251	0
	Mealy bug	0	0	0	0	0	321

e)

Figure 5. Confusion matrix result of a) 1st, b) 2nd, c) 3rd, d) 4th and e) 5th fold for ResNet for batch sizes for 16

Table 5. Detection CA of individual folds in the 5-fold CVM process each batch size

Fold Number	Number of images	Batch sizes for 8			Batch sizes for 16			
		Detected number of images	Missed number of images	CA(%)	Detected number of images	Missed number of images	CA(%)	
Fold 1	1646	1645	1	99.94	1645	1	99.94	
Fold 2	1645	1641	4	99.76	1641	4	99.76	
Fold 3	1645	1640	5	99.70	1640	5	99.70	
Fold 4	1645	1641	4	99.76	1640	5	99.70	
Fold 5	1646	1641	5	99.70	1639	7	99.57	
Total				99.77	Total			99.73

In Table 6, we presented the class-wise evaluation metrics, including precision, recall, F1-score, and CA, for the ResNet architecture under two different batch sizes 8 and 16. The results demonstrated that the model achieved highly consistent and robust performance across all disease categories, with only marginal fluctuations between the two batch sizes. For batch size 16, the Leaf spot leaf class attained the highest classification accuracy with a CA of 99.99%, followed closely by Diplodia rot with 99.96%, reflecting the model's strong capacity to distinguish these categories. Conversely, the lowest CA value was observed in the Mealy bug class with 99.84% for batch size 8, although this still indicates a highly reliable prediction. Other classes, such as Diplodia rot and Leaf spot leaf, consistently achieved near-perfect metrics across both configurations, highlighting the discriminative power of ResNet in handling subtle inter-class differences.

Table 6. Average performance of ResNet for each class against the others for each batch sizes

Testing performance	Evaluation Metrics (%)							
	Batch sizes for 8				Batch sizes for 16			
	Precision	Recall	F1	CA	Precision	Recall	F1	CA
Anthracnose	99.91	99.53	99.72	99.93	99.91	99.26	99.58	99.89
Black canker	99.66	99.83	99.75	99.89	99.78	99.89	99.83	99.93
Diplodia rot	99.94	99.94	99.94	99.98	100.00	99.82	99.91	99.96
Leaf spot fruit	99.77	99.54	99.65	99.93	99.42	99.42	99.42	99.88
Leaf spot leaf	99.92	99.92	99.92	99.98	99.92	100.00	99.96	99.99
Mealy bug	99.50	99.69	99.60	99.84	99.32	99.75	99.53	99.82

In addition to the class-wise metrics presented in Table 6, we further evaluated the ResNet model using ROC curves and the corresponding AUC values for multi-class classification with a One-vs-Rest (OvR) approach. To ensure statistical robustness, we applied a bootstrap method with 1000 iterations to calculate 95% confidence intervals for the AUC of each disease class. The results, summarized in Table 7, indicate that the model maintains exceptional discriminative ability across all six classes, with AUC values ranging from 0.995 to 0.999 and narrow confidence intervals, confirming the reliability of the predictions. Incorporating 95% confidence intervals provides a

rigorous assessment of model performance by accounting for variability and potential sampling bias.

Table 7. Multi-class AUC analysis with 95% confidence intervals for batch size 8

Class	Batch sizes of 8	
	AUC	95% CI
Anthraco nose	0.998	[0.996, 0.999]
Black canker	0.997	[0.995, 0.998]
Diplodia rot	0.999	[0.998, 0.999]
Leaf spot fruit	0.996	[0.994, 0.998]
Leaf spot leaf	0.998	[0.996, 0.999]
Mealy bug	0.995	[0.993, 0.997]

In this study, the dataset was also classified with GoogleNet to show the effectiveness of the results calculated with ResNet. The classification metrics are shown in the Figure 6 for each architecture and batch size. As can be seen from the table, the best result belongs to the ResNet architecture with a CA of 99.77% for batch size of 8. These results underscore the effectiveness of the proposed method for the 6-class custard apple dataset.

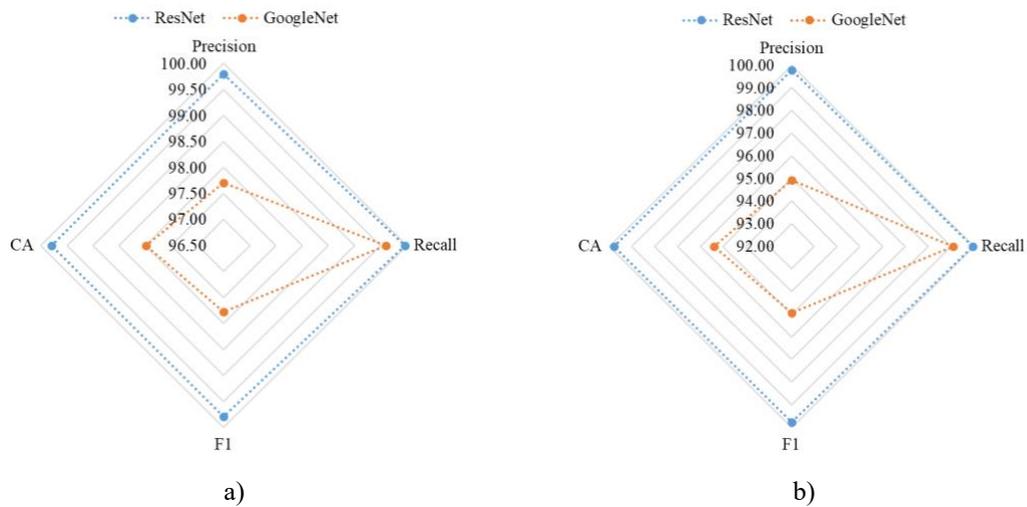


Figure 6. ResNet and GoogleNet classification results a) batch sizes of 8, b) batch sizes of 16

5. Discussion

The preference for ResNet over other pre-trained architectures stems from its unique ability to address the vanishing gradient problem through residual connections, which enable effective training of deeper networks without performance degradation. While models such as VggNet19 and InceptionV3 are well-established and have shown success in plant disease classification, they often struggle with either computational complexity or limitations in capturing hierarchical features across very deep layers. Similarly, DenseNet and InceptionResNetV2 provide strong feature reuse and

multi-scale analysis, but at the expense of significantly higher memory and computational demands, which are less suitable for large-scale agricultural datasets. MobileNet and Xception, on the other hand, are optimized for lightweight applications, making them efficient but less robust in extracting fine-grained features from complex and high-variability images such as those of custard apple diseases. In contrast, ResNet achieves an optimal balance between depth, accuracy, and computational efficiency, allowing it to capture intricate disease patterns while maintaining generalizability across different conditions. These advantages explain why ResNet delivered the highest classification performance in this study and justify its selection as the most suitable architecture for the proposed framework.

Table 8 provides an overview of existing approaches for custard apple disease detection, illustrating the variety of datasets, number of classes, and models applied in prior studies. Previous methods, including traditional machine learning classifiers and shallow CNN architectures, generally achieved lower accuracy or were limited to fewer disease categories. In contrast, the proposed ResNet-based approach demonstrates higher performance, effectively handling six disease classes and achieving a classification accuracy of 99.77%. This comparison highlights the advantage of deep residual networks in capturing complex features and reinforces the robustness and applicability of the proposed method for automated disease identification in custard apple crops.

Table 8. Overview of existing approaches for custard apple

References	Procedure					
	Approaches	Type	Number of Classes	Number of Images	Model	CA(%)
(Wakchaure et al. 2024)	Maturity stages detection	Custard apple	5	2275	k-means clustering and SVM	100.00
(Gaikwad et al. 2021)	Fungi affected fruit leaf disease	Custard apple	10	14181	AlexNet and SqueezeNet	86.80
(Renugadevi et al. 2021)	Classification of custard apple leaves	Custard apple	2	200	CNN	85.00
(Shilaskar et al. 2023)	Detection of mealybug infection	Custard apple	2	1500	CNN, Random Forest, Xgboost and SVM	80.00
Proposed Method	Identification of custard apple diseases	Custard apple	6	8226	ResNet	99.77

6. Conclusion

Agriculture plays a pivotal role in the global economy, not only serving as the foundation for economic growth but also fulfilling the essential need for food security. As the global population

continues to rise and future food shortages are anticipated, the significance of this sector becomes increasingly evident. Agriculture is accountable for approximately 30-40% of global crop losses, which are primarily driven by factors such as plant and fruit diseases. This article focuses on the detection of diseases in custard apple crops, a crucial area of agricultural research. These diseases can lead to the production of mycotoxins—harmful compounds that pose significant risks to both human and animal health by contaminating food and feed sources, potentially causing illness or even death. Thus, the development of an efficient system for the early detection of such diseases in crops is of paramount importance.

The study utilized the Custard Apple Disease dataset, documented by Thite et al., to detect and classify diseases in custard apple crops. The research employed the ResNet model, a CNN-based architecture, to achieve high accuracy in disease identification. The analysis yielded an impressive accuracy rate of 99.77%, demonstrating the potential of DL models for precise disease detection in agriculture. This result marks a significant step forward in enhancing early detection and accurate classification of diseases affecting custard apple crops. In conclusion, this research highlights the potential impact of technological advancements in agriculture, particularly in disease detection. By reducing crop losses through early identification of diseases, such developments can significantly contribute to improving food security and preventing global food crises. Continued exploration and innovation in this domain will be crucial for ensuring the future sustainability of agriculture, offering promising solutions to the challenges faced by the sector.

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Availability of Data and Materials: The experimental datasets used in this study are publicly accessible and can be found at the following link: <https://data.mendeley.com/datasets/jtgh2885yf/2>.

Authors' Contributions

E. Ergün conceptualized the study, designed the methodology, implemented the software, performed data analysis and validation, and wrote the original draft. H. Okumuş contributed significantly during the revision process by providing critical feedback, refining the analysis and discussion, and enhancing the overall clarity and quality of the manuscript.

Statement of Conflicts of Interest

There is no conflict of interest between the authors.

Statement of Research and Publication Ethics

The author declares that this study complies with Research and Publication Ethics.

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