# Benchmarking Hybrid Transfer Learning Architectures (VGG16, ResNet-50, InceptionV3) for Cauliflower Disease Classification

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Plant diseases pose a direct threat to farmers' income and the country's economy. Timely and accurate identification of plant diseases can minimize these losses and associated damages for farmers. Cauliflower is a highly versatile, nutrient-dense cruciferous vegetable consumed daily worldwide. It is rich in fiber and vitamin C and aids digestion. It is cultivated in winter worldwide, particularly in the USA, China, India, Bangladesh, and Pakistan. These plants are highly vulnerable to leaf diseases such as bacterial spot rot, downy mildew, and black rot, which can adversely reduce their yields and have a significant impact on agricultural productivity and food security. manual plant monitoring is difficult, as it is labor-intensive and time-consuming. Automatic plant disease recognition using deep learning algorithms is becoming increasingly common. This study used transfer learning algorithms such as VGG16, ResNet50, and InceptionV3 for feature extraction from cauliflower image datasets. These features are then classified using classical machine learning techniques such as Support Vector Machines (SVM), K-Nearest Neighbors (KNN), Logistic Regression (LR), and Random Forests (RF). The objective of this study was to benchmark the performance of these hybrid models. The ResNet50 features combined with Logistic Regression achieved the highest accuracy of 99.49%, whereas InceptionV3 features with Logistic Regression also performed strongly, reaching 98.98% accuracy. These findings confirm that combining deep feature extraction with conventional classifiers is highly effective, surpassing many current methods reported in the literature.

**Keywords**: Benchmarking; Cauliflower Disease; Hybrid Model; InceptionV3; Precision Agriculture; ResNet50; VGG16.

## Introduction:

Agriculture is fundamental for global food security and economic stability [1]. In developing countries, this sector supports rural communities through employment, income generation, and food provision. In the last two decades, the total economic value generated by agriculture has increased by 89%, reaching close to $3.8 trillion [2]. This growth highlights the importance of agriculture's role in the world's economy. However, plant diseases pose a direct threat to farmers' income and the country's economy, with pathogens causing around 40% of global food crop losses. The annual economic losses due to plant diseases are estimated at roughly $200 billion.

Cauliflower is a widely grown vegetable with high economic and nutritional value. It is rich in fiber and vitamin C and aids digestion. It is cultivated in winter worldwide, particularly in China, India, the USA, Bangladesh, and Pakistan. However, its production faces serious threats from diseases such as bacterial spot rot, downy mildew, and black rot [3]. These infections damage crop quality and reduce yields. Timely and accurate identification of plant diseases can minimize these losses and associated damages for farmers.

Farmers typically diagnose diseases through visual inspection. This approach requires expertise, is time-consuming, and can be inconsistent. Automated systems for detecting diseases from images are becoming increasingly important in modern farming. They enable early detection, consistent decision-making, and broader applicability across farms. Deep learning, particularly Convolutional Neural Networks (CNNs), has demonstrated strong performance in classifying plant diseases. However, standard CNN models require large labeled datasets and significant computational resources. This limitation can make it difficult to deploy in practical scenarios. Hybrid methods offer a viable solution. These methods extract features from deep learning models and classify them using traditional machine learning techniques. They often achieve high accuracy with simpler and faster models.

Our work compares deep learning models for classifying cauliflower leaf diseases using a collected image dataset. Features are extracted from three pretrained models: VGG16, ResNet50, and InceptionV3. These features are classified using four machine learning methods: Support Vector Machines (SVM), K-Nearest Neighbors (KNN), Logistic Regression (LR), and Random Forests (RF). We evaluate all combinations of feature extractors and classifiers to determine the most effective pairing. Our goal is to provide a practical and reliable tool for automated disease detection on farms. The main contributions of this study are:

We provide a detailed comparison of VGG16, ResNet50, and InceptionV3, establishing a clear performance benchmark for cauliflower disease classification.

We demonstrate that using deep networks as feature extractors in combination with standard classifiers improves performance compared to using deep learning models alone.

Our best-performing combination, ResNet50 with Logistic Regression, achieved 99.49% accuracy.

Our experiments show that these hybrid methods outperform several recent techniques reported in the literature.

## Literature Review:

Machine learning and deep learning methods are now widely used to detect plant diseases automatically. These techniques can identify distinguishing features and provide accurate classification. Many researchers have evaluated standard machine learning methods and deep learning models to recognize diseases in cauliflower and other crops.

[4] evaluated four deep learning models—EfficientNetB3, DenseNet121, VGG19, and ResNet50—for cauliflower disease classification, with EfficientNetB3 achieving the highest accuracy of 98%. In [5] k-means clustering was used for image segmentation followed by a Random Forest classifier, yielding 81.68% accuracy. They also evaluated transfer learning

models, including VGG16, ResNet50, MobileNetV2, and InceptionV3, where InceptionV3 achieved the highest accuracy of 90.08%. In [6], researchers developed Cauli-Det, a system based on YOLOv8, to classify and localize cauliflower diseases in smartphone images. Trained on 656 images, the model detected Bacterial Soft Rot, Downy Mildew, and Black Rot with 93.20% precision, 82.6% recall, and 91.10% mean average precision.

[7] developed a system to detect cauliflower leaf diseases using 11,150 images. Their model achieved 96.32% overall accuracy, with both precision and recall exceeding 96%, indicating reliability for early disease detection. A study conducted in Nepal [8] used 729 mobile phone images of cauliflower leaves representing healthy tissue and four diseases. The researchers fine-tuned pretrained CNN models such as NASNet Mobile, ResNet50, and InceptionV3, where ResNet50 achieved the highest accuracy of 93.47%. Another study [9] evaluated several CNN models on approximately 2,500 images of four cauliflower diseases. InceptionV3 achieved the highest test accuracy of 93.93%.

[10] developed a smartphone-based system to diagnose cauliflower diseases. They applied data augmentation, k-means clustering, texture feature extraction, and SMOTE. Among the classifiers evaluated, Logistic Regression achieved the highest accuracy of 90.77%. An online expert system was presented in [11] to identify four cauliflower diseases from mobile images. Using 776 images, the system applied k-means segmentation and extracted statistical and texture features. Random Forest was the best-performing classifier, achieving approximately 89% accuracy. [12] combined a CNN with an SVM in a hybrid model. Their approach achieved 97.52% accuracy on a dataset of 2,000 images, demonstrating strong precision, recall, and consistency across disease categories.

Beyond cauliflower, several studies have highlighted the effectiveness of multimodal and ensemble learning strategies for plant disease detection. In [13], an ensemble framework combining VGG16 and ResNet50 was proposed for potato leaf disease classification using the PlantVillage dataset. Feature-level fusion of both models significantly improved performance, achieving an accuracy of 98.22% compared to individual model accuracies of 95.68% and 96.16%, respectively. Similarly, a hybrid deep learning model named VGG-EffAttnNet was introduced in [14] for chili plant disease classification, integrating VGG16, EfficientNetB0, attention mechanisms, and Monte Carlo Dropout. Trained on a dataset of 5,000 images, the proposed model achieved an accuracy of 99%, outperforming individual networks and existing state-of-the-art methods. Comparative benchmarking of CNN architecture has also been explored for other crops. A study in [15] compared VGG16 and InceptionV3 for grape leaf disease classification using 500 high-resolution images, where InceptionV3 achieved a superior accuracy of 99.33% within only 10 training epochs. Furthermore, a hybrid framework integrating ResNet50 and InceptionV3 was presented in [16] to enhance robustness and generalization for multi-class plant disease classification. The proposed model achieved 97% accuracy and recall, with an F1-score of 96%, demonstrating its suitability for large-scale agricultural monitoring systems. A summary of related work on cauliflower and other crop diseases is provided in Table 1.

**Table 1.** Summary of related work on cauliflower and other crop diseases

| Ref. | Dataset | No. of Images | Techniques | Acc (%) |
|---|---|---|---|---|
| [4] | Cauliflower | 760 | EfficientNetB3, DenseNet121, VGG19, ResNet50 | 98.00 |
| [5] | Cauliflower | 500 | InceptionV3, Mobile NetV2, ResNet50, VGG16 | 90.08 |
| [6] | Cauliflower | 656 | YOLOV8 | 93.20 |
| [7] | Cauliflower | 11150 | Deep Models | 96.32 |

| | | | | |
|---|---|---|---|---|
| [8] | Cauliflower | 729 | NASNet Mobile, ResNet50, and Inception V3. | 93.47 |
| [9] | Cauliflower | 2500 | InceptionV3 | 93.93 |
| [10] | Cauliflower | 1920 | K-means, GLCM, SMOTE | 90.77 |
| [11] | Cauliflower | 776 | Random Forest | 89.00 |
| [12] | Cauliflower | 2000 | CNN–SVM | 97.52 |
| [13] | Potato | 2152 | VGG16, ResNet50, Ensemble VGG16 & ResNet50 | 95.68, 96.16, 98.22 |
| [14] | Chili | 5000 | VGG16, EfficientNetB0, VGG-EffAttnNet | 96.80, 96.50, 99.00 |
| [15] | Grapes | 500 | VGG16, InceptionV3 | 99.33 |
| [16] | Multi-Crops | 87000 | ResNet50, InceptionV3 | 97.00 |

**Materials and Methods:**

**Dataset:**

The VegNet dataset [17] was is a publicly available benchmark dataset from Kaggle. It consists of 656 cauliflower images categorized into four classes: Downy Mildew, Black Rot, Bacterial Spot Rot, and Healthy, as summarized in Table 2. The images were acquired under controlled environmental conditions. Representative sample images are shown in Figure 1. This dataset is designed to facilitate multi-class disease classification tasks and enable reliable disease diagnosis.

**Table 1.** Dataset Class-wise image distribution

| Sr. No | Category | Total Images |
|---|---|---|
| 1 | Bacterial Spot Rot | 173 |
| 2 | Black Rot | 100 |
| 3 | Downy Mildew | 177 |
| 4 | Healthy | 206 |
| | **Total** | **656** |

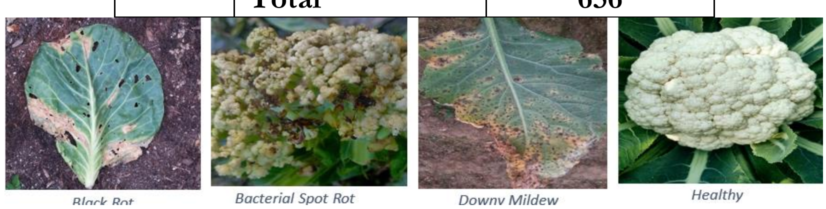


**Figure 1**. Sample Images from VEGNET Dataset

**Preprocessing:**

Several preprocessing steps prepare the images for analysis. All images are resized to 224 × 224 pixels to match the input size expected by the deep learning models. We also apply Contrast Limited Adaptive Histogram Equalization (CLAHE) [18]. This method improves local contrast in the images without excessively amplifying noise. It is especially useful for highlighting visual patterns associated with plant diseases. These steps produce cleaner, more uniform images, improving the quality of extracted features and enhancing classifier performance. Figure 2 shows samples of these preprocessing techniques.


**Figure 2.** Pre-Processing Techniques

**Feature Extraction:**

**VGG16**:

VGG16 is a deep convolutional neural network developed by the Visual Geometry Group at the University of Oxford and originally trained on the ImageNet dataset in 2014. comprising 16 trainable layers, from which the model derives its name[19]. It is distinguished by a uniform and deep structure based on stacked 3 × 3 convolutional filters across multiple layers, enabling the extraction of rich, hierarchical visual features, as illustrated in Figure 3. Due to its architectural simplicity and strong feature extraction capability, VGG16 has been widely used for image classification and object detection tasks, making it a suitable choice for deep feature extraction in this study.

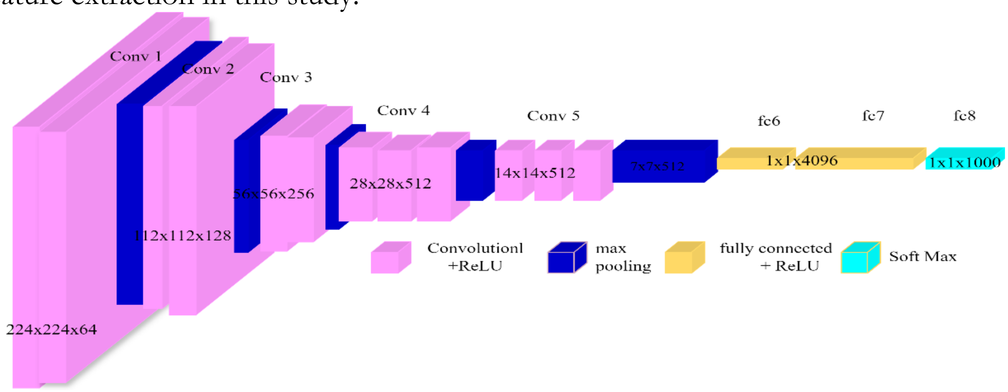


**Figure 3.** Architecture of VGG16

**ResNet50:** ResNet-50 is a 50-layer convolutional neural network designed to improve training efficiency [20]. It addresses common challenges in deep networks, such as vanishing gradients, by incorporating skip connections that allow each layer to refine existing features rather than learn entirely new representations. This approach, known as residual learning, enhances network stability and improves convergence. The model is composed of repeated residual blocks that enable smooth gradient flow during training. Due to its ability to extract robust and meaningful features, ResNet-50 is widely used for image classification, object detection, and applications in medical and agricultural image analysis. Figure 4 illustrates the ResNet50 architecture.

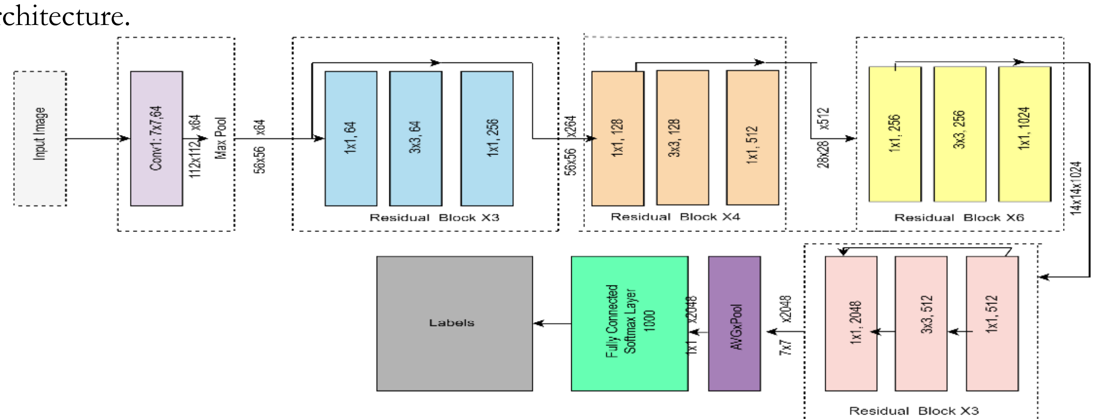


**Figure 4.** Architecture of ResNet50

**InceptionV3:** InceptionV3 is a convolutional neural network designed to be both accurate and efficient [21]. It employs factorized convolutions, asymmetric filters, and auxiliary classifiers. These design choices reduce the parameter count and enhance learning stability. The model's Inception modules capture features at multiple scales, allowing it to identify both fine details and broader patterns. This efficient and effective architecture has made InceptionV3 a popular choice for image classification. Figure 5 illustrates the InceptionV3 architecture.

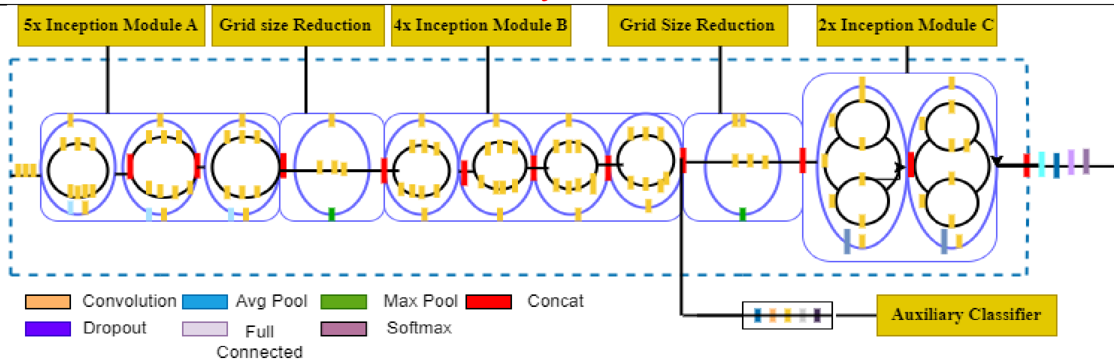


**Figure 5.** Architecture of InceptionV3

**Classification:**

The deep features extracted earlier are classified using four established machine learning classifiers: Support Vector Machine (SVM), K-Nearest Neighbors (K-NN), Logistic Regression (LR), and Random Forest (RF). Classical models typically perform well when training data is limited, whereas deep models generally achieve better results with large amounts of training data. Both types of models have their own strengths and weaknesses, and this study aims to explore the effectiveness of a hybrid approach, where features are extracted using deep models and then classified using traditional machine learning methods. We applied all four classifiers to each extracted deep feature vector, creating a total of 12 different combinations to analyze. This approach leverages the complementary strengths of both techniques. The interpretability and simplicity of classical machine learning combine with the nonlinear power of deep models, resulting in a more robust and reliable classification pipeline. The flow diagram of the model is shown in Figure 6.

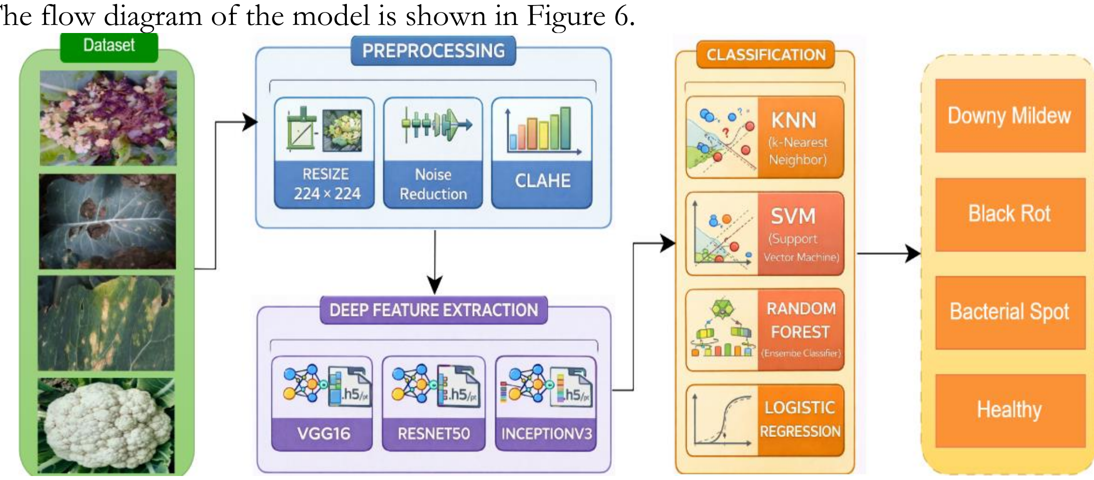


**Figure 6.** Flow diagram of the proposed method

**Results and Discussion:**

The model's performance was evaluated using standard metrics, including accuracy, recall, F1-score, and precision. Accuracy represents the proportion of correctly classified samples among the total number of samples and is calculated using Eq. (1), serving as an indicator of the model's reliability with a balanced number of infected and healthy cauliflower images. Precision evaluates the model's reliability when predicting a specific disease, such as Black Rot, Bacterial Spot, or Downy Mildew, out of all positive predictions and is calculated using Eq. (2). Recall measures the model's ability to identify the proportion of all actual disease samples (true positives) among all ground truths and is computed using Eq. (3). Finally, the F1-score, the harmonic mean of precision and recall, reflects how accurately the model distinguishes between diseased and non-diseased samples and is calculated using Eq. (4). In Equations (1) to (4), the following abbreviations are used: TP corresponds to true positive outcomes, TN stands for true negatives, FP denotes false positives, and FN represents false negatives.

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

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

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

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

Where:

**TP (True Positives):** Correctly predicted positive samples
**TN (True Negatives):** Correctly predicted negative samples
**FP (False Positives):** Incorrectly predicted positive samples
**FN (False Negatives):** Incorrectly predicted negative samples

**Results using InceptionV3 Model:**

The results indicate that transfer learning using InceptionV3 provides strong performance for cauliflower disease detection when combined with traditional machine learning classifiers. Logistic Regression demonstrates the highest performance, achieving an accuracy of 98.98%, a precision of 99.22%, a recall of 99.05%, and an F1-score of 99.12%. These values indicate a well-balanced model that effectively identifies diseased leaves while minimizing both false positive and false negative rates. Support Vector Machine (SVM) also performs strongly, with accuracy, precision, recall, and F1-score of 97.46%, 97.54%, 97.25%, and 97.36%, respectively. These findings suggest that SVM is a reliable and robust approach for cauliflower disease detection. Random Forest achieves an accuracy of 94.42%, with a precision of 94.65%, a recall of 94.05%, and an F1-score of 94.28%. Although these results are satisfactory, they indicate that tree-based methods may be less suited to the deep features extracted in this case. The K-Nearest Neighbor (KNN) classifier shows the lowest performance among the tested models, with accuracy, precision, recall, and F1-score of 92.39%, 92.02%, 92.89%, and 91.77%, respectively. Overall, the performance ranking suggests that linear classifiers, such as Logistic Regression and SVM, are highly effective in leveraging the pre-trained patterns learned by InceptionV3, which capture discriminative features such as leaf texture and visual disease characteristics. Table 3 presents the numerical results, and the corresponding confusion matrices are illustrated in Figure 7 for performance analysis.

**Table 3.** Evaluation results using InceptionV3

| Sr No | Classifier | Accuracy (%) | Precision (%) | Recall (%) | F1-Score (%) |
|---|---|---|---|---|---|
| 1 | KNN | 92.39 | 92.02 | 92.89 | 91.77 |
| 2 | SVM | 97.46 | 97.54 | 97.25 | 97.36 |
| 3 | Random Forest | 94.42 | 94.65 | 94.05 | 94.28 |
| 4 | Logistic Regression | 98.98 | 99.22 | 99.05 | 99.12 |

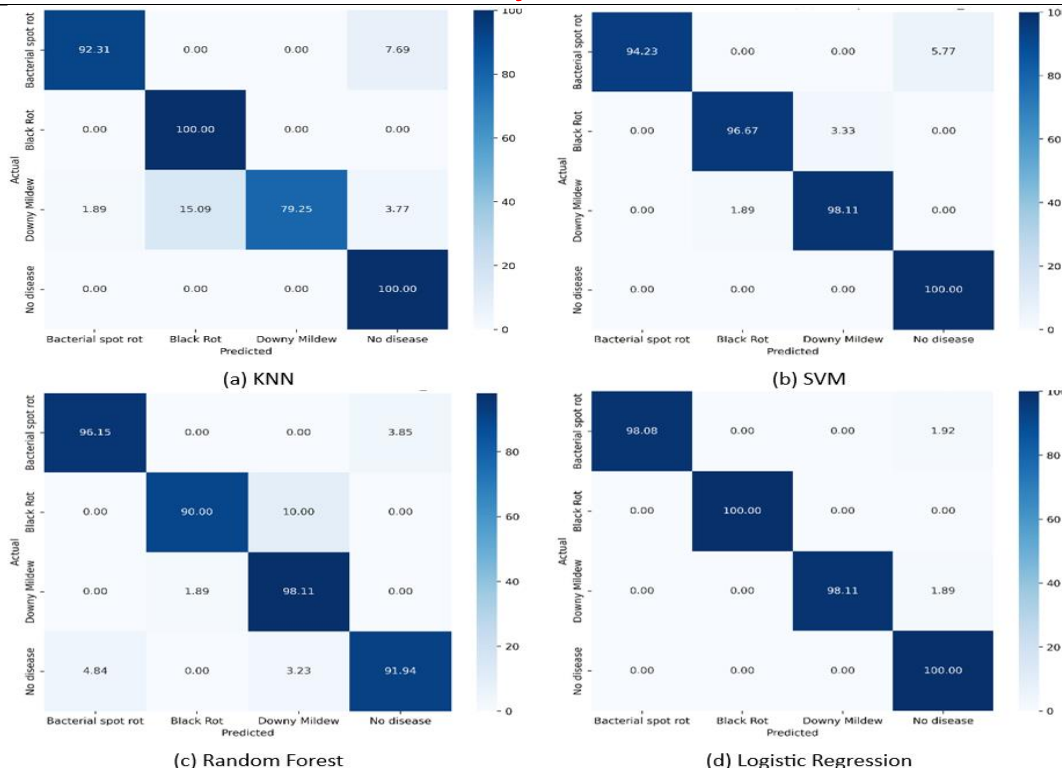


**Figure 7.** Confusion matrices for InceptionV3 features across different classifiers: (a) k-NN, (b) SVM, (c) Random Forest, and (d) Logistic Regression

**Results for VGG16:**

The results obtained from VGG16 show a consistent classifier ranking, with Logistic Regression achieving the highest performance, reaching an accuracy of 97.97%, a precision of 97.83%, a recall of 98.16%, and an F1-score of 97.99%. These values indicate a well-balanced and robust model capable of accurately identifying diseased areas. Support Vector Machine (SVM) follows closely, attaining an accuracy of 95.94%, a precision of 95.61%, a recall of 96.05%, and an F1-score of 95.82%. The consistent performance of SVM suggests its suitability for practical field applications and reliable decision-making. Random Forest (RF) achieves an accuracy of 94.42%, with a precision of 95.28%, a recall of 93.10%, and an F1-score of 93.90%. Although the model shows stable performance, the lower recall suggests slightly reduced sensitivity to diseased cases. K-Nearest Neighbor (KNN) exhibits the lowest performance, with accuracy, precision, recall, and F1-score of 91.37%, 90.20%, 91.58%, and 90.16%, respectively, suggesting that distance-based methods may be less effective with the high-dimensional features extracted by VGG16. Overall, the results indicate that the deep feature representations extracted by VGG16 integrate well with linear classifiers, especially Logistic Regression, which effectively constructs discriminative decision boundaries by leveraging complex textures and disease-specific patterns. The complete quantitative results are presented in Table 4, while the corresponding confusion matrices are illustrated in Figure 8.

**Table 4.** Evaluation results using VGG16

| Sr. No. | Classifier | Accuracy (%) | Precision (%) | Recall (%) | F1-Score (%) |
|---|---|---|---|---|---|
| 1 | KNN | 91.37 | 90.20 | 91.58 | 90.16 |
| 2 | SVM | 95.94 | 95.61 | 96.05 | 95.82 |
| 3 | Random Forest | 94.42 | 95.28 | 93.10 | 93.90 |
| 4 | Logistic Regression | 97.97 | 97.83 | 98.16 | 97.99 |

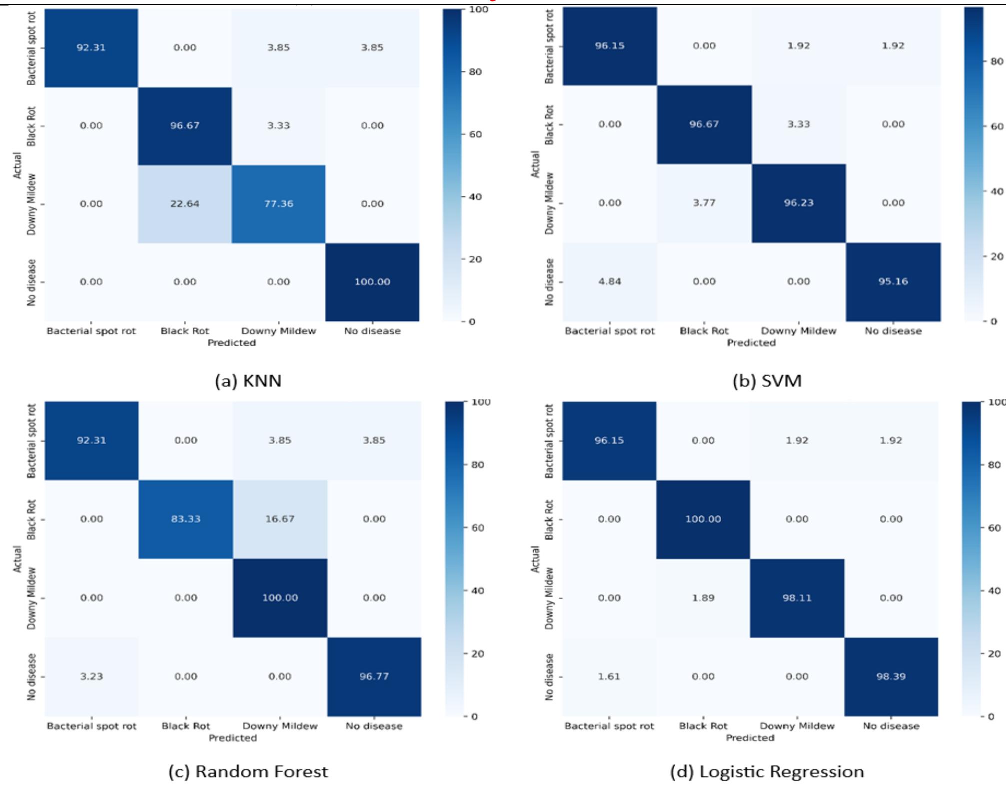


**Figure 8.** Confusion matrices for VGG16 features across different classifiers: (a) k-NN, (b) SVM, (c) Random Forest, and (d) Logistic Regression

**Results for ResNet50:**

The results obtained using ResNet-50-based transfer learning also exhibit the best performance for cauliflower disease detection. Logistic Regression achieves the highest overall performance, with an accuracy of 99.49%, a precision of 99.60%, a recall of 99.52%, and an F1-score of 99.56%. These results indicate accurate disease identification with minimal misclassification. SVM also delivers strong results, achieving an accuracy, precision, recall, and F1-score of 98.98%, 99.09%, 98.69%, and 98.87%, respectively. This performance demonstrates the reliable nature of SVM for prompt and accurate decision-making in practical agricultural applications. Random Forest achieves an accuracy of 96.45%, with a precision of 96.83%, a recall of 95.74%, and an F1-score of 96.18%, showing balanced performance suitable for real-world field applications. KNN exhibits the lowest performance, achieving an accuracy of 95.43%, with a precision, recall, and F1-score of 95.38%, 95.69%, and 95.32%, respectively. The results suggest that KNN is comparatively less effective for the rich and high-dimensional feature representations extracted by ResNet50. Overall, these findings indicate the strong compatibility of ResNet50 features with linear classifiers, especially Logistic Regression, which effectively constructs precise decisions based on complex visual patterns of plant images. The complete numerical results are shown in Table 5, and the corresponding confusion matrices are provided in Figure 9.

**Table 5.** Evaluation results using ResNet50

| Sr No | Classifier | Accuracy (%) | Precision (%) | Recall (%) | F1-Score (%) |
|---|---|---|---|---|---|
| 1 | KNN | 95.43 | 95.38 | 95.69 | 95.32 |
| 2 | SVM | 98.98 | 99.09 | 98.69 | 98.87 |
| 3 | Random Forest | 96.45 | 96.83 | 95.74 | 96.18 |
| 4 | Logistic Regression | 99.49 | 99.60 | 99.52 | 99.56 |

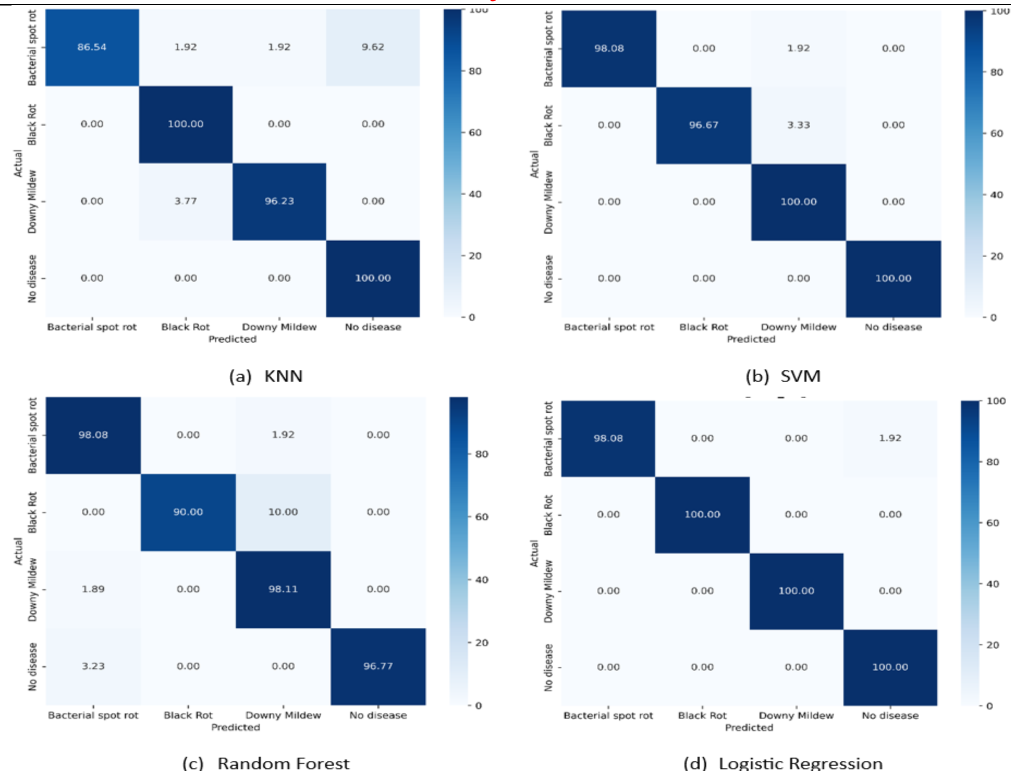


**Figure 9.** Confusion matrices for ResNet50 features across different classifiers: (a) k-NN, (b) SVM, (c) Random Forest, and (d) Logistic Regression

**Discussion:**

Among the transfer learning models evaluated, ResNet50 combined with Logistic Regression performs best for detecting cauliflower diseases. It achieves an accuracy of 99.49%, precision of 99.60%, recall of 99.52%, and an F1-score of 99.56%. The residual connections in ResNet50 allow the network to learn detailed disease patterns, such as early blight or Alternaria leaf spots, without suffering from gradient degradation. This makes the model well-suited for capturing subtle visual details in agricultural images. InceptionV3 with Logistic Regression also performs strongly, achieving 98.98% accuracy and metrics close to 99% across the board. Its multi-scale convolutional design helps it capture lesions of different sizes effectively. However, it does not reach the highest level of refinement shown by ResNet50.

VGG16 paired with Logistic Regression yields more moderate results, with an accuracy of 97.97% and other metrics around 98%. Its straightforward stacking of convolutional filters works reliably for detecting edges and textures. Still, its simpler architecture can sometimes overfit on uniform crop backgrounds, which may slightly limit its performance. KNN proves consistently weakest across all backbones, ranging from 91.37% to 95.43% accuracy, as distance metrics falter in the high-dimensional spaces created by deep feature extractors, where noise from lighting or angles gets amplified. On average, SVM and Random Forest perform in the 94–99% range, with SVM's margin optimization suiting linearly separable features, while Random Forest struggles more with correlated disease traits.

Overall, cleaner embeddings from residual and efficient architectures favor simple linear classifiers, which explains why ResNet50 combined with Logistic Regression delivers the most practical precision for complex plant imagery. The comparison results are presented in Figure 10. As illustrated in Figure 11, the proposed framework demonstrates superior performance on the VegNet dataset compared to existing benchmarks. Specifically, the integration of Logistic Regression with ResNet50 and InceptionV3 achieved state-of-the-art accuracies of 99.49% and 98.98%, respectively.

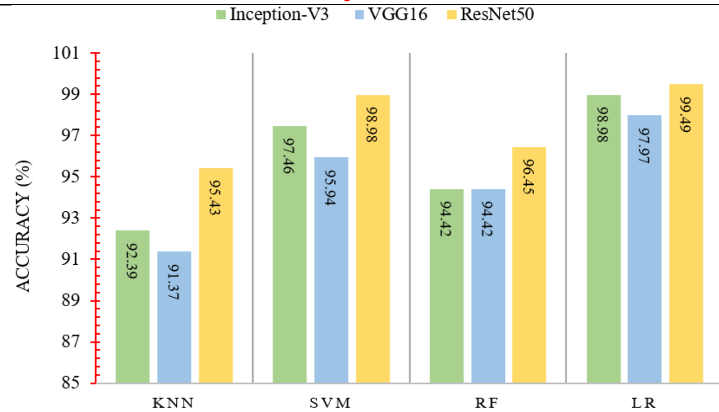


**Figure 10.** Accuracy comparison of different classifiers

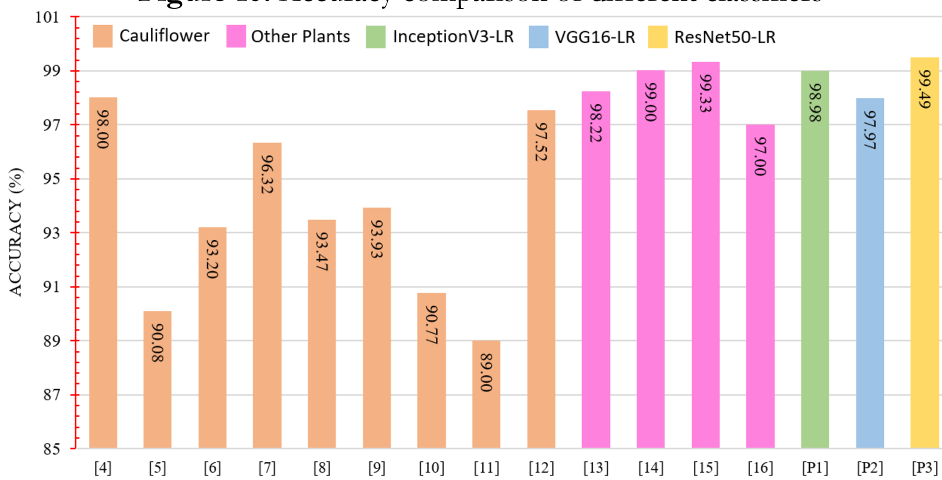


**Figure 11:** Accuracy comparison with state-of-the-art techniques

## Conclusions:

This study evaluates hybrid transfer learning frameworks for classifying cauliflower diseases. The results demonstrate clear performance improvements from combining deep feature extraction with conventional statistical classifiers. By testing VGG16, ResNet50, and InceptionV3 with multiple machine learning classifiers, we identified the ResNet50 and Logistic Regression combination (ResNet50-LR) as the most effective approach. It achieved a peak accuracy of 99.49%. Our experiments consistently show that these hybrid setups perform better than standalone deep learning models and several current methods reported in recent literature. The findings validate that using pretrained networks to extract features, followed by statistical classification, creates a reliable tool for early disease detection. This approach is important for safeguarding crop yields and supporting the adoption of digital tools in sustainable agriculture. In future work, we aim to implement this optimized hybrid framework in lightweight mobile applications and IoT edge devices. T This implementation would enable real-time, on-site disease monitoring for farmers. Future research will also aim to expand the dataset to cover additional cauliflower growth stages and diverse environmental conditions.

**Author Contributions:** Conceptualization: SP and WA; Methodology: SP, WA, and SMA; Software and Validation: SP; Formal analysis: SP, WA, and SMA; Data curation: SP; Original draft preparation: SP; Review and editing: WA; Supervision: WA; All authors have read and agreed to the published version of the manuscript.

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**Data Availability Statement:** The dataset used in this research is publicly available at https://www.kaggle.com/datasets/musabbirarrafi/vegnet-organized-dataset-of-cauliflower-disease. Further inquiries can be directed to the corresponding author.
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**Conflicts of Interest:** The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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