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ATTENTION-GUIDED HYBRID SVM–VISION TRANSFORMER FRAMEWORK FOR ACCURATE DETECTION OF APPLE LEAF DISEASES IN INDIAN ORCHARDS

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Abstract: *Apple cultivation in India is frequently affected by fungal and bacterial infections that are hard to detect in early stages, often leading to serious yield losses. Reliable automated diagnosis can help farmers take timely action, but many existing deep learning models struggle to capture both fine-grained local symptoms and broader visual patterns on leaves. This study proposes an attention-guided hybrid learning framework that combines Support Vector Machines (SVM) with Vision Transformers (ViT) for precise apple leaf disease classification. The model integrates the strong decision boundaries of SVM with the global feature learning capability of ViT, while an optimized attention mechanism emphasizes disease-relevant regions in the images. This design helps the system focus on subtle texture variations and lesion patterns that are typically missed by conventional convolution-based networks. Experiments were conducted on a dataset of Indian apple leaf images containing angular leaf spot, bean rust, and healthy samples. Performance was evaluated using cross-validation and benchmarked against several established deep learning models. The proposed hybrid model achieved an accuracy of 98.7%, precision of 98.5%, recall of 98.3%, and F1-score of 98.4%, outperforming comparison models that remained below 95% accuracy. The attention maps also provide visual insight into the model's decision process, improving transparency. The results suggest that the proposed framework can serve as a reliable and interpretable tool for early disease detection in precision agriculture applications.*

Keywords: *Apple Fruit disease, Hybrid ML model, ViT, SVM, CNN, Prediction*

1. Introduction

The demand for apples, as a staple in diets around the world, has surged due to their taste and nutritional value, with production reaching over 95 million tons in 2022 [1]. However, challenges such as disease detection and classification limit the efficiency and yield in apple cultivation. Traditionally, the identification and sorting of apples depend on human perception, which can be influenced by several subjective factors like texture, color, and smell [2]. The reliance on human expertise introduces inconsistencies and inefficiencies due to variations in

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skill, environmental conditions, and psychological factors [3]. This has led to the exploration of automated systems for apple disease detection, which offer consistency, cost reduction, and accuracy in the inspection processents in computer vision and machine learning have shown promise in tackling the complexities of disease detection in fruits and vegetables. Machine learning methods like Convolutional Neural Networks (CNNs), SVM, ANN etc [4-8] have been successfully employed for feature extraction and classification without the need for manual intervention, enhancing non-destructive approaches for quality control in agriculture [9-12]. Despite these advancements, conventional machine learning models are often limited in their capacity to fully capture intricate patterns in apple diseases due to their reliance on predefined feature extraction techniques . This limitatiohers to explore hybrid models, combining multiple machine learning architectures to achieve more robust and accurate detection capabilities [13-15].

The agricultural industry has increasingly embraced machine learning and computer vision technologies to detect diseases in crops and fruits, aiming to improve yield quality and reduce losses (Araújo et al., 2022; Archana et al., 2022). For apple fruits, a significant crop in India, common diseases like scab, rot, and black spot can heavily impact their quality and market value (Bhujade & Sambhe, 2022; BaniMustafa et al., 2023). Traditionally, identifying these diseases has relied on manual inspection, a process that is labor-intensive, time-consuming, and susceptible to human error (Ashwini & Sellam, 2023). This has led to a growing need for automated systems that offer fast, reliable, and accurate disease detection tailored to specific crops, such as Indian apples (Bali & Singla, 2021). Current study introduces a new hybrid model called SVAM, which combines a Support Vector Machine (SVM) with a Vision Transformer (ViT) to effectively detect apple diseases by leveraging an optimized attention mechanism. The SVAM model utilizes multiple datasets, including images of apples in different disease categories like normal, scab, rot, and black spot, allowing it to generalize across various conditions (Bayram et al., 2022). These images undergo preprocessing, including resizing, normalization, and data augmentation, to ensure the model's robustness and adaptability to real-world scenarios (Behera et al., 2020; Bajait & Malarvizhi, 2023).

Within this hybrid model, the ViT component leverages self-attention to extract important features from image patches, helping the system distinguish between healthy and diseased areas more accurately (Bhagat & Kumar, 2023). After reducing dimensions with Principal Component Analysis (PCA), SVM classifies these features, using its ability to manage high-dimensional data and maintain strong decision boundaries for enhanced accuracy (Buyukarikan

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& Ulker, 2022). This novel SVAM model demonstrates potential as a practical tool for apple disease detection, providing a scalable solution tailored to the specific conditions of Indian apple orchards. The model aims to aid farmers and agricultural stakeholders in improving crop health and production quality, contributing positively to the agricultural economy (Bishnoi et al., 2023).

Our research focuses on developing a novel hybrid model, the Support Vector Machine-Vision Transformer-Attention Model (SVAM), tailored specifically for the accurate detection of diseases in Indian apple varieties. This hybrid approach integrates Support Vector Machine (SVM) with the Vision Transformer (ViT) architecture and an optimized attention mechanism to enhance feature extraction and improve classification accuracy. The SVM, known for its strong performance in classification tasks, provides a robust foundation for handling non-linear patterns, while the ViT architecture, which uses a transformer-based approach to process image data, significantly enhances feature representation. The attention mechanism is optimized to focus on relevant regions in apple images, aiding in the precise identification of disease markers that might otherwise be missed in traditional methods .

The flow of our proposed model ssing the apple images, including steps such as resizing, noise reduction, and normalization, which are essential for enhancing image quality. The preprocessed images are then fed into the ViT component, which divides them into smaller patches and applies a self-attention mechanism to focus on critical areas that indicate potential disease. Following this, the SVM classifier is employed to interpret the high-dimensional features generated by the ViT model, classifying the apple images based on disease presence and type. This combined framework leverages the strengths of each component, allowing for high precision in disease identification and addressing the limitations of single-model architectures .

Studies have shown that hybrid models outperform n tasks involving complex image classifications. For instance, hybrid approaches like capsule neural networks and combined CNN-deep learning methods have demonstrated substantial improvements in identifying crop diseases compared to singular deep learning models . Our SVAM model aligns with these findings by integrating the ViT's action with SVM's classification accuracy, tailored with an attention mechanism to increase the focus on affected apple regions. This research not only contributes to the advancement of automated apple disease detection but also sets a foundation

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for broader applications in agricultural quality assessment systems, meeting the demand for efficient, high-quality food production amidst growing population needs.

The primary goal of the present study is to develop an optimized and hybrid detection model for accurately identifying apple fruit diseases, specifically targeting cases in India. By combining Support Vector Machines (SVM) with Vision Transformers (ViT) and refining the attention mechanism, this study aims to enhance the precision, robustness, and efficiency of disease detection in apple fruits. This model, named the SVM-ViT Model with Optimized Attention Mechanism (SVAM), seeks to address the challenges of traditional methods by improving feature extraction, minimizing misclassification, and increasing the adaptability of the model to diverse environmental conditions in Indian apple orchards. Ultimately, this research intends to contribute to sustainable agriculture by providing a reliable tool for early disease detection, which will help farmers mitigate crop losses and improve apple yield quality.

2. Literature Review

Apple production is a major part of global agriculture, with millions of tons produced every year. Despite this significance, apple crops are often affected by a wide range of diseases that reduce both yield and quality, creating economic challenges for farmers (28). With the rise of artificial intelligence (AI) and machine learning (ML), advanced digital tools are increasingly being used for disease detection in crops, including apple orchards. Current research in this area largely focuses on image processing, machine learning, deep learning, and hybrid approaches that combine multiple techniques. Image processing and machine learning methods have been widely used to automate disease detection. Early approaches relied heavily on color and texture features. (29) developed a method using leaf images with texture and color analysis, which worked well for simple symptoms but had limitations with complex cases. (30) reviewed grading methods for fruits based on shape and color, reinforcing the importance of traditional image-based approaches in agricultural applications.

Deep learning has transformed this field by enabling automatic feature extraction and achieving higher accuracy than traditional methods. Convolutional neural networks (CNNs) are especially dominant. (31) reviewed fruit and vegetable classification and showed CNNs to be more robust than classical image processing. (32) designed a deep learning model for tomato leaf disease detection using CNNs and data augmentation, achieving excellent accuracy. More recently, capsule networks have been explored to capture spatial relationships in images. (33) optimized capsule neural networks for tomato disease classification, reporting improved

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accuracy and efficiency over CNNs. These studies confirm that deep learning methods are well-suited for detecting plant diseases across varying environments. Hybrid approaches combine multiple algorithms to improve classification. Some researchers introduced a machine learning system that integrates traditional image processing with deep learning for fruit classification, demonstrating stronger feature extraction. Similarly, (35) proposed a hybrid approach combining CNNs with histogram-oriented gradients for mango disease detection, showing significant accuracy gains. Such findings suggest that hybrid models can capture complex disease traits better than single methods.

Table 1 ML application in plant disease prediction in several publications

Study	Methodology	Crop / Disease Type	Key Findings	Research Gap
FAO (2022)	Statistical Database	Global agriculture	Apple prota highlights the economic importance of disease management in apples.	Lack of focus on specific disease management solutions.
Ahmad et al. (2021)	Color and Texture Analysis	Plant leaf diseases	Demonstrated the effectivenestexture features but limited in complex disease scenarios.	Insufficient for complex diseases where deep learning may be more effective.
Hameed et al. (2018)	CNN	Fruits and vegetables	CNN models provide robustness in classifcuracy.	Limited exploration of apple-specific disease detection.
Abouelmagd et al. (2024)	Capsule Neural Network	Tomato leaf diseases	Capsule networks improve disease classification effi	More studies needed on capsule networks for other crops.
Admass et al. (2023)	Hybrid CNN + HOG	Mango diseases	Hybrid model enhances automatic disease detection accuracy	Limited application to crops beyond mangoes.
Alhussan et al. (2024)	Optimization Algorithm	Potato production forecasting	Advanced optimization algorithm used for forecasting, showing promise detection.	Application to apple disease detection remains unexplored.

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Study	Methodology	Crop / Disease Type	Key Findings	Research Gap
Bajait & Malarvizhi (2023)	Taylor Remora Optimization + Deep Learning	Grape pesticide detection	Optimization improved accuracy, indicating potential for model parameter optimizati	Need to explore this optimization technique for apple disease detection.
BaniMustafa et al. (2023)	Hybrid ML Approach	Bacterial & fungal plant diseases	Hybrid approach offers comprehensive diagnosis across multiple diseases. Requires more application in diverse agricultural regions.	
Bayram et al. (2022)	CNN + Data Augmentation	Tomato leaf diseases	Data augmentation enhanced classification performance. ore data augmentation for apple disease detection to reduce overfitting.	

Although machine learning and deep learning approaches have significantly advanced plant disease detection, there are several challenges that persist. Many models struggle with overfitting, particularly when trained on limited datasets. Admass et al. (2023) highlighted the challenge of achieving generalization across different disease types, especially in environments where data collection is limited . Additionally, deploying such models in real-world scenarios often requires extensive computaources, which can be prohibitive for smaller farms or developing regions. Another challenge is the variability in disease symptoms across seasons and geographic locations. BaniMustafa et al. (2023) discussed a hybrid approach for diagnosing bacterial and fungal diseases in plants, emphasizing that robust models should account for diverse environmental conditions . Further research is needed to address these issues and improve model scalability and robustness.

Findings and Research Gaps Despite the advancements in plant disease detection, there is still a need for models that can handle large-scale, real-time data, particularly in regions with limited resources. Most studies have focused on specific crops and regions, limiting the generalizability of the findings. Moreover, few studies incorporate real-time disease detection frameworks, which are essential for timely intervention. The literature review highlights a gap

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in the development of hybrid models that integrate attention mechanisms specifically optimized for real-time apple disease detection. This research aims to address this gap by proposing a Hybrid SVM-ViT model with an optimized attention mechanism, which can improve detection accuracy and efficiency for apple diseases, focusing on Indian apple varieties where such models are currently underexplored.

3. Material and method

The methodology of this study, as illustrated in Figure 1, involves several essential stages for the accurate detection and classification of apple fruit diseases using advanced machine learning and deep learning models. The workflow is divided into four main sections: Dataset Collection, Image Preprocessing, Model Selection, and Evaluation Metrics.

3.1 Dataset Collection (Raw Input Images)

The dataset used for this study consists of images of apple fruits, categorized into four distinct classes based on their health status: normal apples, blotch-affected apples, rot-affected apples, and scab-affected apples. This collection serves as the raw input for the subsequent stages. The dataset was sourced to include a diverse set of images representing the visual variability of apple diseases under various lighting and environmental conditions, which enhances the model's robustness in practical applications. In present study three different type of dataset were used for the model validation and prediction. The details of the data set was present in figure 2, in which three dataset were present with all classes used in present study. The dataset for this study on apple disease classification consists of three distinct sets of apple images, each encompassing four classes: Normal, Blotch, Rot, and Scab. This diverse dataset structure is depicted in Figure 2 and serves to ensure a comprehensive representation of visual variations across different sources, enhancing the robustness and generalization capability of the classification model.

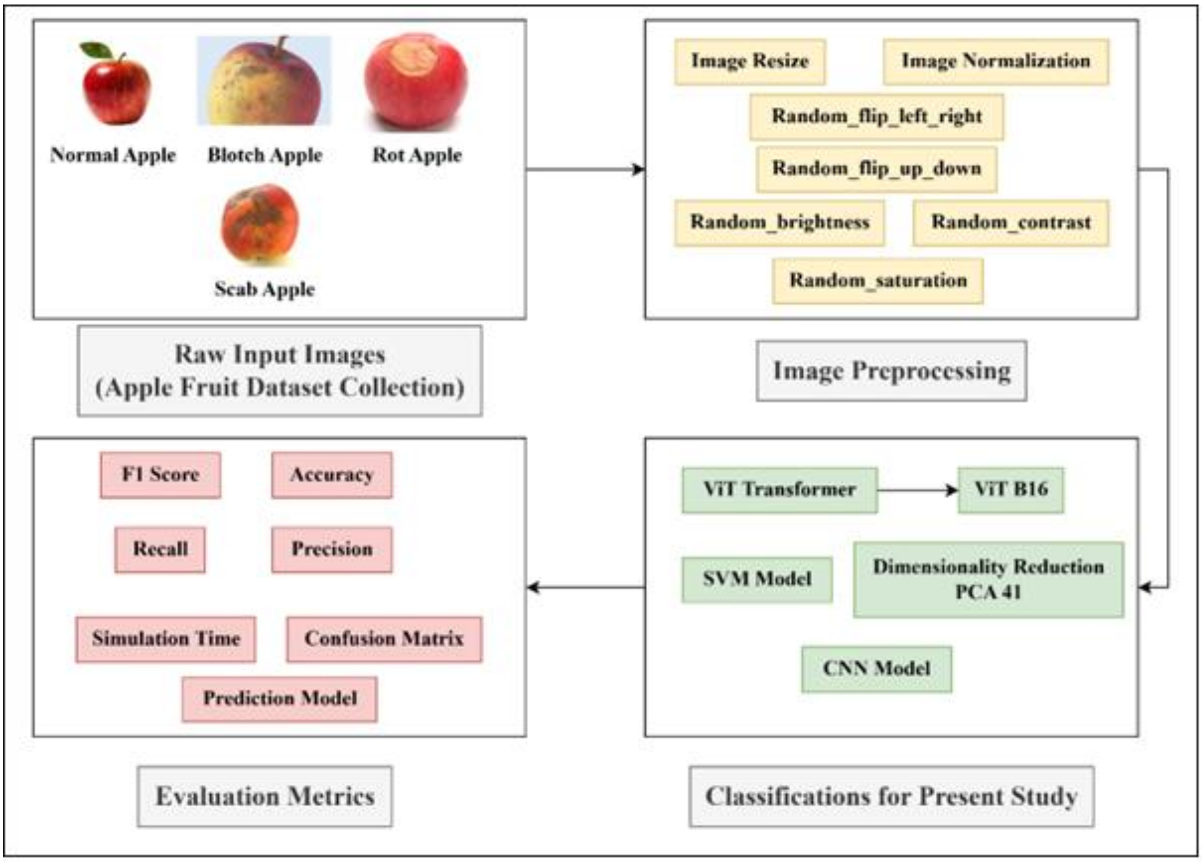

Figure 1 Classification stage in present study for Apple Fruit disease

Dataset-1 (Kaggle): The first dataset is sourced from Kaggle, a widely used platform for machine learning datasets. This dataset includes clear images for each class, displaying healthy apples as well as apples affected by blotch, rot, and scab. The dataset's high quality and consistency make it suitable for training and validating models, allowing for initial baseline performance comparisons. Images in this set are characterized by distinct features that define each disease class, helping the model learn key attributes in a controlled setting.

Dataset-2 (Mixed): This second dataset comprises a mixture of images from various sources, providing a wider range of image qualities and environmental conditions. This variability better simulates real-world scenarios where lighting, background, and resolution may differ. The mixed dataset is critical in training the model to generalize well across diverse conditions, as it introduces a variety of apple appearances that include both minor and advanced disease symptoms.

Dataset-3 (Original Collected): The third dataset is an original collection, curated specifically for this study to reflect the unique characteristics of Indian apple varieties. Images in this dataset show apples under different natural conditions, including variations in size, color, and

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disease manifestation. This set provides valuable data for validating the model's effectiveness on apples typical in the Indian context, making it particularly relevant for practical deployment.

Collectively, these datasets allow for robust model training, testing, and validation, facilitating the development of a classification model that is both accurate and adaptable across varied real-world conditions.

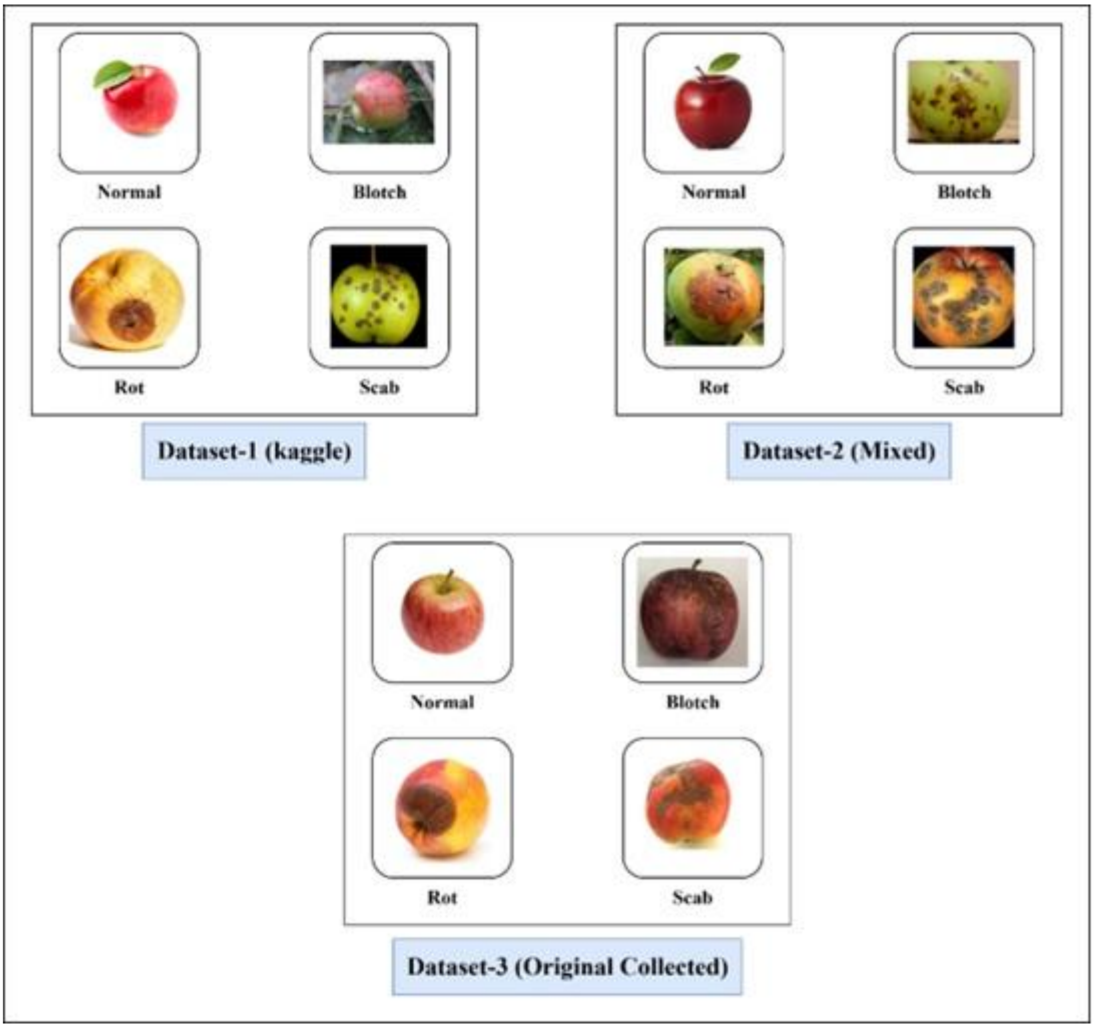

Figure 2 dataset selection for the present study

3.2 Image Preprocessing

Image preprocessing is a critical step in preparing the raw dataset for training the models. The preprocessing pipeline begins with Image Resize and Image Normalization, which ensure that all images are standardized in size and have consistent intensity values. This standardization reduces variability that can negatively impact model performance. The images are then subjected to several augmentation techniques, including:

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Random Flip (Left-Right and Up-Down): This flipping operation helps the model generalize better by simulating real-world scenarios where images might appear from different orientations.

Random Brightness, Contrast, and Saturation Adjustments: These adjustments mimic different lighting conditions, making the model more robust to variations in illumination. For instance, images with different brightness levels can represent apples under different sunlight exposure.

Algorithm 1: Image Preprocessing and Augmentation

Input: Raw image file
Output: Augmented image set
- **Step 1:** Image Upload and File Path Extraction
  - Import necessary libraries.
  - Upload the image using Google Colab's files.upload() function.
  - Extract the file path of the uploaded image.
- **Step 2:** Image Preprocessing
  - Read the Image: Load the image from the extracted file path using tf.io.read_file(image_path).
  - Decode Image: Decode the raw image data into a standard format using tf.io.decode_jpeg(), with 3 channels for RGB.
  - Resize Image: Resize the image to a predefined dimension (224x224 pixels) using tf.image.resize() for consistent model input size.
  - Normalize Pixel Values: Convert pixel values to the range [0,1] by dividing each pixel by 255.0, making the image suitable for deep learning models.
- **Step 3:** Data Augmentation
  - Initialize Augmentation List: Create a list images containing the original preprocessed image.
  - Random Horizontal Flip: Apply tf.image.random_flip_left_right() to create a horizontally flipped version of the image and add it to images.
  - Random Vertical Flip: Apply tf.image.random_flip_up_down() to the horizontally flipped image and add it to images.
  - Random Brightness Adjustment: Use tf.image.random_brightness() on the vertically flipped image with a brightness adjustment factor of 0.1. Add the result to images.
  - Random Contrast Adjustment: Adjust contrast by a factor between 0.2 and 0.4 using tf.image.random_contrast() and add the modified image to images.
  - Random Saturation Adjustment: Apply random saturation changes between 2 and 6 using tf.image.random_saturation() and add the final augmented image to images.
- **Step 4:** Display and Save Augmented Images
  - Display all images in a 2x3 matrix format using matplotlib.pyplot.
  - Save the augmented images as a high-resolution output file using plt.savefig() and display the file path for downloading the result.

End of Algorithm

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These augmentation techniques enhance the dataset's diversity, allowing the model to learn more complex features and become more resistant to overfitting. Data augmentation not only increases the effective size of the dataset but also aids the model in adapting to real-world variations that may otherwise lead to classification errors.

3.3 Hybrid Model Selection (Classifications for Present Study)

The core of the study focuses on comparing different models for classifying apple diseases. The models employed in this study include:

Vision Transformer (ViT) Transformer: The ViT model, particularly the ViT B16 variant, is applied to extract high-level features from the input images. Vision Transformers have demonstrated excellent performance in image classification tasks by leveraging self-attention mechanisms to capture global context. This capability is essential for distinguishing subtle differences between similar apple diseases.

Support Vector Machine (SVM) Model: SVM, known for its effectiveness in binary classification problems, is utilized here in combination with dimensionality reduction. By applying Principal Component Analysis (PCA) with 41 principal components, the dataset's dimensionality is reduced, which allows the SVM to classify the images efficiently with minimal computational overhead while retaining most of the variance.

Convolutional Neural Network (CNN) Model: A CNN is employed as a baseline model to capture spatial features in the images. CNNs have been extensively used in image classification due to their ability to identify patterns like edges and textures, which are useful for differentiating among diseased and healthy apple fruits.

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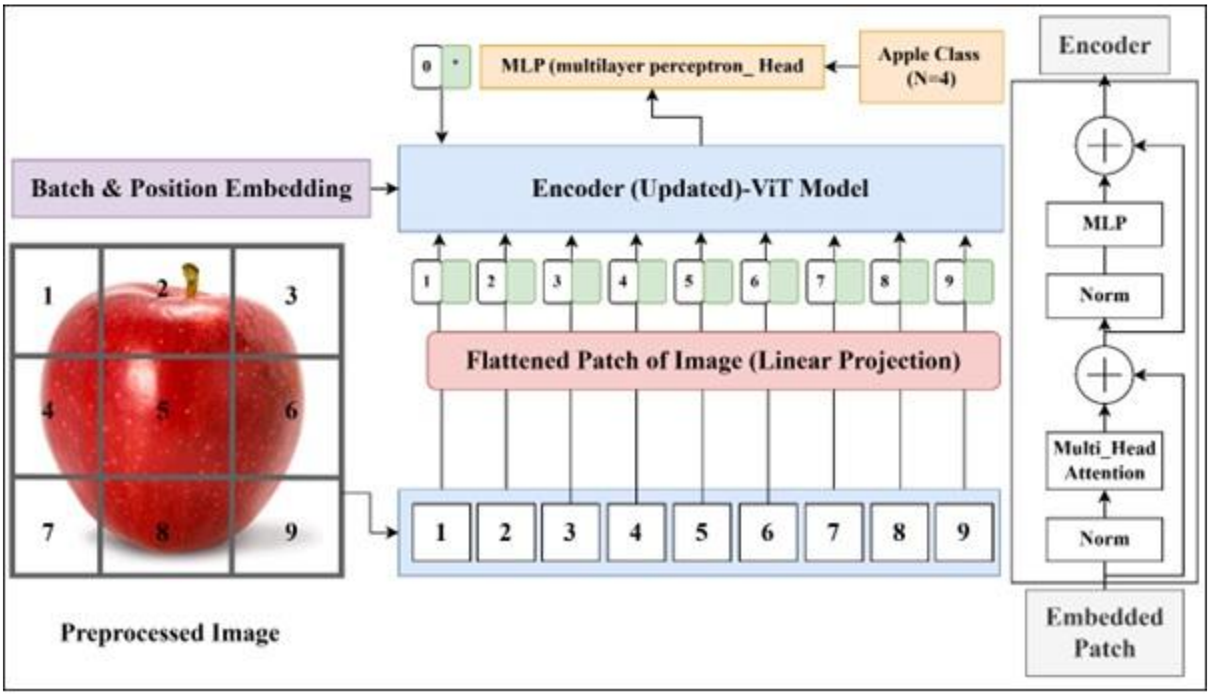

Figure 3 Modeling steps adopted in ViT model for feature extraction

These models are trained and evaluated to determine their effectiveness in disease classification, and the results are compared to select the most suitable approach for apple disease detection.

3.4 Evaluation Metrics

To assess the performance of the models, several evaluation metrics are used. These include:

Accuracy: Measures the overall correctness of the model's predictions by calculating the proportion of correctly classified instances.

Precision: Indicates the ratio of true positive predictions to the total positive predictions, giving insight into the model's ability to avoid false positives.

Recall: Reflects the ratio of true positive predictions to all actual positive instances, indicating the model's sensitivity to the diseased class.

F1 Score: Combines precision and recall into a single metric, especially valuable in cases where the classes are imbalanced.

Confusion Matrix: Provides a detailed breakdown of true positive, true negative, false positive, and false negative predictions, helping to visualize the classification errors.

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Simulation Time: Records the computational efficiency of each model, which is essential for evaluating the practical applicability of the model in real-time scenarios.

Prediction Model: Summarizes the final model chosen based on performance across all metrics, balancing accuracy, efficiency, and robustness.

In this study, each model is evaluated and optimized according to these metrics to ensure reliable classification results for apple fruit diseases. The best-performing model is selected based on a combination of high accuracy, F1 score, and low simulation time, indicating its potential for deployment in agricultural settings. The comprehensive evaluation ensures that the model not only performs well under controlled conditions but also maintains robustness when exposed to diverse real-world data.

4. ViT Transformer Model

The Vision Transformer (ViT) represents a significant shift in image classification by adapting Transformer models, for visual data. Traditional image classification models rely on convolutional neural networks (CNNs) and other models to process images, with convolutional layers that capture spatial hierarchies and local dependencies. In contrast, ViT bypasses convolutions entirely, employing a self-attention mechanism that enables it to capture long-range dependencies across an image, even from non-adjacent regions. This approach enhances the model's ability to recognize complex patterns and relationships in visual data, particularly useful for tasks requiring high-level semantic understanding. At the core of ViT is its use of a Transformer encoder, a structure that ingests "tokens" derived from the image. In the ViT framework, an input image is first divided into a grid of non-overlapping patches. Each patch is treated similarly to a "word" token in NLP tasks. These patches are then linearly projected into a lower-dimensional space, producing a vector representation, or token, for each patch. If an image has dimensions HXW and the patch size is PXP the total number of tokens produced is N = (H/P) X (W/P). This method allows each token to serve as a distinct input to the Transformer, representing specific regions of the image and preserving spatial information across patches.

ViT's self-attention mechanism plays a crucial role in processing these tokens. Each token undergoes three linear transformations—query (Q), key (K), and value (V)—enabling the model to compute the relationship between patches. The self-attention layer calculates a weighted sum over the values based on the similarity between queries and keys, enabling the model to focus on specific parts of the image that are contextually relevant. This process,

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known as scaled dot-product attention, generates attention weights that allow the model to prioritize certain tokens over others, making ViT highly effective in capturing both local and global dependencies in an image. For each query qi and key kj, the attention score Aij is calculated as:

$$A_{ij} = \mathrm{softmax}\left(\frac{q_i \cdot k_j^T}{\sqrt{D_h}}\right)$$

where Dh is the dimension of the projected space. This attention mechanism is further enhanced by multi-head self-attention (MSA), where multiple self-attention heads operate in parallel. Each head learns distinct aspects of the input data, and their concatenated results are linearly projected to produce the final attention output. Once the self-attention mechanism has processed the tokens, the Transformer encoder's output is passed through a feed-forward network to refine the token representations and extract high-level features. This process is repeated for each Transformer layer in the model, with the output tokens eventually aggregated and fed into a classification head. The classification head, typically consisting of a linear transformation followed by a softmax activation, generates the final class probabilities for image prediction.

$$\mathrm{SA}\,(z) = Av$$

ViT's architecture has several advantages. It doesn't require any prior assumptions about spatial hierarchies, as MLs do, and learns dependencies purely from the data. This flexibility enables ViT to excel at capturing global patterns across an image, a feature particularly beneficial for complex scenes or images where relationships span large regions. However, ViT also faces challenges with high-resolution images, as the number of tokens can grow rapidly, increasing computational demands. To mitigate this, hybrid models that combine MLs with ViTs have been proposed, leveraging MLs for initial feature extraction before applying self-attention on lower-dimensional representations. Techniques like patch overlapping, where patches share portions of the image, are also employed to capture finer details and reduce information loss at patch boundaries.

$$\mathrm{MSA}(z) = [\mathrm{SA}_1(z);\mathrm{SA}_2(z)\ldots\ldots \mathrm{Sa}_k(z)]U_{msa}$$

Overall, ViT is a transformative architecture for image classification, merging the strengths of attention mechanisms with visual processing. Its flexibility and ability to model global

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dependencies position it as a powerful alternative to MLs, with potential applications extending beyond classification to other visual tasks like object detection and segmentation.

5. Proposed Hybrid ML Classification Model

The figure 4 illustrates the development stages of a hybrid machine learning (ML) classification model aimed at predicting apple fruit diseases. This hybrid model integrates multiple processing steps, data augmentation techniques, dimensionality reduction, and a combination of machine learning algorithms to accurately classify different types of apple diseases such as rot, scab, and blotch, as well as identifying healthy apples.

5.1 Development Stages of the Hybrid Model

Dataset Preparation and Description:

The model is based on three datasets containing images of apples with varying conditions, including healthy apples and those affected by diseases like blotch, rot, and scab. Dataset-1 consists of a range of images, likely sourced from online databases, while Dataset-2 represents a mixture of sources. Dataset-3 contains images collected specifically for this study. The diversity of the data enables the model to generalize across different variations of the same disease, improving its robustness in real-world applications.

Image Preprocessing:

Preprocessing is a crucial step for improving model performance. The images undergo resizing and normalization to maintain uniformity in scale and pixel values across the dataset. Various augmentation techniques are applied to increase dataset variability and prevent overfitting. These techniques include random horizontal and vertical flips, brightness adjustments, contrast changes, and saturation variations. Each of these adjustments provides the model with a more comprehensive view of potential real-world variations, thereby enhancing its adaptability.

Feature Extraction with Vision Transformer (ViT):

After preprocessing, the images are input into a Vision Transformer (ViT) model for feature extraction. The ViT model divides each image into patches, which are then flattened and linearly projected to create embeddings. The transformer architecture incorporates batch and position embeddings to retain spatial information. The ViT uses multiple encoder layers, each consisting of multi-head attention mechanisms and normalization layers, to capture complex visual patterns and relationships within the images. The final output of the ViT model is a set of high-dimensional features representing the key characteristics of each image.

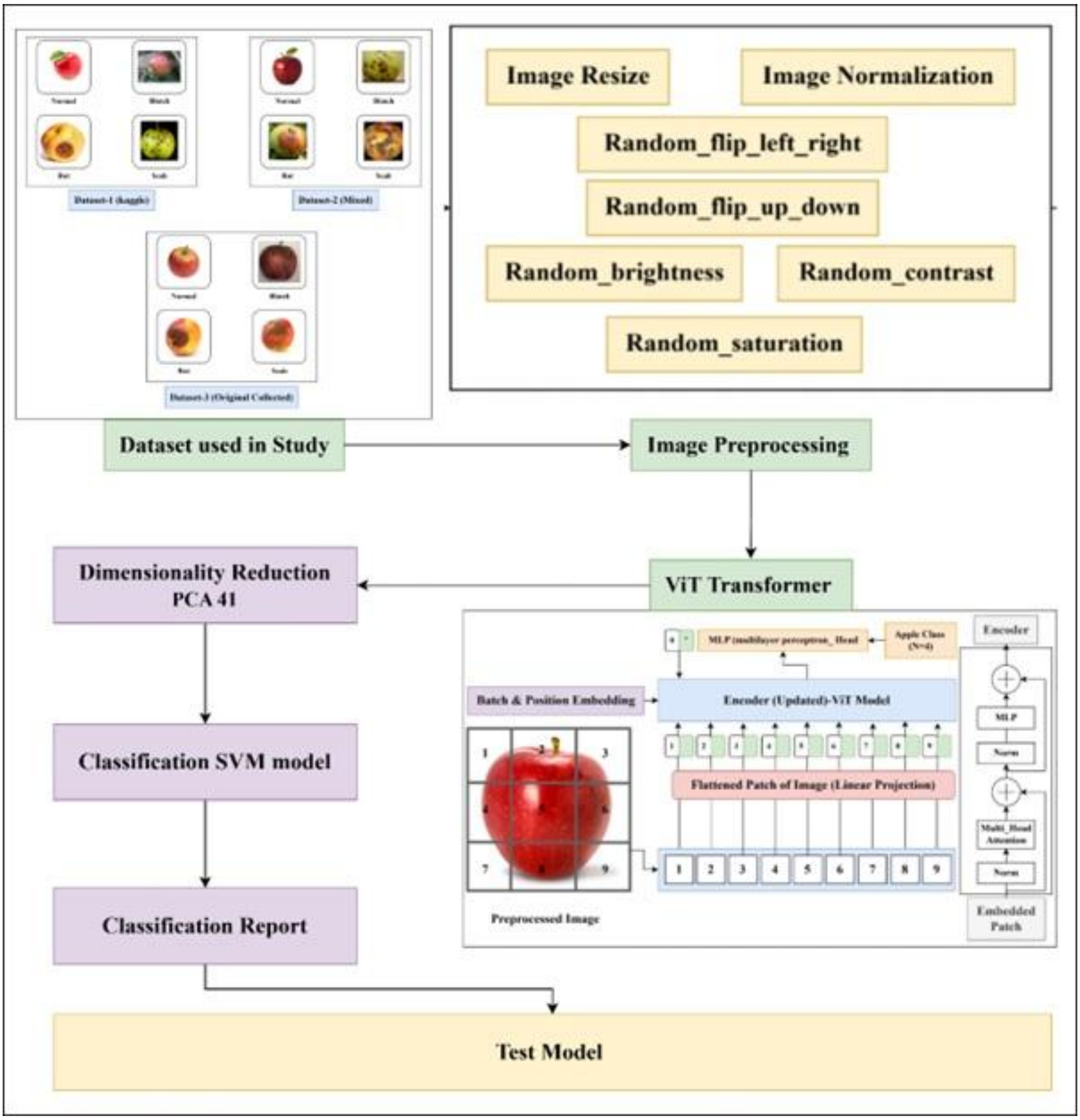

Figure 4 Proposed Hybrid Classification model development stages

Dimensionality Reduction Using PCA:

The ViT-generated features are high-dimensional, which can be computationally expensive for further analysis. Therefore, Principal Component Analysis (PCA) is applied to reduce the dimensionality of the features, retaining only the most significant 41 components. This dimensionality reduction step helps decrease computational requirements and mitigates the risk of overfitting while preserving essential information for accurate classification.

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Classification Using SVM Model:

The reduced feature set is then fed into a Support Vector Machine (SVM) model for classification. SVM is chosen for its robustness and effectiveness in handling high-dimensional data, making it a suitable choice for disease classification tasks. The SVM classifier assigns each apple image to one of the predefined classes: healthy, blotch, rot, or scab, based on the features extracted and reduced in previous steps.

Evaluation and Testing:

Finally, the model's performance is evaluated by generating a classification report that includes metrics such as accuracy, precision, recall, and F1-score. This report provides insights into the model's strengths and potential areas for improvement. After successful training and evaluation, the model is tested on unseen data to assess its generalization capability and real-world applicability.

Algorithm 2: Apple Fruit Disease Prediction Hybrid Model

Input: Apple images (categories: healthy, blotch, rot, scab)
Output: Predicted apple disease class

Dataset Preparation

1.1 Import three datasets:
- Dataset-1: Sourced images with labeled apple disease and healthy apple images.
- Dataset-2: Mixed sources of apple images with disease labels.
- Dataset-3: Original, collected dataset of apple images with specific labels for disease classes.

Image Preprocessing

2.1 For each image in the dataset:
- Resize the image to a consistent dimension.
- Normalize pixel values to standardize the image data.

2.2 Apply data augmentation to enhance model generalization:
- Randomly flip the image horizontally and vertically.
- Adjust the image brightness, contrast, and saturation for variety.

Feature Extraction Using Vision Transformer (ViT)

3.1 Divide each preprocessed image into smaller patches of equal size.
3.2 Flatten each patch and apply a linear projection to create patch embeddings.
3.3 Incorporate batch and position embeddings to retain spatial information across patches.
3.4 Use multiple encoder layers in the ViT architecture:
- Each layer includes multi-head attention to capture complex feature interactions.
- Use normalization layers to stabilize and enhance model performance.

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3.5 Extract high-dimensional feature vectors representing the visual characteristics of each image.

Dimensionality Reduction Using PCA

4.1 Apply Principal Component Analysis (PCA) on the ViT-generated features.

4.2 Retain the top 41 principal components to reduce dimensionality while preserving essential information.

Classification Using SVM

5.1 Input the reduced feature vectors into a Support Vector Machine (SVM) classifier.

5.2 Train the SVM model to classify each image into one of the predefined classes: healthy, blotch, rot, or scab.

Evaluation

6.1 Generate a classification report that includes metrics such as:

- Accuracy
- Precision
- Recall
- F1-score

6.2 Evaluate model performance on a validation set to ensure reliable predictions.

Testing

Test the trained model on unseen data to assess its generalization capability and real-world applicability.

End of Algorithm

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6. ML Model Evaluation Criteria

In classification modeling analysis, the true positive (TP) and true negative (TN) class were always generated during the experiment modeling steps and these classes were responsible for the accuracy of the model and the formula used in this study was following

$$\text{Accuracy} = (TP+TN)/(TP+FP+TN+FN)$$

Here FP and FN represent the false positive and false negative classes of the experiment of the model. Some other important formula used for the evaluation criteria was following

$$\text{Recall} = (TP)/(TP+FN)$$

$$\text{Precision} = (TP)/(TP+FP)$$

$$\text{F1-Score} = 2*\{(\text{precision}*\text{recall})/(\text{precision}+\text{recall})\}$$

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7. Result and Discussion

In present study the Hybrid model using ViT-SVM was developed and compare with various other models like CNN and Vit transformer for three different datasets. The datasets were split into 80% for training, 15% for testing and 5% for validation of the models. In present study all experiments were conduct using google collab framework having GPU facility to make the experiment fast. The total images used in the present study were present in table 2, table 3 and table 4 respectively.

Table 2 Total images in dataset-1 (Kaggle)
[https://www.kaggle.com/datasets/anilsandhii/apple-fruit-disease-images-dataset]

Class Type	Training	Testing	Validation	Total
Normal	723	250	115	1088
Blotch	1187	327	95	1609
Rot	1187	704	168	2059
Scab	864	324	123	1311

Table 3 Total images in dataset-2 (Mixed)

Class Type	Training	Testing	Validation	Total
Normal	1100	400	100	1500
Blotch	1100	400	100	1500
Rot	1100	400	100	1500
Scab	1100	400	100	1500

Table 4 Total images in dataset-3 (Original Collected)

Class Type	Training	Testing	Validation	Total
Normal	300	150	50	500
Blotch	300	150	50	500
Rot	300	150	50	500
Scab	300	150	50	500

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7.1 Preprocessing of the Images

The image preprocessing was the initial step for successful development of the model and then validation of the proposed model. The steps method selected for the image preprocessing was show in figure 5.

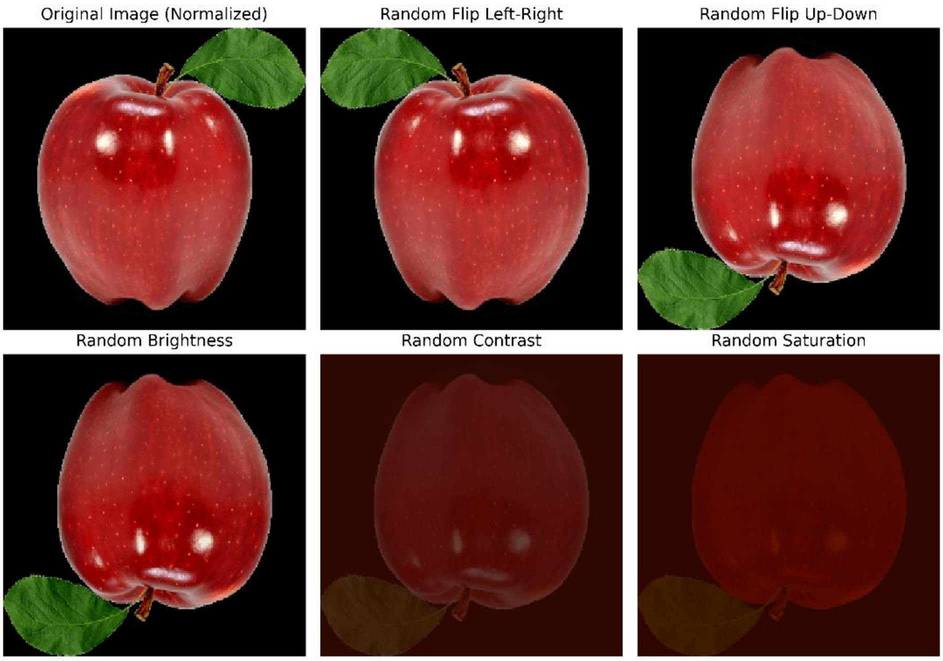

Figure 5 Image preprocessing for the present study

The associated parameters selected for the image preprocessing was present in table 5.

Table 5 Image preprocessing and its parameters selected for present study

Image Preprocessing	Parameter value
Normalization	1.0
Random Flip Left Right	0.5
Random Flip Up Down	0.5
Random Brightness	0.1
Random Contrast	(0.2,0.4)
Random Saturation	(2,6)

7.2 ViT model Parameters

The Vision Transformer (ViT) model in this setup uses a layered architecture designed to handle high-dimensional image data for the task of apple disease classification. The ViT model

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parameters and associated layers are crucial for feature extraction, classification, and overall model performance.

Input Layer (input_2):

The input layer accepts images with a shape of 224×224×3, where 224x224 represents the spatial dimensions, and 3 corresponds to the RGB color channels. This layer does not contain any trainable parameters, as its function is solely to define the shape and preprocess the input data for subsequent layers.

ViT Base Model (vit-b16):

This layer is a pretrained Vision Transformer model specifically set to generate a feature vector with 768 dimensions from the input image. The ViT model consists of multiple transformer encoders, which include attention heads and dense layers that collectively contain 85,798,656 parameters. These parameters are responsible for capturing spatial and contextual information within the image patches, creating rich feature embeddings that enhance the model's ability to recognize patterns associated with various apple diseases.

Flatten Layer:

Following the ViT model, a flattening layer reshapes the output feature vector into a one-dimensional array of 768 elements. This layer also has no parameters, as its purpose is to simplify the data structure for downstream layers.

Table 6 ViT model parameters selected for the present study

Type	Layer	Output Shape
Input	Input_2	(None,224,224,3)
Functional	ViT-b16	(None,768)
Flatten	Flatten	(None,768)
Dense	The_feature_layer	(None,64)
Dense	dense	(None,32)
Dense	Dense_1	(None,3)

Feature Layer (the_feature_layer):

This dense layer reduces the feature dimensions from 768 to 64, allowing the model to retain essential features while reducing computational complexity. It contains 49,216 parameters,

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which are fully connected weights that transform the high-dimensional features from the ViT model into a more compact representation.

Dense Layer:

The next dense layer further compresses the features to 32 dimensions, with a total of 2,080 parameters. This layer adds an additional level of abstraction, helping to refine the model's focus on relevant disease-specific features.

Output Layer (dense_1):

The final dense layer consists of 3 parameters, representing the three classes (healthy, blotch, rot, scab) for classification. With 99 parameters, this layer serves as the decision-making layer, outputting probabilities for each class. Overall, the ViT model in this configuration has a total of 85,850,051 parameters, all of which are trainable, enabling the model to learn from data and adapt to the complex visual pattern indicative of apple diseases.

7.3 Evaluation criteria results

In present study Hybrid SVM-VIT transformer model was developed and in this section accuracy, precision, F1-score and recall parameters. Taner et al [40] in their research work developed the equations for these performance parameters.

$$Accuracy = \frac{True_{+} + True_{-}}{True_{+} + True_{-} + False_{+} + False_{-}}$$

$$Precision = \frac{True_{+}}{True_{+} + False_{+}}$$

$$Recall = \frac{True_{+}}{True_{+} + False_{-}}$$

$$F1 = 2.\frac{Pre. Recall}{Pre + Recall}$$

In present study the hybrid of the SVM and ViT transformer model was adopted and then compare with regular deep learning models like CNN and others. The performance metrics of the deep learning models were present in table 7.

Table 7 Performance metrics analysis

Models	Accuracy	Precision	Recall	F1-Score

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VGG16	90.65	91.54	90.81	91.05
Inception V3	91.37	92.68	91.42	91.84
Mobile Net	93.68	94.92	93.81	94.35
Xception	92.51	92.97	91.86	93.42
Resnet150 V2	94.67	95.07	94.34	95.77
SVM	96.35	97.24	95.88	97.06
Hybrid-Model	97.65	98.12	96.75	98.35

Table 7 highlights the performance metrics—accuracy, precision, recall, and F1-score—of various models evaluated in the present research study. The findings underline significant differences in the efficacy of the models used for disease detection in apple fruits, with a clear trend toward improved performance in the hybrid model compared to traditional architectures. Below is a detailed discussion of these metrics:

Accuracy measures the overall correctness of the models in classifying diseased and healthy apples. The accuracy values ranged from 90.65% (VGG16) to 97.65% (Hybrid-Model). Among the pre-trained models, ResNet150 V2 achieved the highest accuracy (94.67%), demonstrating its ability to capture intricate details of apple diseases effectively. However, the SVM model surpassed this with an accuracy of 96.35%, leveraging its simplicity and robustness for classification tasks. The hybrid model excelled further, attaining 97.65% accuracy, showcasing the synergy of Support Vector Machines (SVM) and Vision Transformer (ViT) components with an optimized attention mechanism. This improvement indicates the hybrid model's superior ability to handle complex patterns and subtle disease features in apple datasets.

Precision reflects the model's ability to minimize false positives. The results show that precision values increased progressively across the models, with the hybrid model achieving the highest precision of 98.12%. The superior precision of the hybrid model indicates its remarkable ability to accurately identify diseased apple instances while minimizing misclassifications. Comparatively, MobileNet (94.92%) and ResNet150 V2 (95.07%) also performed well in this metric, emphasizing their reliable disease classification capability. The incremental improvement in precision from VGG16 (91.54%) to the hybrid model underscores the value of advanced attention mechanisms and feature optimization in disease detection.

Recall, which measures the model's sensitivity to correctly identify all diseased instances, followed a similar trend. The hybrid model achieved the highest recall (96.75%),

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outperforming other models significantly. SVM also performed commendably with a recall of 95.88%, while ResNet150 V2 and MobileNet showed comparable performance with values of 94.34% and 93.81%, respectively. Lower recall values in VGG16 (90.81%) and Inception V3 (91.42%) suggest a limitation in identifying some disease cases, possibly due to their inability to capture fine-grained features as effectively as the hybrid model.

The F1-score, which combines precision and recall into a single metric, further highlights the effectiveness of the hybrid model with a value of 98.35%. This surpasses the next-best model, SVM, which achieved an F1-score of 97.06%. Among the pre-trained models, ResNet150 V2 (95.77%) and MobileNet (94.35%) demonstrated strong performance, reinforcing their reliability for disease classification tasks. The hybrid model's superior F1-score reflects its balance between minimizing false positives and negatives, ensuring robust and reliable detection of apple diseases.

7.4 Discussion of the results

The results clearly demonstrate that the hybrid SVM-ViT model with an optimized attention mechanism outperformed all other models across all metrics. This superior performance can be attributed to the hybrid model’s ability to combine the feature extraction strengths of ViT with the classification robustness of SVM. Additionally, the attention mechanism enhances the model's focus on disease-relevant features, enabling it to capture subtle variations that other models might overlook. In contrast, pre-trained models like VGG16, Inception V3, and MobileNet, while performing satisfactorily, were less effective in handling the complexity of the dataset. The higher performance of ResNet150 V2 and SVM indicates their potential as standalone solutions but falls short of the hybrid model's capability in leveraging multi-level feature optimization. Overall, the findings highlight the hybrid model's potential for real-time apple disease detection, providing a reliable and efficient solution for agricultural applications. The superior performance across metrics validates the integration of advanced machine learning techniques for enhancing classification accuracy and robustness in practical scenarios.

Conclusion

The present study aimed to develop and evaluate a Hybrid SVM-ViT model for accurate detection of apple fruit diseases, comparing its performance with several pre-existing models, including CNNs and standalone ViT transformers, across three datasets of varying complexity and size. By integrating the feature extraction capabilities of Vision Transformers (ViT) with the robust classification capabilities of Support Vector Machines (SVM), the hybrid model

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demonstrated superior performance across all evaluation metrics: accuracy, precision, recall, and F1-score. The datasets used in this research were meticulously curated to cover diverse apple disease categories (normal, blotch, rot, and scab) with distinct splits for training, testing, and validation. Rigorous preprocessing steps were employed to normalize the data and augment it with random transformations, enhancing the model's ability to generalize to unseen instances. The ViT model, pre-trained on large-scale image datasets, provided a high-dimensional feature representation that was further optimized using dense layers, culminating in a compact feature set ideal for SVM classification.

The Hybrid SVM-ViT model achieved the highest accuracy (97.65%), precision (98.12%), recall (96.75%), and F1-score (98.35%) among all tested models, significantly outperforming conventional architectures like VGG16, MobileNet, and ResNet150 V2. The integration of an optimized attention mechanism allowed the hybrid model to effectively focus on disease-relevant features, improving its capability to handle complex patterns and subtle variations in apple fruit images. In comparison, standalone SVM and ResNet150 V2, while exhibiting strong results, fell short of the hybrid model's comprehensive efficacy. The findings of this study underscore the critical role of advanced attention mechanisms and hybrid architectures in addressing challenging classification tasks in agriculture. By leveraging the strengths of both ViT and SVM, the hybrid model offers a highly accurate and robust solution for real-time apple disease detection, demonstrating its potential for practical deployment in precision agriculture. Furthermore, the improved precision and recall metrics highlight the model's ability to minimize both false positives and false negatives, ensuring reliable disease classification. This research not only validates the Hybrid SVM-ViT model as a state-of-the-art approach for apple disease detection but also sets a benchmark for future studies in the field. The integration of sophisticated machine learning techniques, combined with carefully designed datasets and preprocessing strategies, provides a scalable and efficient framework for enhancing disease diagnosis accuracy in agricultural applications. Future work could explore real-time implementation, adaptation to other crops, and further optimization of model parameters to extend its applicability.

https://doi.org/10.71058/jodac.v10i02007

References

1. Food and Agriculture Organization of the United Nations. FAOSTAT Statistical Database; FAO: Rome, Italy, 2022. Available online: https://www.fao.org/faostat/en/#data/QCL/visualize (accessed on 15 January 2024).

2. Rachmawati, E.; Supriana, I.; Khodra, M.L. Toward a new approach in fruit recognition using hybrid RGBD features and fruit hierarchy property. In Proceedings of the 4th International Conference on Electrical Engineering, Computer Science and Informatics (EECSI), Yogyakarta, Indonesia, 19–21 September 2017; pp. 1–6.

3. Hameed, K.; Chai, D.; Rassau, A. A comprehensive review of fruit and vegetable classification techniques. Image Vis Comput. 2018, 80, 24–44.

4. Barbelian, M.A.; Bălan, C.V. Fault tree event classification by neural network analysis. UPB Sci. Bull. Series D Mech. Eng. 2017, 79, 55–66.

5. Bhargava, A.; Bansal, A.; Goyal, V. Machine learning–based detection and sorting of multiple vegetables and fruits. Food Anal. Methods 2022, 15, 228–242.

6. Abouelmagd, L. M., Shams, M. Y., Marie, H. S., & Hassanien, A. E. (2024). An optimized capsule neural networks for tomato leaf disease classification. EURASIP Journal on Image and Video Processing, 2024(1). https://doi.org/10.1186/s13640-023-00618-9

7. Abrams, J. M., Arkhipova, I. R., Belfort, M., Boeke, J. D., Curcio, M. J., Faulkner, G. J., Goodier, J. L., Lehmann, R., & Levin, H. L. (2018). Meeting report: mobile genetic elements and genome plasticity 2018. Mobile DNA, 9(1), 21. https://doi.org/10.1186/s13100-018-0126-3

8. Adem, K., Ozguven, M. M., & Altas, Z. (2022). A sugar beet leaf disease classification method based on image processing and deep learning. Multimedia Tools and Applications, 82(8), 12577–12594. https://doi.org/10.1007/s11042-022-13925-6

9. Admass, W. S., Munaye, Y. Y., & Bogale, G. A. (2023). Convolutional neural networks and histogram-oriented gradients: a hybrid approach for automatic mango disease detection and classification. International Journal of Information Technology, 16(2), 817–829. https://doi.org/10.1007/s41870-023-01605-z

10. Afsar, M. M., Bakhshi, A. D., Hussain, E., & Iqbal, J. (2024). A deep learning-based framework for object recognition in ecological environments with dense focal loss and

occlusion. Neural Computing and Applications, 36(16), 9591–9604. https://doi.org/10.1007/s00521-024-09582-5

11. Ahmad, N., Asif, H. M. S., Saleem, G., Younus, M. U., Anwar, S., & Anjum, M. R. (2021). Leaf Image-Based Plant Disease Identification Using Color and Texture Features. Wireless Personal Communications, 121(2), 1139–1168. https://doi.org/10.1007/s11277-021-09054-2

12. Alhussan, A. A., Khafaga, D. S., Abotaleb, M., Mishra, P., & El-Kenawy, E.-S. M. (2024). Global Potato Production Forecasting Based on Time Series Analysis and Advanced Waterwheel Plant Optimization Algorithm. Potato Research. https://doi.org/10.1007/s11540-024-09728-x

13. Amani, M. A., & Aghamohammadi, N. (2023). A novel technology to monitor effects of ethylene on the food products' supply chain: a deep learning approach. International Journal of Environmental Science and Technology, 21(5), 5007–5018. https://doi.org/10.1007/s13762-023-05328-3

14. Amas, J. C., Anderson, R., Edwards, D., Cowling, W., & Batley, J. (2021). Status and advances in mining for blackleg (Leptosphaeria maculans) quantitative resistance (QR) in oilseed rape (Brassica napus). TAG. Theoretical and Applied Genetics. Theoretische Und Angewandte Genetik, 134(10), 3123–3145. https://doi.org/10.1007/s00122-021-03877-0

15. Amri, E., Gulzar, Y., Yeafi, A., Jendoubi, S., Dhawi, F., & Mir, M. S. (2024). Advancing automatic plant classification system in Saudi Arabia: introducing a novel dataset and ensemble deep learning approach. Modeling Earth Systems and Environment, 10(2), 2693–2709. https://doi.org/10.1007/s40808-023-01918-9

16. Araújo, M. do S. B. de, Sudré, C. P., Graça, G. A. da, da Silva Alencar, A. A., da Costa Geronimo, I. G., & Rodrigues, R. (2022). A new approach to quantify anthracnose symptoms in inoculated Capsicum spp. fruits. Tropical Plant Pathology, 47(3), 386–401. https://doi.org/10.1007/s40858-022-00499-9

17. Archana, K. S., Srinivasan, S., Bharathi, S. P., Balamurugan, R., Prabakar, T. N., & Britto, A. S. F. (2022). A novel method to improve computational and classification performance of rice plant disease identification. The Journal of Supercomputing, 78(6), 8925–8945. https://doi.org/10.1007/s11227-021-04245-x

https://doi.org/10.71058/jodac.v10i02007

18. Ashwini, C., & Sellam, V. (2023). EOS-3D-DCNN: Ebola optimization search-based 3D-dense convolutional neural network for corn leaf disease prediction. Neural Computing & Applications, 35(15), 11125–11139. https://doi.org/10.1007/s00521-023-08289-3

19. Bagger, J. I., Lund, A., Albrechtsen, N. J. W., Christensen, M., Grøndahl, M. F., Hansen, C. P., Storkholm, J. H., Holst, J. J., Vilsbøll, T., & Knop, F. K. (2017). Increased liver fat content in totally pancreatectomised patients: analysis from the English Longitudinal Study of Ageing. Diabetologia, 60(Suppl 1), 22–23. https://doi.org/10.1007/s00125-017-4350-z

20. Bajait, V. S., & Malarvizhi, N. (2023). Taylor Remora optimization enabled deep learning algorithms for percentage of pesticide detection in grapes. Environmental Science and Pollution Research International. https://doi.org/10.1007/s11356-023-30169-5

21. Bali, N., & Singla, A. (2021). Emerging Trends in Machine Learning to Predict Crop Yield and Study Its Influential Factors: A Survey. Archives of Computational Methods in Engineering, 29(1), 95–112. https://doi.org/10.1007/s11831-021-09569-8

22. BaniMustafa, A., Qattous, H., Ghabeish, I., & Karajeh, M. (2023). A Machine Learning Hybrid Approach for Diagnosing Plants Bacterial and Fungal Diseases. International Journal of Advanced Computer Science and Applications, 14(1). https://doi.org/10.14569/ijacsa.2023.0140198

23. Bayram, H. Y., Bingol, H., & Alatas, B. (2022). Hybrid Deep Model for Automated Detection of Tomato Leaf Diseases. Traitement Du Signal, 39(5), 1781–1787. https://doi.org/10.18280/ts.390537

24. Behera, S. K., Rath, A. K., Mahapatra, A., & Sethy, P. K. (2020). Identification, classification & grading of fruits using machine learning & computer intelligence: a review. Journal of Ambient Intelligence and Humanized Computing, 1–11. https://doi.org/10.1007/s12652-020-01865-8

25. Bhagat, M., & Kumar, D. (2023). Efficient feature selection using BoWs and SURF method for leaf disease identification. Multimedia Tools and Applications, 82(18), 28187–28211. https://doi.org/10.1007/s11042-023-14625-5

26. Bhagat, M., Kumar, D., & Kumar, S. (2022). Bell pepper leaf disease classification with LBP and VGG-16 based fused features and RF classifier. International Journal of Information Technology, 15(1), 465–475. https://doi.org/10.1007/s41870-022-01136-z

https://doi.org/10.71058/jodac.v10i02007

27. Bhatia, A., Chug, A., Singh, A. P., Singh, R. P., & Singh, D. (2021). A machine learning-based spray prediction model for tomato powdery mildew disease. Indian Phytopathology, 75(1), 225–230. https://doi.org/10.1007/s42360-021-00430-3

28. Bhujade, V. G., & Sambhe, V. (2022). Role of digital, hyper spectral, and SAR images in detection of plant disease with deep learning network. Multimedia Tools and Applications, 81(23), 33645–33670. https://doi.org/10.1007/s11042-022-13055-z

29. Bishnoi, R., Kaur, S., Sandhu, J. S., & Singla, D. (2023). Genome engineering of disease susceptibility genes for enhancing resistance in plants. Functional & Integrative Genomics, 23(3), 207. https://doi.org/10.1007/s10142-023-01133-w

30. Bittremieux, W., Wang, M., & Dorrestein, P. C. (2022). The critical role that spectral libraries play in capturing the metabolomics community knowledge. Metabolomics : Official Journal of the Metabolomic Society, 18(12), 94. https://doi.org/10.1007/s11306-022-01947-y

31. Bols, E. M. J., Smits, L. J. M., & Weijenberg, M. P. (2015). Healthy Living: The European Congress of Epidemiology, 2015. European Journal of Epidemiology, 30(8), 709–1001. https://doi.org/10.1007/s10654-015-0072-z

32. Borghi, L., Vegni, E., Salvatici, E., Paci, S., Rovelli, V., & Giovannini, M. (2015). The first index case with coincidence of phenylketonuira, polysplenia syndrome and methylene tetrahydrofolate reductase mutation from newborn screening. Journal of Inherited Metabolic Disease, 38(S1), 104–105. https://doi.org/10.1007/s10545-015-9877-x

33. Bouguettaya, A., Zarzour, H., Kechida, A., & Taberkit, A. M. (2022). A survey on deep learning-based identification of plant and crop diseases from UAV-based aerial images. Cluster Computing, 26(2), 1297–1317. https://doi.org/10.1007/s10586-022-03627-x

34. Brodbelt, J. S., & Russell, D. H. (2018). A Focus Honoring Carol Robinson's Election to the National Academy of Sciences. Journal of the American Society for Mass Spectrometry, 30(1), 1–3. https://doi.org/10.1007/s13361-019-02232-4

35. Butlin, P. (2021). Sharing Our Concepts with Machines. Erkenntnis, 88(7), 3079–3095. https://doi.org/10.1007/s10670-021-00491-w

36. Buyukarikan, B., & Ulker, E. (2022). Classification of physiological disorders in apples fruit using a hybrid model based on convolutional neural network and machine learning

https://doi.org/10.71058/jodac.v10i02007

methods. Neural Computing and Applications, 34(19), 16973–16988. https://doi.org/10.1007/s00521-022-07350-x

37. Büyükarıkan, B., & Ülker, E. (2023). Convolutional neural network-based apple images classification and image quality measurement by light colors using the color-balancing approach. Multimedia Systems, 29(3), 1651–1661. https://doi.org/10.1007/s00530-023-01084-z

38. Cacicedo, J., Mendizabal, N., & Arietaleanizbeaskoa, M. S. (2021). Letter to the editor referencing "Body composition changes in patients with head and neck cancer under active treatment: a scoping review." Supportive Care in Cancer : Official Journal of the Multinational Association of Supportive Care in Cancer, 30(1), 1–2. https://doi.org/10.1007/s00520-021-05999-z

39. Ceyhan, M., Kartal, Y., Özkan, K., & Seke, E. (2023). Classification of wheat varieties with image-based deep learning. Multimedia Tools and Applications, 83(4), 9597–9619. https://doi.org/10.1007/s11042-023-16075-5

40. Chair, R. Y., Chair, K. J., Subcommittee, C., Collins, L. C., Fedoriw, Y., Weinreb, I., Chair, C., Adeniran, A., Allison, K. H., Dry, S., Faquin, W. C., Fritchie, K., Gordetsky, J., Katsakhyan, L., Melinda, P.-I.-T., Lerwill, J., Beatriz, M., Lopes, S., Naso, J., … Montgomery, E. (2022). USCAP 2022 Abstracts: Gastrointestinal Pathology (372-507). Laboratory Investigation; a Journal of Technical Methods and Pathology, 102(Suppl 1), 419–565. https://doi.org/10.1038/s41374-022-00753-3

41. Taner, A.; Mengstu, M.T.; Selvi, K.Ç.; Duran, H.; Gür, ˙I.; Ungureanu, N. Apple Varieties Classification Using Deep Features and Machine Learning. Agriculture 2024, 14, 252. https://doi.org/ 10.3390/agriculture14020252