

## ConvNeXt-Based Deep Feature Engineering and Machine Learning Approach with Explainable Artificial Intelligence for Guava Fruit Disease Classification

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### Abstract

Guava (*Psidium guajava*) is an important part of tropical agriculture with its high nutritional value and economic return. However, diseases in this fruit cause serious losses in productivity and product quality. The manual and subjective nature of traditional diagnostic methods is insufficient to meet the speed and accuracy requirements of modern agriculture. Therefore, the aim of the study is to identify guava fruit using a model that combines ConvNeXt and machine learning. In this study, ConvNeXt-Tiny, ConvNeXt-Small, ConvNeXt-Base, ConvNeXt-Large and ConvNeXt-XLarge architectures were used as feature extractors. The features extracted from these variants were classified using Support Vector Machines (SVM), Random Forest (RF) and Logistic Regression (LR) algorithms. In addition, different numbers of features (50, 100 and 200) were selected from each ConvNeXt variant by SelectKBest method and new feature vectors were created by combining these features. The classification performances of these feature vectors were also evaluated with SVM, RF and LR. According to the experimental results, the ConvNeXt-XLarge-SVM model achieved an accuracy of 0.997. The CS200-ConvNeXt-SVM model after feature selection and feature fusion achieved

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1.000 in all performance metrics. Contextual Importance and Utility (CIU), one of the explainable artificial intelligence methods, was used to identify the features that contribute to the decision mechanism of the proposed model. The contributions of the features determined by the CIU method for the CS200-ConvNeXt-SVM model were analyzed on a class basis, and the top 10 features with the highest contribution were identified for each class. It was found that the F570 feature contributed the most in the Healthy guava class, the F625 feature contributed the most in the Anthracnose class, and the F626 feature contributed the most in the Fruit fly class. In addition, evaluations were conducted across different datasets to assess the generalization performance of the proposed model. The findings suggest that combining ConvNeXt variants and machine learning algorithms is an effective approach for guava fruit disease classification.

## 1. Introduction

The ongoing growth of the world population, along with the prediction that food demand will double by 2050, underscores the importance of sustainable, efficient agricultural practices. Therefore, increasing food demand necessitates strategies to maintain product quality and productivity (Hunter et al., 2017; Mirvakhabova et al., 2018). Agricultural production, which extends beyond meeting basic nutritional requirements to serve as a significant economic driver, includes guava (*Psidium guajava*) as a strategically important crop due to its high nutritional value, industrial versatility, and substantial value-added potential (Joseph and Priya, 2011). The global guava market is expected to reach billions of dollars in volume by 2033. This market continues to increase its commercial value every day, driven by its steady growth trend (Ahmed et al., 2025). Guava fruit, which is cultivated in tropical and subtropical climates, is eaten fresh because of its nutritional value and is also utilized for making fruit juice and jam (Amin et al., 2024; Kılıcı and Koklu, 2024). Guava fruit, which is a super fruit because of its four times more vitamin C content than that of orange and its antioxidant properties, is attacked by a variety of diseases, resulting in a considerable loss of yield (Paramesha et al., 2025).

In traditional agricultural practices, disease diagnosis largely relies on farmers or agrarian experts physically observing the field with the naked eye. However, this manual monitoring process, which requires expertise and relies on human factors, falls short of meeting the speed and accuracy requirements of modern agriculture due to its limited applicability across large areas, its time-consuming nature, and its subjectivity, which depends on the observer's experience (Ahmed et al., 2025). Furthermore, it leads to incorrect or delayed diagnoses in the early stages of diseases with similar visual symptoms, triggering irreversible yield losses. This situation not only increases production costs

and environmental pollution but also brings serious commercial obstacles, such as product rejection in export markets due to pesticide residues (Arnal Barbedo, 2013; Paramesha et al., 2025).

The need to improve the accuracy and speed of diagnosis has led to the prominence of digital technologies in agricultural disease management, thus increasing the popularity of Precision Agriculture and Smart Farming practices (Mohanty et al., 2016). In this regard, Convolutional Neural Networks (CNNs), which are deep learning (DL) models, have proven to be more effective in fruit disease image classification than conventional image processing techniques because of their capability to automatically and efficiently extract features from images (Krizhevsky et al., 2012). Studies on guava have typically used well-known classical CNN architectures such as VGGNet, GoogLeNet, ResNet, DenseNet, and EfficientNet, which have achieved high classification performance (Doutoum et al., 2023; Kaur et al., 2024; Mostafa et al., 2022). However, due to its superior performance, the ConvNeXt architecture has recently been widely adopted across many fields, including agriculture (Kanimalar and Karthikeyan, 2025; KP and Gowrishankar, 2023).

ConvNeXt is a DL model that unifies the structural efficiency of CNN-based architectures and the powerful representation learning of Transformer-based architectures. The ConvNeXt model is available at different scales, including Tiny, Small, Base, Large, and XLarge. The main difference between these scales is their depth and capacity (Liu et al., 2022). This allows ConvNeXt to be easily adapted to different datasets and computational requirements. However, end-to-end training of ConvNeXt architectures may increase the risk of overfitting in agricultural datasets due to high computational costs and the need for large-scale labeled data. Therefore, the classification of features extracted from ConvNeXt architectures using machine learning (ML) algorithms is widely used (An et al., 2024; Gao et al., 2023; Solmaz and Tasci, 2025).

The aim of this study is to classify the diseases in guava fruit using an approach that combines ConvNeXt variants and ML algorithms. This present study used a publicly available dataset containing the classes Anthracnose, Fruit Flies, and Healthy. The features were extracted using the dataset, where the ConvNeXt-Tiny, ConvNeXt-Small, ConvNeXt-Base, ConvNeXt-Large, and ConvNeXt-XLarge architectures were utilized, followed by classification using the Support Vector Machine (SVM), Random Forest (RF), and Logistic Regression (LR) algorithms. Moreover, the features extracted using the ConvNeXt variants were also selected using the SelectKBest method. The selected features were combined based on their number, and feature vectors

of varying sizes were created. These vectors were evaluated using SVM, RF, and LR classifiers. Furthermore, to increase transparency into the decision-making mechanism of the high-performing model, an explainable artificial intelligence (XAI) analysis was conducted using the Contextual Importance and Utility (CIU) method. In addition, the behavior of the proposed model on different datasets was also examined. The main contributions of this study to the literature are summarized below:

(i) This study presented an approach for classifying guava fruit diseases using different scales (Tiny, Small, Base, Large, and XLarge) of the ConvNeXt architecture and evaluating the obtained features using ML algorithms.

(ii) Using guava fruit, 50, 100, and 200-dimensional feature vectors were generated from features obtained from ConvNeXt architectures by applying the SelectKBest method, and the effect of these vectors on the performance of ML algorithms was investigated.

(iii) To increase the transparency of the model showing the high performance, a contextual analysis of the decision mechanism was performed using the CIU method.

(iv) The proposed model was evaluated on different datasets to demonstrate its generalization capability.

## **2. Related Work**

The earliest approaches in the literature for detecting guava diseases rely on basic image processing techniques and classical ML algorithms. The main characteristic of studies during this period is that extracting meaningful information from raw images relies on handcrafted features that require human intervention and domain knowledge. For example, Almutiry et al. (2021) classified features extracted using Local Binary Pattern (LBP) and Principal Component Analysis (PCA) with a cubic-SVM model, achieving 98.6% accuracy. Similarly, Almadhor et al. (2021) achieved 99% accuracy using LBP and Bagged Trees. Asim et al. (2023) classified tissue features extracted from guava leaves using the Instant Base Identifier model, achieving an accuracy of 87.125%.

On the other hand, researchers preferred CNN models to overcome the limitations of hand-crafted features. In this context, AlexNet, DenseNet, and ResNet architectures were widely used. Mostafa et al. (2022) classified guava diseases using AlexNet, SqueezeNet, GoogLeNet, ResNet-50, and ResNet-101, achieving the highest accuracy of 97.74% with ResNet-101. Similarly, Tewari et al. (2024) achieved 99% accuracy with the DenseNet169

model on a dataset with four disease classes. Hashan et al. (2024) achieved 93% accuracy using the AlexNet model on a dataset of 612 images. Kaur et al. (2024) reported that, when using Adam optimization with their DenseNet-based model, they achieved 98.76% accuracy.

The goal of disease detection systems is to integrate this technology into easily accessible mobile devices or drone systems with limited processor and battery capacity. In this context, lightweight models that balance parameter count and accuracy stand out for guava damage classification. Doutoum et al. (2023) achieved 94.93% accuracy in their study classifying guava leaf diseases using the EfficientNet-B3 model. In another study, Nath Nandi et al. (2022) reduced the size of the GoogleNet model to 0.143 MB using model quantization techniques and achieved approximately 97% accuracy. Similarly, Mustak Un Nobi et al. (2023) achieved 98% accuracy with their proposed MobileNet-based model. They also evaluated the model's robustness using XAI, employing Grad-CAM. On the other hand, combining the powerful feature extraction capabilities of CNN models with ML algorithms, Kılıcı and Koklu (2024) classified features extracted using SqueezeNet with the Gradient Boosting algorithm, achieving an accuracy of 95.6% with their proposed model. In another study, Kılıcı and Koklu (2025) combined InceptionV3 with an SVM and achieved 99.74% accuracy with their proposed model.

These studies in the field of guava fruit and leaf disease classification have demonstrated high accuracy with known CNN architectures. However, modern architectural structures such as ConvNeXt have not been sufficiently investigated for the classification of these diseases in the current literature. Furthermore, explainability analysis of which features the model's decision processes are based on has been largely neglected. Therefore, the primary motivation of this study is to extract features of diseases observed in guava fruit using ConvNeXt-based architectures, classify these features using ML, and evaluate the features that affect the model's performance using XAI.

### **3. Materials and Methods**

#### **3.1. Dataset Details**

This study used the Guava Disease Dataset downloaded from the Mendeley Data platform. This dataset consists of three classes such as Anthracnose, Fruit Flies, and Healthy guava fruit. The images in the dataset were captured in July in orchards in the cities of Rajshahi and Pabna, Bangladesh, and were labeled and verified by a plant pathologist. Furthermore, all images are 512 × 512 pixels in size and in PNG format. Preprocessing techniques such as unsharp masking and Contrast-Limited Adaptive Histogram Equalization

were applied to improve the image quality of the Guava Disease Dataset. This dataset, consisting of 3784 images, has been divided into training, validation, and test sets at ratios of 70%, 20%, and 10%, respectively (Amin et al., 2024). In this study, the existing data division was preserved, and no re-division process was applied. All images in the dataset were resized to  $224 \times 224$ . The distribution of the number of images per class in the dataset is shown in Table 1.

*Table 1. Distribution of images across classes in the Guava Disease Dataset*

Class	Training set	Validation set	Test set
Anthraxnose	1080	308	156
Fruit Flies	918	262	132
Healthy Fruits	649	185	94
Total number of images	2647	755	382

## 3.2. ConvNeXt-Based Deep Feature Extraction and Classification

### 3.2.1. ConvNeXt architecture

ConvNeXt, proposed by Liu et al. (2022), is a CNN architecture designed based on the principles of Vision Transformer (ViT) architectures. In the ConvNeXt architecture,  $7 \times 7$  depthwise convolutions, Layer Normalization, the GELU activation function, and inverted bottleneck structures are used instead of the small-kernel convolutions commonly used in classical CNNs. Furthermore, some design elements from the ResNet architecture have been simplified, with layer normalization preferred over batch normalization. These architectural adjustments have both increased ConvNeXt's training efficiency and strengthened its generalizability across different scales (Liu et al., 2022; Noda and Hashimoto, 2025).

Depending on resource constraints, the ConvNeXt architecture has different variants according to model capacity: Tiny, Small, Base, Large and XLarge (Liu et al., 2022). In scenarios where hardware capacity is limited, ConvNeXt-Tiny and ConvNeXt-Small stand out as efficient options that lighten the computational load by optimizing the number of parameters (Lekkala et al., 2025; Roshanzadeh et al., 2025; Shabrina et al., 2023). The ConvNeXt-Base and ConvNeXt-Large variants offer medium model capacity, providing a trade-off between performance and computational cost (Nan et al., 2025). ConvNeXt-XLarge is an architecture with the highest parameter capacity.

### 3.2.2. Classification algorithms

SVM is a robust supervised learning algorithm that aims to find the optimal decision hyperplane that maximizes the separation between classes (Cortes and Vapnik, 1995). This algorithm positions itself to maximize the margin, a gap between training data, thereby increasing the model's generalization ability and minimizing overfitting. SVM's reliance on the principle of structural risk minimization and its resilience to outliers make it particularly effective for small- and medium-sized datasets (Hosmer Jr et al., 2013).

LR is a fundamental statistical classification algorithm used to model the relationship between classes when the dependent variable is categorical. Unlike linear regression, this algorithm uses a sigmoid function that limits the probability that the dependent variable belongs to a specific class to values between 0 and 1 (Cox, 1958). The algorithm optimizes the coefficients using the maximum likelihood estimation method and delivers high-performance results even on high-dimensional datasets (Hosmer Jr et al., 2013).

RF is a classification algorithm based on ensemble learning, where multiple decision trees are randomly split and trained, and their predictions are combined to produce a single, stable result. This algorithm builds many decision trees during training and classifies using randomly selected feature subsets at each node. The predictions from individual trees are combined using majority voting to make the final classification decision. The algorithm uses both random sampling from the dataset and selecting a random subset of features at each node when constructing each tree (Breiman, 2001). This randomness mechanism minimizes the risk of overfitting by reducing the correlation between trees and increases prediction accuracy by reducing variance (Hastie, 2009).

### 3.3. Proposed Approach

In this study, an approach combining feature extraction, feature selection, and ML algorithms with ConvNeXt variants is proposed for the classification of diseases observed in guava fruit. The proposed approach consists of two stages, as shown in Figure 1.

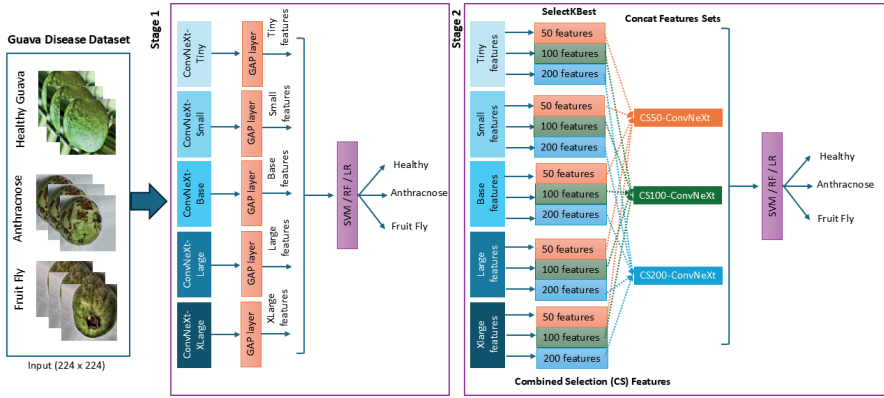


Figure 1. Diagram of the proposed approach

In the first stage, ConvNeXt-Tiny, ConvNeXt-Small, ConvNeXt-Base, ConvNeXt-Large, and ConvNeXt-XLarge architectures were initialized with pre-trained weights from the ImageNet-1k dataset. Global Average Pooling (GAP) was applied to the output of the last convolutional layer of each ConvNeXt variant, and fixed-size feature vectors were obtained. Accordingly, 768-dimensional feature vectors were obtained from the ConvNeXt-Tiny and ConvNeXt-Small architectures, 1024-dimensional feature vectors from the ConvNeXt-Base architecture, 1536-dimensional feature vectors from the ConvNeXt-Large architecture, and 2048-dimensional feature vectors from the ConvNeXt-XLarge architecture. These feature vectors were classified using SVM, RF, and LR algorithms.

In the second stage, the Mutual Information-based SelectKBest feature selection method was applied to these features obtained from each ConvNeXt architecture. The first K distinctive features were selected from each feature extractor. Feature selection was performed only on the training data, and data leakage was prevented by applying the same selective transformations to the validation and test data. In this context, 50, 100, and 200 features were selected from the feature sets extracted by each ConvNeXt architecture in the study. Then, these features were combined based on the number of selections to form feature sets (named Combined Selection (CS) feature count). Accordingly, using all ConvNeXt variants, there are 250 features in the CS50-ConvNeXt feature set, 500 features in the CS100-ConvNeXt feature set, and 1000 features in the CS200-ConvNeXt feature set. Table 2 lists the hyperparameters used in training the ML models and their values. The hyperparameters used in the study were determined based on the validation set performance. Finally, the

CIU method was used to increase the transparency of the model's decision-making mechanism, achieving the highest performance.

All experiments in the study were performed using the Python programming language in the Google Colaboratory environment, and the models were evaluated using the Keras library on v5e-1 TPU. The scikit-learn library was used for training the ML models.

*Table 2. Hyperparameters and their values used in ML algorithms*

Model	Parameter	Value
SVM	Kernel	rbf
	C	10
	Gamma	scale
RF	n_estimators	500
	max_depth	None
	random_state	42
	n_jobs	-1
LR	max_iter	5000
	solver	lbfgs
	n_jobs	-1

### 3.4. Performance Metrics

In this study, accuracy, precision, recall, F1-score, and Cohen's Kappa were used to evaluate the classification performance of the proposed models quantitatively. These metrics are calculated using True Positive (TP), True Negative (TN), False Positive (FP), and False Negative (FN) values. The metrics module of the Scikit-learn library was used to calculate these metrics in this study.

Accuracy is the ratio of correctly predicted examples to the total number of examples and indicates the model's overall success. The accuracy metric is calculated using the mathematical expression given in Equation 1.

$$Accuracy = \frac{TP + TN}{TP + TN + FP + FN} \quad (1)$$

Precision indicates how many of the predicted positives are actually positive. The mathematical expression for the precision metric is given in Equation 2.

$$Precision = \frac{TP}{TP + FP} \quad (2)$$

Recall measures the proportion of true positives correctly captured by the model. The mathematical expression for calculating the recall metric is given in Equation 3.

$$Recall = \frac{TP}{TP + FN} \quad (3)$$

The F1-score is the harmonic mean of precision and recall. This metric reflects the model's balanced performance on imbalanced datasets. The F1-score is calculated using the mathematical expression given in Equation 4.

$$F1 - score = 2 * \frac{Precision * Recall}{Precision + Recall} \quad (4)$$

Cohen's Kappa measures the difference between observed accuracy and the accuracy expected by chance, evaluating the consistency between the classifier and the actual labels. The mathematical expression used to calculate Cohen's Kappa is given in Equation 5. Here,  $P_o$  represents the observed accuracy, and  $P_e$  represents the expected chance agreement.

$$\text{Cohen's Kappa} = \frac{P_o - P_e}{1 - P_e} \quad (5)$$

## 4. Experimental Results and Discussion

### 4.1. Classification of Features Extracted from ConvNeXt Variants Using Machine Learning Algorithms

The performance results obtained with SVM, RF, and LR classifiers on the Guava Disease Dataset, using features extracted from ConvNeXt variants, are listed in Table 3. According to the findings, all performance metrics increased as the ConvNeXt scale increased. This indicates that deeper, higher-capacity ConvNeXt architectures can represent image discriminative features more effectively. SVM-based models achieved the highest performance across all

ConvNeXt variants. The classification performed with the ConvNeXt-XLarge-SVM model achieved 0.997 accuracy, 0.996 precision, 0.998 recall, 0.997 F1-score, and 0.996 Cohen's Kappa values, respectively.

LR-based models showed a slight performance drop compared to SVM. However, the ConvNeXt-Base-LR and ConvNeXt-XLarge-LR models produced quite competitive results. In contrast, RF-based models achieved the lowest performance results across all scales compared to the other proposed models.

*Table 3. Classification performance of ConvNeXt-based features with ML classifiers*

Model	Accuracy	Precision	Recall	F1-score	Cohen's Kappa
ConvNeXt-Tiny-SVM	0.940	0.934	0.936	0.935	0.908
ConvNeXt-Tiny-RF	0.874	0.882	0.865	0.872	0.806
ConvNeXt-Tiny-LR	0.914	0.906	0.904	0.905	0.868
ConvNeXt-Small-SVM	0.969	0.968	0.964	0.966	0.952
ConvNeXt-Small-RF	0.840	0.849	0.827	0.835	0.753
ConvNeXt-Small-LR	0.942	0.941	0.937	0.939	0.912
ConvNeXt-Base-SVM	0.984	0.985	0.983	0.984	0.976
ConvNeXt-Base-RF	0.895	0.898	0.890	0.893	0.839
ConvNeXt-Base-LR	0.979	0.974	0.980	0.977	0.968
ConvNeXt-Large-SVM	0.974	0.972	0.975	0.973	0.960
ConvNeXt-Large-RF	0.893	0.897	0.884	0.889	0.835
ConvNeXt-Large-LR	0.976	0.979	0.975	0.977	0.964
ConvNeXt-XLarge-SVM	<b>0.997</b>	<b>0.996</b>	<b>0.998</b>	<b>0.997</b>	<b>0.996</b>
ConvNeXt-XLarge-RF	0.945	0.947	0.944	0.945	0.916
ConvNeXt-XLarge-LR	0.992	0.994	0.991	0.992	0.988

The best results are shown in bold font.

The confusion matrices for evaluating features extracted using the ConvNeXt-XLarge architecture with different classifiers are shown in Figure 2. The ConvNeXt-XLarge-SVM model (Figure 2a) correctly predicted almost all classes. The ConvNeXt-XLarge-RF model (Figure 2b) mostly misclassified the classes. The ConvNeXt-XLarge-LR model (Figure 2c) showed limited confusion in some classes.

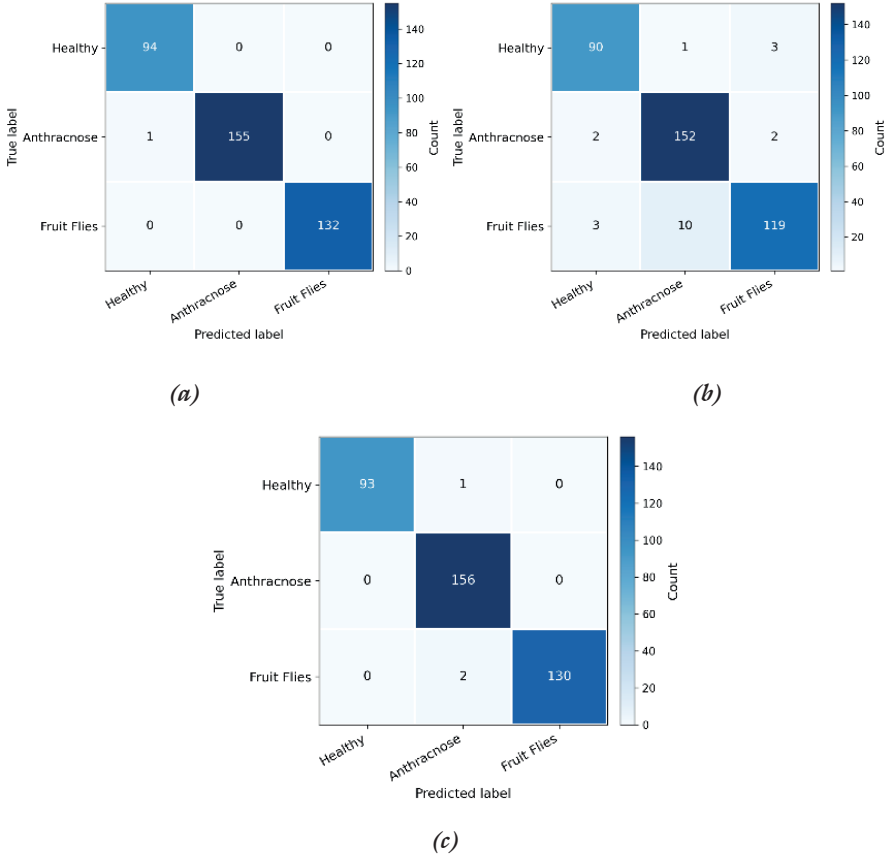


Figure 2. Confusion matrices for ConvNeXt-XLarge-based models, (a) ConvNeXt-XLarge-SVM, (b) ConvNeXt-XLarge-RE, (c) ConvNeXt-XLarge-LR

#### 4.2. Combining Selected Features from ConvNeXt Variants and Classifying Them with Machine Learning Algorithms

The performance results of classifying the vectors obtained by combining the subsets determined by applying feature selection to ConvNeXt-based deep features using SVM, RE, and LR are reported in Table 4. In this context, 50, 100, and 200 features were selected from each ConvNeXt variants. According to the experimental results, the CS200-ConvNeXt-SVM model achieved the highest performance among all models. This model reached a value of 1.000 in all accuracy, precision, recall, F1-score, and Cohen’s Kappa metrics.

When examining SVM-based models, it was observed that increasing the number of features from 250 to 1000 raised the accuracy rate from 0.982 to 1.000. LR-based models ranked second among the groups, with performance

increasing steadily as the number of features increased. In this context, the accuracy of 0.950 in the CS50-ConvNeXt-LR model increased to 0.984 in the CS200-ConvNeXt-LR model. In contrast, the RF algorithm performed worse than other classifiers, and a slight downward trend in accuracy was observed as the number of features increased. However, the fact that Cohen's Kappa values remained above 0.85 in all SVM and LR-based models indicates that the classification successes achieved were not random. In other words, it reveals a high level of consistency between the classifier outputs and the actual labels.

*Table 4. Classification performance of ML classifiers using combined feature vectors after feature selection*

Model	Sum Feature counts	Accuracy	Precision	Recall	F1-score	Cohen's Kappa
CS50-ConvNeXt-SVM	250	0.982	0.982	0.981	0.981	0.972
CS100-ConvNeXt-SVM	500	0.997	0.998	0.997	0.998	0.996
CS200-ConvNeXt-SVM	1000	<b>1.000</b>	<b>1.000</b>	<b>1.000</b>	<b>1.000</b>	<b>1.000</b>
CS50-ConvNeXt-RF	250	0.921	0.923	0.920	0.921	0.880
CS100-ConvNeXt-RF	500	0.914	0.914	0.909	0.911	0.867
CS200-ConvNeXt-RF	1000	0.908	0.909	0.904	0.906	0.859
CS50-ConvNeXt-LR	250	0.950	0.947	0.951	0.949	0.924
CS100-ConvNeXt-LR	500	0.971	0.968	0.971	0.969	0.956
CS200-ConvNeXt-LR	1000	0.984	0.984	0.984	0.984	0.976

The best results are shown in bold font.

The CS50-ConvNeXt-SVM model (Figure 3a) made a limited number of misclassifications between classes. In the CS100-ConvNeXt-SVM model (Figure 3b), misclassifications have been significantly reduced, and the distinction between classes has improved markedly. Here, the nearly error-free classification of the Anthracnose class demonstrates that the selected features represent disease-specific visual patterns more effectively. However, there is a limited level of error in the fruit fly class. Finally, the confusion matrix for the CS200-ConvNeXt-SVM model in Figure 3c demonstrates perfect classification performance, with all classes correctly identified.

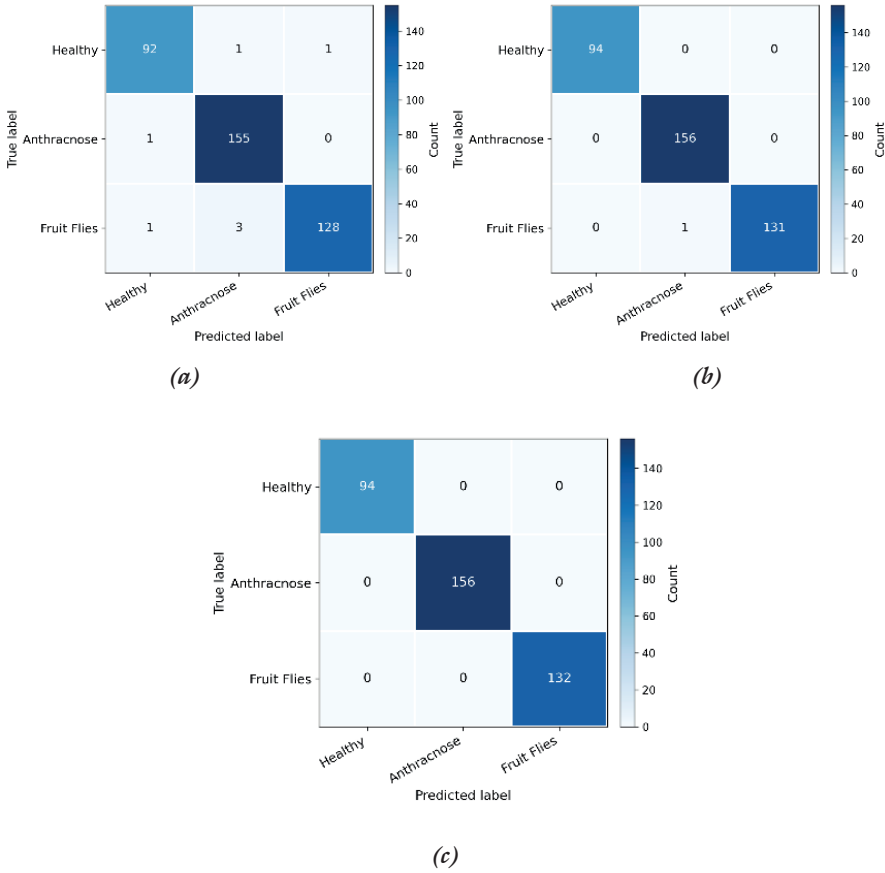


Figure 3. Confusion matrices of models with different feature counts, (a) CS50-ConvNeXt-SVM, (b) CS100-ConvNeXt-SVM, (c) CS200-ConvNeXt-SVM

### 4.3. Explainable Artificial Intelligence Evaluation of the Proposed Model

Figure 4 presents the class-based average CIU values calculated from correctly classified examples in the CS200-ConvNeXt-SVM model. The top 10 features contributing most to the average CI value for each class have been identified.

Upon examining the results, the F570 feature stood out in the Healthy guava class, with both high average Contextual Importance (CI) and Contextual Utility (CU) values. The F570 was followed by the F861, F952, F925, F896, F761, F529, F449, F520, and F852 features, respectively, based on their average CI values. On the other hand, the features that provide the highest contribution differ in the Anthracnose and Fruit fly classes. In other

words, the proposed model makes decisions based on discriminative and class-specific feature representations for each class. The highest contribution in the Anthracnose class was obtained from the F625 feature, and the highest contribution in the Fruit fly class was obtained from the F626 feature.

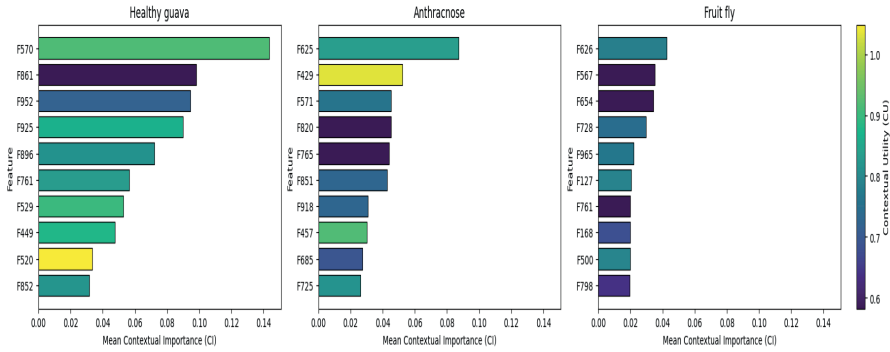


Figure 4. CIU analysis results for the CS200-ConvNeXt-SVM model

#### 4.4. Cross-Dataset Evaluation of the Proposed Model

To evaluate the generalization performance of the proposed model against different data distributions, the results obtained on various publicly available guava datasets are presented in Table 5. The datasets evaluated differ in terms of the number of classes, the number of images, and the content. Both datasets contain images of guava leaves and fruits. The datasets were divided into 70% training and 30% testing ratios. The proposed model achieved high performance in datasets with a relatively high number of images, while it exhibited relatively low performance in smaller datasets. These findings reveal that the model’s performance varies depending on the data volume and that it can generalize better in larger datasets.

*Table 5. Performance results of the proposed model on different datasets*

Dataset	Type	Number of images and classes	Accuracy	Precision	Recall	F1-score
Guava Disease Dataset (Rajbongshi et al., 2022)	Leaf and fruit	4899 images and 5 classes	0.994	0.995	0.994	0.994
Guava Disease Detection Dataset (Shihab et al., 2024)	Leaf and fruit	606 images and 6 classes	0.737	0.746	0.757	0.749

#### 4.5. Discussion

As seen in the studies summarized in Table 6, CNN-based architectures have been predominantly used for the classification of guava fruit and leaf diseases. However, since these studies used different datasets, numbers of classes, and image types (guava fruit or guava leaf), the comparison was limited to the methods used.

Mostafa et al. (2022) achieved 97.74% accuracy with the ResNet-101 model on a dataset of 2889 images across 5 classes. Tewari et al. (2024) obtained 99% accuracy in classifying a 4-class guava disease dataset comprising 681 images using the DenseNet169 model. Hashan et al. (2024) achieved a 93% accuracy rate in classifying guava fruit diseases using the AlexNet model. Kaur et al. (2024) achieved an accuracy rate of 98.76% with their proposed model. Doutoum et al. (2023) achieved 94.93% accuracy in classifying guava leaf diseases using the EfficientNet-B3 model. Nath Nandi et al. (2022) achieved approximately 97% accuracy with their proposed approach. Although most of these studies report high classification accuracies, analyses of the explainability of model decisions remain limited. Mustak Un Nobil et al. (2023) achieved 98% accuracy with their proposed model, which incorporates a Grad-CAM-based XAI approach.

On the other hand, hybrid approaches also show noteworthy performance results in detecting guava diseases. In this context, Kılıcı and Koklu (2024) achieved 95.6% accuracy using SqueezeNet and Gradient Boosting models on a dataset of 3784 images across 3 classes. Kılıcı and Koklu (2025) reached an accuracy rate of 0.9974 on the same dataset using the InceptionV3-SVM model.

In this study, the ConvNeXt-XLarge-SVM model achieved an accuracy rate of 0.997, while the CS200-ConvNeXt-SVM model, which used 1000 features, achieved an accuracy of 1.000. Furthermore, the features influencing model decisions were analyzed using the CIU method.

*Table 6. Comparison of studies in the literature on the classification of guava diseases*

Reference	Dataset structure: number of images	Method	Use of explainable models	Highest accuracy value
Mostafa et al. (2022)	2889 images and 5 classes	ResNet-101	-	97.74%
Tewari et al. (2024)	681 images and 4 classes	DenseNet169	-	99%
Hashan et al. (2024)	612 images and 5 classes	AlexNet	-	93%
Kaur et al. (2024)	527 images and 5 classes	DenseNet	-	98.76%
Doutoum et al. (2023)	1834 images and 5 classes	EfficientNet-B3	-	94.93%
Nath Nandi et al. (2022)	8525 images and 6 classes	GoogleNet	-	97%
Mustak Un Nobi et al. (2023)	Dataset 1: 1842 images and 5 classes Dataset 2: 527 images and 5 classes	MobileNet	Grad-CAM	98%
Kılıcı and Koklu (2024)	3784 images and 3 classes	SqueezeNet and Gradient Boosting	-	95.6%
Kılıcı and Koklu (2025)	3784 images and 3 classes	InceptionV3 and SVM	-	0.9974
This study	3784 images and 3 classes	ConvNeXt-XLarge-SVM	-	0.997
This study	3784 images and 3 classes	CS200-ConvNeXt-SVM	CIU	1.000

#### 4.6. Limitations of the Study

The proposed ConvNeXt-based ML approach achieves high performance in classifying guava fruit diseases but also has limitations. These limitations are explained below:

- (i) ConvNeXt variants were used only as feature extractors in this study; no end-to-end training evaluations were performed.
- (ii) ML algorithms such as SVM, RF, and LR were used in the study, and the hyperparameters of these algorithms were kept fixed.
- (iii) This study used a single dataset. The fact that this dataset contains three different classes may limit the model's performance in more complex and multi-class scenarios.
- (iv) The performance of the proposed model is evaluated over the training, validation and testing partitions in the 70:20:10 % defined in the original dataset. Strategies such as K-fold or nested cross-validation were not applied in this study.

## 5. Conclusions and Future Works

In this study, features obtained from ConvNeXt variants (Tiny, Small, Base, Large, XLarge) were classified using ML algorithms (SVM, RF and LR) for the classification of diseases observed in guava fruit. The Guava Disease Dataset, comprising 3784 images across three classes (healthy, anthracnose, fruit fly), was used in the study.

According to the experimental results, the ConvNeXt-XLarge-SVM model achieved the highest performance among the models evaluated. This model achieved values of 0.997, 0.996, 0.998, 0.997, and 0.996 for accuracy, precision, recall, F1-score, and Cohen's Kappa, respectively. On the other hand, the CS200-ConvNeXt-SVM model achieved a value of 1.000 in all metrics. Furthermore, the contribution of the features selected using the CIU method to the CS200-ConvNeXt-SVM model was evaluated on a class-by-class basis. It was determined that the highest contribution in the Healthy guava class came from feature F570, in the Anthracnose class from feature F625, and in the Fruit fly class from feature F626. Furthermore, evaluations across different datasets demonstrated that the model performs well under variable datasets. Future studies may explore the integration of the ViT architectures with various ML algorithms, along with cross-validation strategies and hyperparameter optimization.

### Dataset

The Guava Disease Dataset utilized in this study is publicly available on the Mendeley Data repository, and the citation is provided in the reference list. The dataset can be accessed at: <https://data.mendeley.com/datasets/bkdkc4n835/1> [07.08.2025]

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