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PROTOINCNET: A PROTOTYPICAL NETWORK-BASED DEEP LEARNING APPROACH FOR CLASSIFYING RICE LEAF DISEASES

Muhammad Adeel Zafar[*1], Muhammad Noman Zafar[2], Abdul Manan Zafar[3], Iftikhar Sarwar[4]

[1]*Department of Artificial Intelligence, The Islamia University of Bahawalpur, Bahawalpur 63100, Pakistan*
[2]*Department of MSE Management, The University of Hertfordshire, Hatfield AL10 9AB, England*
[3]*Department of Computer Science, Bahria University Lahore Campus, Lahore 54000, Pakistan*
[4]*Department of Artificial Intelligence, The Islamia University of Bahawalpur, Bahawalpur 63100, Pakistan*

[*1]adeelbhai78945@gmail.com, [2]mz24abm@herts.ac.uk, [3]mannanfiver2000@gmail.com, [4]iftikhar.sarwar1032@gmail.com

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Corresponding Author: *
Muhammad Adeel Zafar

Abstract

Rice disease is always a challenge worldwide, particularly with the harmful threats of Leaf Blast, Brown Spot, and Hispa to rice crops. This study proposes a comprehensive meta- learning framework, ProtoIncNet, that integrates InceptionV3 for feature extraction and Prototypical Networks for classification, combining advanced deep learning techniques to effectively address the challenges of rice leaf disease classification. The proposed model was trained on the Rice Crop Dataset, which consists of images representing four rice leaf categories: Leaf Blast, Brown Spot, Hispa, and Healthy, capturing intricate patterns and features associated with each disease. The model was comprehensively trained on this complex dataset to identify subtle distinctions that determine the presence of these paddy diseases. This approach shows that combining transfer learning with few-shot learning enables accurate disease detection even with limited data, offering a scalable path toward explainable and farmer-friendly digital agriculture systems. To evaluate its effectiveness, we compared ProtoIncNet with ResNet50, VGG16, and EfficientNet under the same experimental conditions. The proposed approach achieved the highest accuracy of 98.3%, significantly outperforming these baseline models. Its deployment can help large-scale farmers mitigate crop losses and promote the adoption of digital agriculture systems in developing regions.

1 INTRODUCTION

Rice is a vital staple food that significantly influences global economies, diets, and cultures, sustaining millions worldwide. It serves as a critical driver of food security, playing a central role in social stability and economic growth Azim et al. (2021). Geographical factors, such as resource availability, environmental conditions, and cultural practices, have a large impact on rice production and consumption. As a staple for over 70 percent of the global population, particularly in Asia, Africa, and America, rice is essential for preventing malnutrition and ensuring food security USD.

From 2018/19 to 2022/23, the top rice-producing countries were China, producing an annual average of 147.691 million tons, followed by India with 125.038 million tons, Bangladesh with 35.511 million tons, and Indonesia with 34.360 million tons Ric (a); Li et al. (2024). India has dominated global rice exports since 2012, peaking at 22.1 million tons in 2022 Top; Mehnaz and Islam (2025).

Despite its significance, rice faces major threats from diseases such as rice blast, a devastating microbial infection caused by the filamentous ascomycete fungus Aggarwal and Mall (2002). This cyclic disease infects rice tissues above ground through asexual spores called conidia. The pathogen adheres to the rice cuticle with adhesive at the apex of the spore and generates turgor pressure up to 8.0 MPa to penetrate it. Once inside, the fungus produces invasive spores and releases toxins that weaken the immune system of the host, allowing rapid spread Ghatak et al. (2013). Rice blast poses a significant threat to global food security by reducing rice production, a staple for much of the world's population. Integrated management focuses on early prevention to mitigate yield losses. A deeper understanding of the pathogen, its interaction with hosts and the environment, and its dispersal under global warming can improve management strategies Deng et al. (2017).

Rice production faces challenges from climate change, extreme weather events, and environmental pollution. Programs like Africa's "New Rice for Africa" and crop simulation models such as CERES-Rice and ORYZA aim to improve rice resilience and improve yields under varying climate scenarios Asibi et al. (2019); Rao (2020). In Vietnam's LMD region, ground-level ozone pollution caused 9593.52 tons of rice yield loss, valued at 2761.01 thousand dollars, emphasizing the need for emissions controls to safeguard rice cultivation Bui and Nguyen (2023). Integrated policies and advanced technologies are essential for sustainable rice production and food security Chen and Wang (2023).

Compares global mean temperature, average global rice yield and highest national rice yield from 1961 to 2018. The yellow line represents the steadily increasing average yield of world rice, showing continuous improvements over time, probably due to advancements in agricultural technology, irrigation, and crop management practices. The magenta dotted line shows the top yield, which fluctuates significantly, reflecting the variability of peak productivity in different nations during certain years. The green line corresponds to the global mean temperature, which shows a gradual but consistent upward trend in figure 1, highlighting the impact of global warming over the observed period Cai et al. (2022). The figure emphasizes the concurrent rise in average rice yields despite increasing global temperatures, suggesting a complex relationship between climate change and rice production. This relationship demonstrates the need for sustainable agricultural practices to mitigate the possible adverse effects of climate change on rice yields.

Key Contributions:

- Developed a highly accurate rice leaf disease classification system, achieving 98.33% accuracy by fine-tuning the InceptionV3 model within the ProtoIncNet framework and applying few-shot learning (4-way 15-shot).

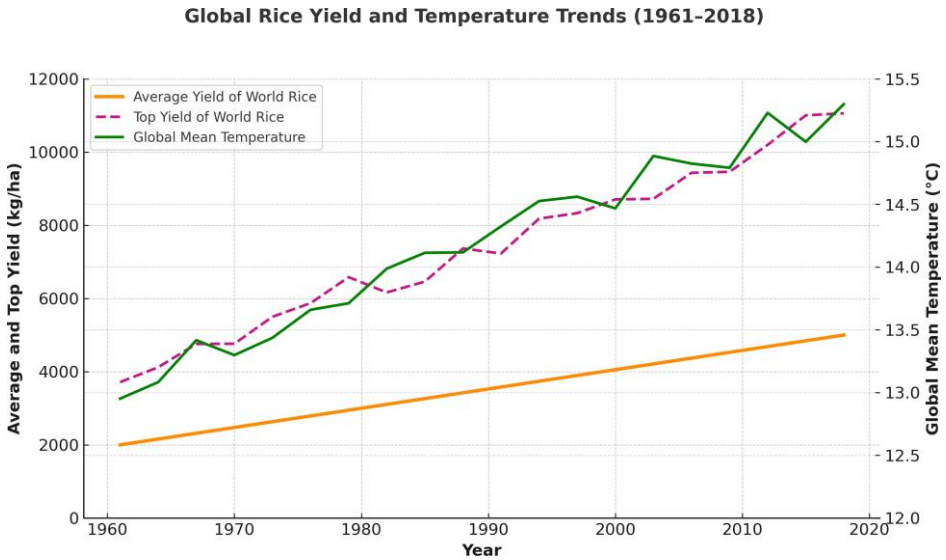


Figure 1: Average and top yields (kg/ha) of world rice yields have increased steadily from 1961 to 2018, global temperatures (°C) have also risen, highlighting a potential link between climate change and agricultural productivity

- Leveraged Prototypical Networks to enable strong performance even with limited training data, making the system suitable for real-world agricultural scenarios where labeled data is scarce.
- Designed the system with real-time deployment in mind, with future plans to integrate it into mobile applications or edge devices. The approach is also scalable to other crops and supports the incorporation of **explainable AI** for greater transparency.

Conventional machine learning models often depend on extensive labeled datasets, which are difficult to obtain for certain plant diseases. This highlights the need for a system capable of performing accurately with limited data while ensuring reliable disease detection in practical farming scenarios.

Address the problem by fine-tuning the InceptionV3 model combined with few-shot learning techniques like Prototypical Networks. This approach allows the model to achieve high accuracy despite the small dataset, making it practical for real-world agricultural applications. To ensure a fair and comprehensive evaluation, this study includes a comparative analysis with widely used CNN architectures such as ResNet50, VGG16, and EfficientNet, which serve as strong baselines in medical image classification tasks.

Focuses on building an efficient rice plant disease detection system that works even when limited training data is available. It targets four main categories: Leaf Blast, Hispa, Brown Spot, and Healthy Leaves, with the aim of supporting farmers with an easy-to-use and reliable solution.

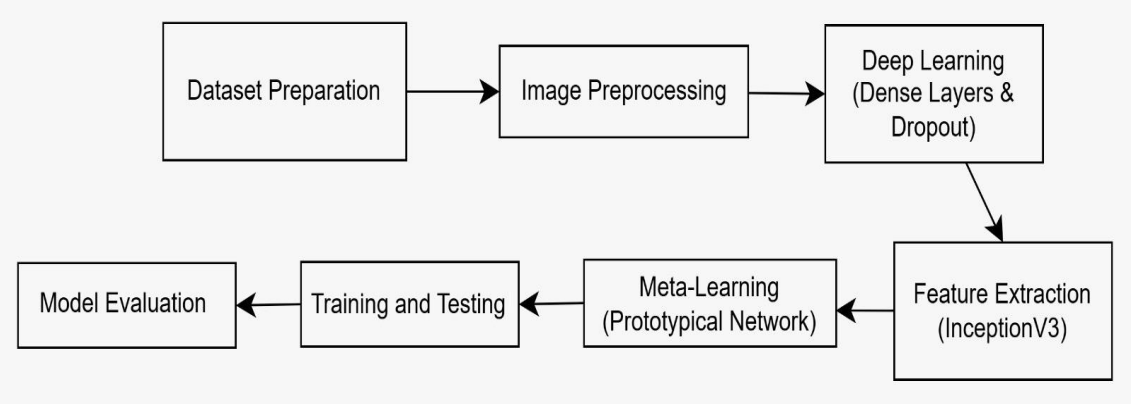


Figure 2: Overview of the proposed rice leaf classification framework (ProtoIncNet). The pipeline consists of four main stages: (i) data preprocessing, (ii) feature extraction using InceptionV3, (iii) meta-learning-based classification with Prototypical Networks, and (iv) model evaluation across multiple metrics.

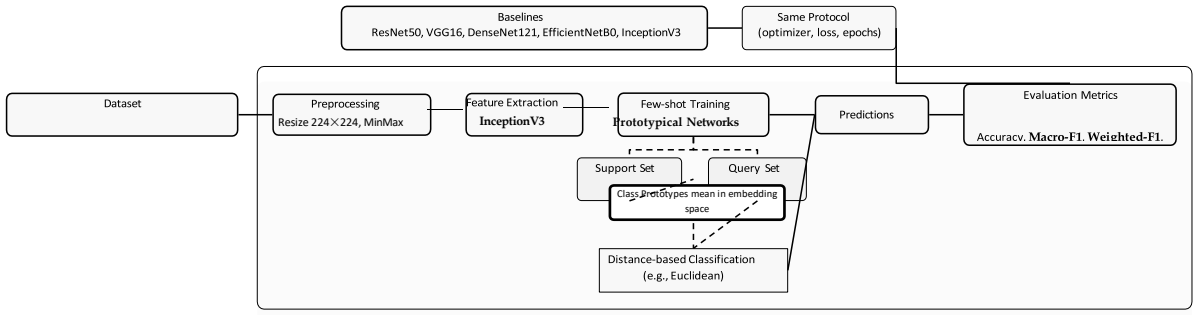


Figure 3: Overview of the proposed ProtoIncNet based rice leaf classification pipeline. The main flow includes preprocessing, feature extraction with InceptionV3, few-shot learning with Prototypical Networks (support/query, prototype computation, distance-based classification), and evaluation (Accuracy, Macro-/Weighted-F1, Cohen's κ, Hamming Loss). The upper branch shows baseline models trained under the same protocol and evaluated for comparison.

Figure 3 illustrates the streamlined workflow of the proposed rice leaf classification system. After dataset preparation and image preprocessing, InceptionV3 extracts deep features, which are refined through dense layers with dropout. A Prototypical Network-based meta-learning approach then enables few-shot classification. The model is trained using an 80/20 split and evaluated for robust performance.

The rest of this paper is organized as follows. Section 2 reviews recent research and related work in rice leaf disease classification. Section 3 details the proposed methodology, including model architecture and learning strategies. Finally, Section 4 presents the experimental setup, dataset, and results and Section 5 concludes the paper with future research directions.

2 Literature analysis

Examines the state-of-the-art studies used for rice disease classification, focusing on machine learning methods for predicting Leaf Blast, BrownSpot, and Hispa. It highlights the precision and efficiency of the proposed InceptionV3-based prototypical network, comparing it with existing approaches to address gaps in current research. Several studies have employed architectures such as ResNet50, VGG16, and EfficientNet for lung disease classification, reporting accuracies in the range of 90–96%. These models were therefore selected as baselines for comparison in this study. Johnson and Chandrakumar (2025). Rice sustains 50% of the global population, making effective disease control essential Tabassum et al. (2025). The author focuses on brown spot, bacterial leaf blight, and leaf smut, using hue and saturation thresholding for image preprocessing and feature extraction K. (2025). The gradient boosting decision tree achieved 86.58% accuracy on the UCI rice leaf dataset, outperforming previous methods with consistent accuracy across diseases Azim et al. (2021). Rice diseases, caused by bacteria, viruses, and fungi, pose significant threats to global rice production Zhaoxing Li et al. (2024). Mekha et al. classifies an image based dataset of rice leaf diseases, including BSR disease, using algorithms like Random Forest, Decision Tree, Gradient Boosting, and Naive Bayes. Performance was evaluated using accuracy, precision and recall, and Random Forest achieved the highest classification accuracy of 69.44% Mekha and Teeyasuksaet (2021). Rice leaf diseases like Brown Spot, Leaf Blast, and Hispa threaten crop yields and food security in India. Deep learning models were found more effective than traditional methods, with a 5-layer convolutional model achieving 78.2% accuracy, outperforming VGG16 at 58.4% Tejaswini et al. (2022).

Rice, a staple for over half the world, is vital in India, where agriculture supports 70% of the population and contributes significantly to GDP Atul Tiwari1 (2023). Deep learning have been applied to automate the identification of rice leaf disease, addressing challenges in manual detection. Using images processed from 32 pre-trained models, EfficientNetV2B3 with ET and HGB classifiers achieved an impressive 93–94% accuracy Aggarwal et al. (2023). The model demonstrates reliable and effective prediction of diseases like bacterial blight, blast, and brown spot, ensuring improved agricultural outcomes. Maheswaran et al. (2022) Traditional methods for detecting diseases of rice plants are costly and subjective, leading to financial losses for farmers Sharma (2022). This study proposes an automated system based on color features for diagnosing rice plant diseases, analyzing 14 color schemes and extracting 172 characteristics. Using a dataset of 619 images across four categories (Bacterial Leaf Blight, Rice Blast, Sheath Blight, and Healthy Leaves), the support vector machine (SVM) achieved the highest classification accuracy of 94.65% Shrivastava and Pradhan (2021). These results underscore the significance of color features in disease classification, aiding farmers in improving crop yield and quality through timely preventive actions.

Rice production is heavily affected by environmental and biological factors, with farmers relying on costly, error-prone manual disease detection. Making effective use of the Inception ResNetV2 model with transfer learning for rice leaf disease classification, achieving a high accuracy of 95.67%, offering an efficient automated solution for farmers Krishnamoorthy et al. (2021); Rodrigo et al. (2024). Deep learning utilized for automated rice disease detection, evaluating VGG-16 and Google Net CNN models through transfer learning with threefold cross-validation. Achieving average accuracies of 91.28% and 92.24%, respectively, the method classifies symptoms from a dataset of 12,000 annotated images, aiding disease management and farming practices Pandiyaraju et al. (2024); Yakkundimath

et al. (2022). New plant disease variations challenge farmers due to insufficient early detection methods. The study Li et al. (2024); Rallapalli and Saleem Durai (2021) proposes M-Net, an enhanced CNN architecture based on AlexNet, for effective plant disease identification using datasets from Kaggle and UCI ML Repository. M-Net outperformed traditional models, achieving a precision of 71% on rice disease datasets.

Table 1: Comparison of Rice Leaf Disease Classification Methods

Ref.	Year	Technique	Acc.	Dataset
Azim et al. (2021)	2021	XGBoost	86.58%	Leaf blight, brown spot, leaf smut
Mekha and Teeyasuksaet (2021)	2021	Decision Tree, Gradient Boosting, Naïve Bayes	69.44%	Brown Spot, Bacterial Leaf Blight
Tejaswini et al. (2022)	2021	CNN	78.20%	Brown spot, Leaf Blast, Hispa
Aggarwal et al. (2023)	2023	EfficientNetV2B3	94.00%	Bacterial Blight, Blast, Brown Spot
Shrivastava and Pradhan (2021)	2020	SVM	94.65%	Bacterial Leaf Blight, Rice Blast, Sheath Blight, Healthy Leaves
Krishnamoorthy et al. (2021)	2021	Inception-ResNetV2	95.67%	Not specified
Yakkundimath et al. (2022)	2021	VGG-16	92.24%	12,000 labeled images
Rallapalli and Saleem Durai (2021)	2021	M-Net	71.00%	Rice Leaf Diseases Dataset
Deb et al. (2021)	2021	InceptionV3	96.23%	Healthy, Bacterial Leaf Blight, Brown Spot, Leaf Blast, Leaf Smut
Sudhesh et al. (2023)	2023	XceptionNet	94.33%	Bacterial Blight, Leaf Blast, Brown Spot, Tungro
Thai-Nghe et al. (2021)	2021	EfficientNet	95.00%	Brown Spot, Hispa, Leaf Blast, Healthy Rice Leaf
Gunawan et al. (2021)	2021	ANN	66.30%	Brown Spot, Leaf Smut
Shrivastava et al. (2021)	2021	VGG-16	93.11%	Rice Blast, Bacterial Leaf Blight, Brown Spot, Sheath Blight, Sheath Rot, False Smut, Healthy
Sharma et al. (2021)	2021	CNN	94.00%	Hispa

Accurate plant disease identification is crucial for preventing production loss, with AI offering safer alternatives to chemical methods. The author evaluated five CNN models on 7,096 paddy leaf images, with InceptionV3 achieving the highest accuracy of 96.23% Deb et al. (2021); Mehnaz and Islam (2025). Agriculture in India faces growing threats from plant diseases and pests. Convolutional neural networks (CNNs) utilized with pre-processing techniques like hue-based background exclusion to classify paddy leaf diseases, including sheath rot, paddy blast, and bacterial leaf blight. The method achieved high accuracy, helping farmers detect diseases early and

prevent crop damage Abasi et al. (2023); Maheswaran et al. (2022). The author addresses challenges in identifying rice leaf diseases due to symptom similarities and irrelevant noise in global images. Using a dataset of 3,416 images across four diseases (bacterial blight, blast, brown spot, tungro), it proposes a Static Mode Compression method with attention-driven pre-processing via dynamic mode decomposition (DMD). DenseNet121 achieved 93.87% accuracy, while XceptionNet with SVM on DMD-preprocessed images reached 100% test accuracy. The attention-driven approach significantly improved disease detection by focusing on damaged areas, with XceptionNet achieving 94.33% accuracy on on-field images. Models trained on DMD- processed data showed superior performance across precision, recall, and F1-score metrics kumar S. Sakthivel (2025); Sudhesh et al. (2023). Mobile-compatible deep learning method presents by using EfficientNet and transfer learning to detect rice diseases like brown spot, hispa, and leaf blast. Trained on 1,790 images, the model achieved 95% accuracy and was converted to TFLite for mobile use. An Android app identifies diseases in 1.7 seconds, aiding farmers effectively K. (2025); Thai-Nghe et al. (2021). The author aims to classify rice diseases like brown spot and leaf smut using an artificial neural network (ANN) based on color and form features from leaf images. The model achieved an accuracy of 66.3% in disease classification Gunawan et al. (2021); Padhi et al. (2025).

Rice, a staple crop, faces yield and quality losses due to various diseases, making early detection essential. A Comparison of pre-trained deep CNN models was conducted for classifying seven rice plant diseases using 1,216 field images, with VGG16 achieving the highest accuracy of 93.11%. The model serves as a practical tool for early disease identification and prevention Shrivastava et al. (2019, 2021). The present research aims to develop a rice disease detection (RDD) system for hispa rice disease using live images from Punjabi rice fields and a CNN-based machine learning model. To train and validate the proposed CNN model, the dataset is initially processed in Matlab and then partitioned into a 70 to 30 ratio, yielding a 94% accuracy rate. The lack of an existing RDD system specifically for hispa disease serves as the driving force behind this work, emphasizing the necessity of a trained and effective system to detect rice hispa disease Sharma et al. (2021); Wang et al. (2023).

2.1 Critical discussion about research gap

Through the analysis of the literature, several research gaps have been identified.

- Most research in agricultural disease detection primarily uses traditional CNNs like ResNet, VGG16, and some Inception-based models for feature extraction.
- These models generally rely on large datasets, with data augmentation techniques often used to overcome the challenge of limited labeled data.
- The major problem in these approaches is the lack of robustness, especially in small dataset scenarios, where models tend to overfit and fail to generalize well.
- Evaluation metrics in existing studies often focus mainly on accuracy, without incorporating more comprehensive metrics like Cohen's Kappa or Hamming Loss, which can better reflect model reliability.
- Few-shot learning techniques, like Prototypical Networks, are underexplored, and models based on these methods are less common in agricultural disease classification.
- This study uses InceptionV3 for feature extraction and integrates a Prototypical Network to address data scarcity by enabling effective few-shot learning.
- Unlike previous approaches, this research focuses on meta-learning, specifically using class prototypes to improve classification accuracy with limited labeled samples.
- The methodology in existing literature often struggles with generalization to unseen classes or new diseases, limiting the model's practical application.
- The choice of Prototypical Networks allows for more effective learning with few examples, directly addressing data limitations that hinder traditional methods.
- This study fills the gap by combining advanced feature extraction (InceptionV3) and meta- learning (Prototypical Networks) for improved classification accuracy and generalization, achieving 98.3% accuracy.

3 Proposed Methodology

The model combines InceptionV3 for feature extraction and a Prototypical Network for

classification. Alongside the primary models (InceptionV3 and DenseNet), ResNet50, VGG16, and EfficientNet were trained under identical preprocessing and hyperparameter settings to provide a fair basis for performance comparison. The InceptionV3 model, pre-trained on ImageNet, is used to extract features from input images, which are then processed through a series of dense layers to learn complex patterns and relationships. Our novel proposed methodology for disease classification of rice is illustrated in Figure 4. The Prototypical Network is a meta-learning classifier that performs well in few-shot learning tasks, making it highly effective for classifying rice leaf diseases with limited data. The training process includes data preprocessing, such as normalization with MinMaxScaler and data augmentation to improve model generalization. The entire pipeline involves feature extraction, meta-learning for classification, and a carefully structured evaluation to assess model performance.

- Step 1: Feature extraction is performed using the InceptionV3 model, which processes input images (224x224x3) and applies convolutional layers to extract features like edges, textures, and patterns.
- Step 2: Activation functions are applied: ReLU for hidden layers to introduce non-linearity, and Softmax in the output layer to convert logits into probabilities for multi-class classification.
- Step 3: The feature maps from the convolutional layers are flattened into a 1D array, transforming the data to be suitable for input into the fully connected dense layers.
- Step 4: Three dense layers (64, 128, and 256 neurons) with ReLU activation are used to capture complex patterns, while a dropout layer with a 50% rate helps prevent overfitting during training.
- Step 5: The final dense layer with 500 neurons applies Softmax activation to produce a probability distribution over the 500 possible classes, ensuring that the probabilities sum to 1.
- Step 6: Prototypical network setup for episodic training involves selecting 4 classes, with 15 support examples for training and 30 query examples for testing in each episode. The model classifies query samples based on their distance to class prototypes.
- Step 7: MinMaxScaler is applied to normalize feature values between 0 and 1, and the dataset is split into 80% training and 20% testing for model evaluation.
- Step 8: The model is trained using a combination of InceptionV3 for feature extraction and Prototypical Networks for meta-learning, allowing it to perform few-shot learning by creating class prototypes and classifying query samples based on their proximity to these prototypes.

3.1 Exploratory data analysis

The dataset used in the proposed approach was sourced from Kaggle Ric (b), a widely recognized platform for machine learning datasets. It contains high-quality, RGB images of rice leaf

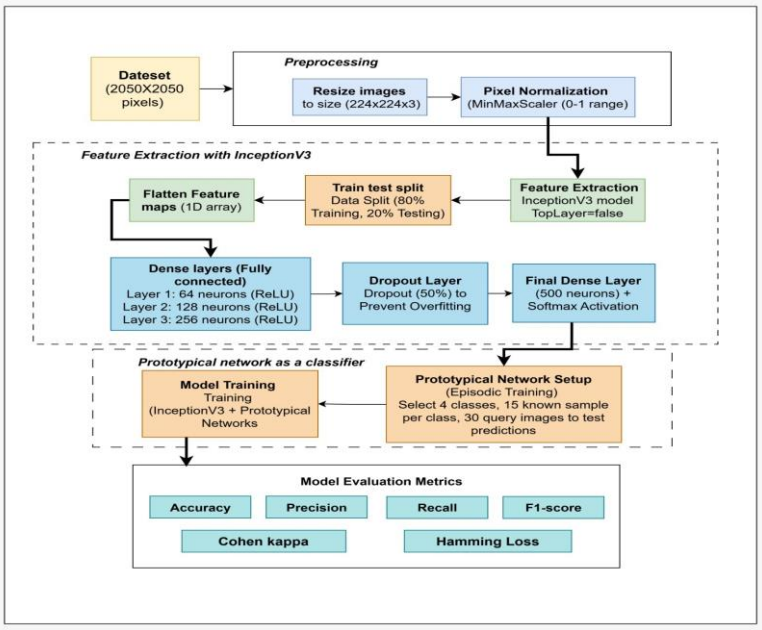


Figure 4: The diagram illustrates the proposed methodology for rice leaf disease classification, incorporating pre- processing, InceptionV3-based feature extraction, normalization, and data partitioning. A Prototypical Network is employed for classification under few-shot learning settings, followed by comprehensive model evaluation.

diseases, offering a diverse collection of images showcasing various stages and types of disease conditions. The dataset includes four categories: BrownSpot, Healthy, Hispa, and LeafBlast, each representing a different class of rice leaf health as shown in figure 5. These categories are central to the classification task that the study aims to accomplish using advanced machine learning techniques.

The total data set comprises 3355 images as shown in table 2 with the distribution of images in each category as follows. BrownSpot Leaf (523 images), Healthy Leaf (1488 images), Hispa Leaf (565 images), and LeafBlast Leaf (779 images). These images were initially recorded at an average resolution of 2050 × 2050 pixels, ensuring high detail and clarity, which is crucial for accurate feature extraction and classification. However, to improve processing efficiency and meet the input size requirement for the InceptionV3 model, all images were resized to 224 × 224 pixels.

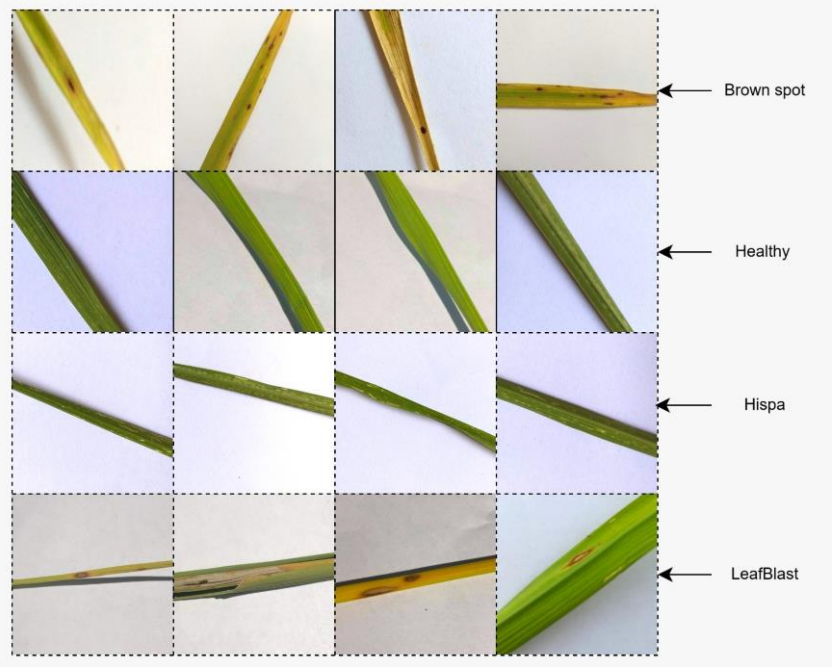


Figure 5: Sample images from the rice leaf disease dataset: The 4x4 grid showcases different disease types including Healthy, BrownSpot, Hispa, and LeafBlast. Each category represents a distinct class of rice leaf health used for training a classification model. Images are resized to 224 × 224 pixels and preprocessed using MinMax scaling.

Table 2: Dataset Composition and Image Specifications

Class	Number of Images	Label	Original Resolution	Resized Resolution
BrownSpot	523	0	2050×2050	224×224
Healthy	1488	1	2050×2050	224×224
Hispa	565	2	2050×2050	224×224
LeafBlast	779	3	2050×2050	224×224

The images are stored in JPG format, and each image consists of three color channels (RGB), providing rich color information vital for distinguishing between the different disease types and healthy conditions. For efficient processing and to maintain consistent input dimensions, the images were scaled using the MinMaxScaler. This step ensures that all pixel values lie between 0 and 1, improving the model's performance by maintaining uniformity in the data as illustrated in 6.

In order to convert the categorical disease labels into a format suitable for machine learning, a label mapping process was applied. The four disease categories were assigned unique integer values: BrownSpot was mapped to 0, Healthy to 1, Hispa to 2, and LeafBlast to 3. This transformation ensures that the labels are numerically represented, making them compatible with the classification algorithms used in the study.

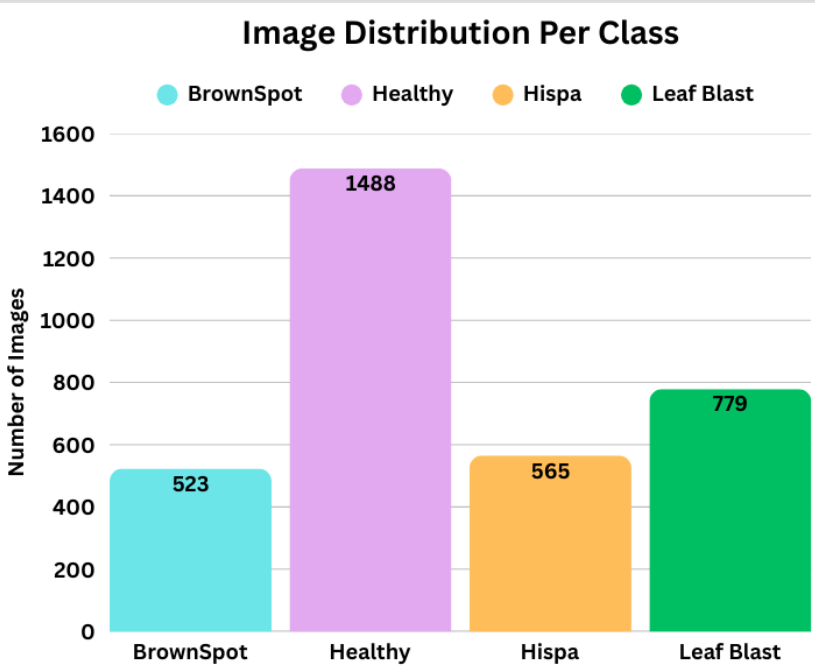


Figure 6: Bar chart showing the number of images in each rice leaf disease category.

The dataset was split into training and testing sets, with 80% of the images allocated for training and the remaining 20% used for testing the model. This division is crucial for evaluating the model's ability to generalize to unseen data, thereby providing a more accurate measure of its performance.

3.2 Feature Extraction using InceptionV3

InceptionV3 is a pre-trained Convolutional Neural Network (CNN) model that is used for feature extraction in this study. It leverages a deep architecture to extract hierarchical features from input images, which in this case are rice leaf images (224x224x3).

The process of feature extraction begins by passing the input images through the convolutional layers of the InceptionV3 model as illustrated in a sample Figure 7. These layers are designed to automatically learn low- and high-level features such as edges, textures, and patterns, which are crucial for identifying the subtle differences **between various rice leaf disease states.**

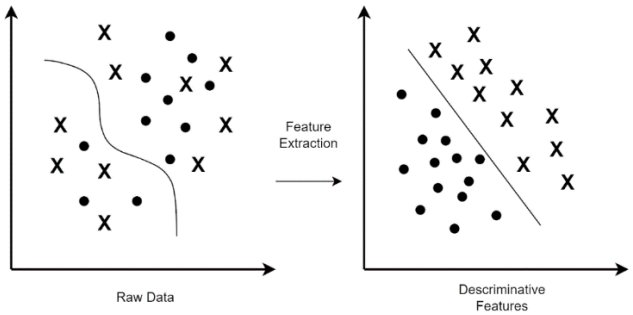


Figure 7: Feature extraction transforms raw, non-linearly separable data into a space with discriminative features that enable linear class separation.

The first key component of InceptionV3 is its use of convolutional layers, which apply a set of learnable filters (or kernels) to the input image. These filters move across the image, performing element-wise multiplication with the image pixels, producing feature maps that highlight the patterns and structures present in the image. These convolutions capture essential features like edges, corners, and textures that are critical for recognizing the different types of rice leaf diseases. The Rectified Linear Unit (ReLU) activation function is defined as:

$$f(x) = \max(0, x)$$

This function outputs the input x if it is positive, and 0 if x is negative.

After the convolution operation, the output passes through activation functions to introduce non-linearity into the model. The ReLU (Rectified Linear Unit) activation function is applied in hidden layers, allowing the model to learn more complex, non-linear representations. ReLU activates neurons only when the output is positive, ensuring that the model can capture intricate patterns in the data, which is essential for image classification tasks like disease detection.

The InceptionV3 model in this study is loaded with pre-trained weights from the ImageNet dataset. These pre-trained weights enable the model to start with a strong set of learned features that are applicable to a wide range of visual tasks. By leveraging these pre-trained features, the model can effectively extract relevant features from rice leaf images without needing to learn from scratch. This significantly speeds up training and improves the model's performance, especially in domains with limited labeled data like rice disease classification.

The output from the convolutional layers consists of feature maps that represent the extracted features. These maps capture various characteristics of the input image and serve as the basis for further classification tasks. InceptionV3 applies multiple convolutional operations at different scales to capture features at multiple levels, allowing it to learn both fine-grained details and broader patterns.

Once the features are extracted by the convolutional layers, the feature maps are flattened into a one-dimensional vector. This step is necessary to convert the high-dimensional data into a format suitable for input into the fully connected dense layers that follow. Flattening the feature maps helps the dense layers recognize complex relationships between the extracted features and ultimately classify the images into the correct categories (e.g., different types of rice leaf diseases).

By utilizing InceptionV3 for feature extraction, the model effectively leverages state-of-the- art Splitting them into support and query sets. The support set is used to calculate the class prototypes, and the query set is used for evaluation.

- Calculating Prototypes: The class prototypes are computed by averaging the feature vectors of the support examples for each class. The

techniques in convolutional neural networks to learn complex representations of rice leaf images. These features are then passed on to the subsequent layers for classification and further processing, allowing the model to make accurate predictions about the presence of specific diseases.

3.3 Classification using Prototypical Network

The Prototypical Network is a metric-based metalearning model designed to perform classification tasks in few-shot learning scenarios. In the context of rice leaf disease classification, this model excels at identifying rice leaf diseases, such as LeafBlast, Hispa, Healthy, and BrownSpot based on a limited number of labeled examples.

The core idea of Prototypical Networks is to learn an embedding space where instances of the same class are close together, while instances of different classes are far apart. This allows the model to classify unseen data by comparing the query samples to the learned class prototypes.

- Episodes: Prototypical Networks operate on episodes that consist of a small number of classes, with each class having a support set (for training) and a query set (for testing). In each episode, the model learns to classify query samples based on a limited number of support examples.
- Class Prototypes: A prototype represents the central feature vector of a class. In ProtoNet, the prototype for each class is computed by averaging the feature vectors of the support set for that class. These prototypes act as the "centroids" in the embedding space.
- Distance Metric: Once the prototypes are computed, the distance between each query sample and the class prototypes is calculated. Typically, Euclidean distance is used to measure the similarity between the query sample and the prototypes. The query sample is assigned to the class whose prototype is closest to it.

Steps that are included in Prototypical Network

- Sampling the Episode: An episode is sampled by selecting a subset of classes and

Prototype. The prototype c_k for class k is calculated as

$$c_k = \frac{1}{|S_k|} \sum_{\{(x_i, y_i) \in S_k\}} f_{\phi(x_i)}$$

where S_k is the support set for class k, and $f_{\phi(x_i)}$ is the feature vector of the sample x_i these prototypes represent the "center" of each class in the embedding space.

• Loss Calculation: The loss function for Prototypical Networks is based on the distance between query samples and their corresponding prototypes. The prototypical loss is computed by first calculating the Euclidean distances between each query sample and the prototypes. These distances are then transformed using the log softmax function to obtain probabilities for each class. The loss is the negative log probability of the correct class.

$$d(p,q) = \sqrt{\sum_{i=1}^{n}(p_i - q_i)^2}$$

Where:

$-p$ and q are the vectors in the n-dimensional space.

$-n$ is the number of dimensions (or features) in the space.

$-p_i$ and q_i represent the individual components of vectors p and q, respectively.

• Prediction: Once the prototypes are calculated and the model is trained, predictions are made for the query set. For each query example, the Euclidean distance to all the class prototypes is computed. The query is classified as the class whose prototype is closest to the query example. The predicted class is the one with the smallest distance to the query example. The accuracy of the model is then calculated by comparing the predicted class labels to the true labels of the query set.

3.4 Baseline Architectures for Performance Comparison

To evaluate the effectiveness of the proposed ProtoIncNet model, several widely recognized convolutional neural network (CNN) architectures were selected as baselines. Each model was trained on the same rice leaf disease dataset using consistent preprocessing: images were resized to 224 × 224 and normalized using MinMaxScaler, ensuring all pixel values fall within the range [0, 1]. A brief technical overview of each baseline model is provided below, along with key structural advantages.

EfficientNetB0 employs a compound scaling method that uniformly scales depth (d), width (w), and resolution (r) using a fixed set of scaling coefficients. This allows for a balanced increase in model capacity without excessive computational cost. The scaling is defined by:

$$d - \alpha^{\phi}, w - \beta^{\phi}, r = \gamma^{\phi}$$
$$such\ that$$
$$\alpha.\beta^2.\gamma^2 \approx 2$$

where ϕ is the compound coefficient controlling model size. EfficientNetB0, pretrained on ImageNet, is fine-tuned on the rice dataset for transfer learning. Its design emphasizes both performance and parameter efficiency.

DenseNet121 introduces dense connectivity, where each layer receives feature maps from all preceding layers, formalized as:

$$x_\ell = H_\ell([x_0, x_1, \ldots, x_{\{\ell-1\}}])$$

Here, x_ℓ represents the output of the ℓ^{th} layer, $H_\ell(\cdot)$ is a composite function of Batch Normalization, ReLU, and convolution, and $[\cdot]$ denotes concatenation. This connectivity ensures strong gradient flow, minimizes redundancy, and promotes feature reuse.

ResNet50 uses identity-based skip connections to mitigate the vanishing gradient issue in deep networks. Instead of learning the direct mapping H(x), the model learns the residual function F(x) = H(x) − x, making the output:

$$y = F(x) + x$$

This formulation simplifies training by enabling the network to learn identity mappings where needed, especially in deeper layers.

InceptionV3 leverages parallel convolutional kernels of varying sizes within an inception module to extract multi-scale features efficiently. Each module includes 1 × 1, 3 × 3, and 5 × 5 convolutions, allowing the model to capture both local and global patterns simultaneously. This architectural diversity makes it effective for high-resolution visual recognition tasks. In this study, InceptionV3 also serves as the feature extractor backbone for ProtoIncNet.

VGG16 is a deep CNN consisting of 13 convolutional layers followed by 3 fully connected layers. Its architecture relies on a consistent use of 3 × 3 convolution filters with stride 1 and same padding,
followed by 2 × 2 max-pooling layers. The convolution operation in VGG16 can be expressed as:

$$f_{i,j}^{(l)} = \sigma\left(\sum_{m,n} w_{m,n}^{(l)} \cdot x_{i+m,j+n}^{(l-1)} + b^{(l)}\right)$$

where $f_{i,j}^{(l)}$ is the activation at location (i, j) in layer l, w are the convolutional weights, x is the input, b is the bias, and σ is the ReLU activation function. Despite its simplicity, VGG16 remains a strong benchmark for image classification.
All baseline models were trained under identical conditions to ensure fairness in comparison, using the same optimizer, loss function, batch size, and number of epochs.

Table 3: Model-Wise Configuration Table

Model / Classifier	Backbone Params	Pretrained	Ep.	Batch Size	Training Strategy
ProtoIncNet Proposed	~24M	InceptionV3	20	4-way episodic	Meta-Learning
Hybrid + SVM (RBF)	~32M	ImageNet	100	64	Feature Fusion
Hybrid + Dropout MLP	~32M	ImageNet	100	64	Feature Fusion
Hybrid + Shallow MLP	~32M	ImageNet	100	64	Feature Fusion
Hybrid + Linear Soft-max	~32M	ImageNet	100	64	Feature Fusion
Hybrid + Logistic Reg.	~32M	ImageNet	100	32	Feature Fusion
InceptionV3 + Std. MLP	~24M	ImageNet	100	32	Feature Extract

3.5 Comparative Evaluation Setup

To ensure a fair comparison, all models were evaluated using a standardized protocol with an 80-20 stratified train-test split to maintain class balance.

Preprocessing and Configuration: Unlike uniform resizing, we adopted model-specific resolutions to maximize feature quality: 299 × 299 for InceptionV3 and up to 499 × 499 for Hybrid Fusion experiments. Feature vectors were normalized using RobustScaler to mitigate the impact of outliers.
Baseline and Proposed Models: The primary baseline utilized a **Hybrid Feature Fusion** framework, concatenating frozen features from EfficientNetB3 and DenseNet201 (3,456 dimensions). This was evaluated using five distinct classifiers, including SVM (RBF), Dropout-MLP, and Logistic Regression. A standard InceptionV3 model served as a secondary baseline. The proposed **ProtoIncNet** employed a meta-learning approach with episodic training (4-way, 15-shot support, 30-shot query) to specifically address data scarcity.

Training Protocol: Baseline deep learning models were trained for 100 epochs using the Adam optimizer (lr = 1e − 4) and Categorical Cross-Entropy loss, utilizing Early Stopping and learning rate scheduling to prevent overfitting. Batch sizes were set to 64 for Hybrid models and 32 for for classification. These metrics are calculated based on the confusion matrix, which includes the values for True Positive (TP), True Negative (TN), False Positive (FP), and False Negative (FN). The metrics used for evaluation include

$$\text{Accuracy} = \frac{(TP + TN)}{(TP + FP + FN + TN)} \times 100$$

$$\text{Precision} = \frac{TP}{TP + FP} \times 100$$

$$\text{Sensitivity} = \frac{TP}{TP + FN} \times 100$$

$$\text{F1-Score} = 2 \times \frac{(Precision \times Sensitivity)}{(Precision + Sensitivity)} \times 100$$

InceptionV3. Performance was assessed using Accuracy, F1-Score, Cohen's Kappa, and Hamming Loss.

3.6 Evaluation Equations

The following equations represent the key evaluation metrics used in the proposed model Accuracy, Precision, Sensitivity, F1-Score, Hamming Loss, Cohen's Kappa, and Euclidean Distance, all of which provide important insights into the performance of the model.

Equations are

$$\text{Hamming Loss} = \frac{1}{(N \times L)} \sum_{i=1}^{N} \cdot \sum_{j=1}^{L} 1(y_{ij} \neq \hat{y}_{ij})$$

$$\text{Cohen's Kappa } (K) = \frac{(p_o - p_e)}{(1 - p_e)}$$

$$\text{Euclidean Distance } d(p, q) = \sqrt{\left(\sum_{i=1}^{n} (p_i - q_i)^2\right)}$$

4 Results and Discussion

In this section, we present and discuss the results of the model's performance on the rice leaf disease classification task. The results demonstrate the effectiveness of the proposed model, which leverages InceptionV3 for feature extraction and Prototypical Networks for classification. Model Performance Metrics: We evaluate the model's performance using several metrics including Accuracy, Cohen's Kappa and Hamming Loss. These metrics provide insight into the model's ability to correctly classify rice leaf diseases in four categories: LeafBlast, Hispa, Healthy, and BrownSpot.

Table 4 shows the evaluation results for different configurations of the Prototypical Network, varying the number of support and query examples per class. As shown in Table 1, the model demonstrates strong classification performance, with accuracy ranging from 88.63% to 98.3%. The selected configuration (Evaluation 2) achieved the highest accuracy of 98.3%, with a Cohen's Kappa of 0.97 and a low Hamming Loss of 0.0167, indicating excellent agreement between the predicted and true labels. [In addition, several baseline models including ResNet50, VGG16, DenseNet121, and EfficientNetB0 were evaluated on the same dataset for comparison. Table 7 summarizes their performance metrics, showing that ProtoIncNet consistently outperforms these traditional architectures, particularly in handling minority classes like Hispa and LeafBlast.]

Table 4: Performance metrics under various few-shot episode configurations. Highest accuracy (98.33%) is observed with 15 support and 30 query samples.

Evaluation	n_classes	n_support	n_query	Cohen's Kappa	Hamming Loss	Accuracy
1	4	10	30	0.9	0.075	92.5
2(Selected)	4	15	30	0.97	0.0167	98.33
3	4	20	30	0.9	0.075	92.5
4	4	25	30	0.9	0.075	92.5
5	4	30	30	0.94	0.0417	95.83
6	4	35	30	0.91	0.0667	93.33
7	4	15	35	0.9	0.0714	92.85
8	4	15	40	0.96	0.025	97.5
9	4	15	45	0.92	0.0556	94.4
10	4	15	55	0.84	0.1136	88.63
11	4	15	60	0.91	0.0625	93.75
12	4	15	100	0.95	0.0625	96.5

Interpretation of Results: The results show that the model performs exceptionally well with support = 15 and query = 30, which corresponds to the configuration with the highest accuracy. The Cohen's Kappa score of 0.97 in this configuration confirms that the model's predictions are highly reliable, with minimal disagreement between predicted and actual labels.

The Hamming Loss metric is consistently low across different configurations, indicating that the model does not make many errors in classifying the rice leaf diseases. This further supports the effectiveness of the Prototypical Network in achieving accurate classification with limited training data.

The performance of the model is sensitive to the number of support and query examples. As the number of support examples increases from 10 to 15 (Evaluation 2), the accuracy improves significantly. This suggests that providing more support examples helps the model learn more robust prototypes, leading to better classification performance. However, increasing the number of query examples does not seem to have a substantial effect on accuracy, as seen in Evaluations 8 and 9, where the number of query examples increased, but accuracy did not improve proportionally. When comparing our results with other state of the art methods for rice leaf disease classification, our model leveraging the Prototypical Network and demonstrates the competitive performance. The high accuracy, combined with the model's ability to classify diseases with limited training examples, highlights the effectiveness of the few-shot learning approach in agricultural disease classification.

4.1 Evaluation Metric

Table 5 presents the performance metrics of the proposed InceptionV3-based model with dense layers for the classification of rice leaf disease. The model achieves an overall accuracy of 98. 3%, demonstrating its strong ability to distinguish between different types of leaf. Cohen's Kappa score of 0.9777 reflects an almost perfect agreement between the model's predictions and the actual labels, while the Hamming loss of 0.0166 indicates very few errors in label predictions. The model uses a dropout rate of 0.5 to mitigate overfitting and employs ReLU activation for hidden layers and SoftMax for the output layer, ensuring effective classification.

Table 5: Classification performance showing high precision and F1-scores across all classes, with 98.30% accuracy, 0.9777 Cohen's Kappa, 0.0166 Hamming Loss, and a model using ReLU activation with 0.5 dropout.

Metric	Value
Overall Accuracy	98.30%
Cohen's Kappa	0.9777
Hamming Loss	0.0166
Dropout	0.5
Activation Function	ReLu SoftMax
Class 0 (LeafBlast)	Precision 0.97 F1-Score 0.98
Class 1 (Hispa)	Precision 1.00 F1-Score 0.98
Class 2 (BrownSpot)	Precision 0.97 F1-Score 0.98
Class 3 (Healthy)	Precision 1.00 F1-Score 0.98

The precision and F1 scores for each of the four disease classes, LeafBlast, Hispa, BrownSpot, and Healthy, are remarkably high. Both Hispa and Healthy achieve perfect precision scores of 1.00, demonstrating flawless classification for these categories. LeafBlast and BrownSpot also show strong performance, with precision values of 0.97 and F1-scores of 0.98. These results highlight the excellent performance of the model in all classes, effectively identifying and classifying rice leaf diseases with minimal error.

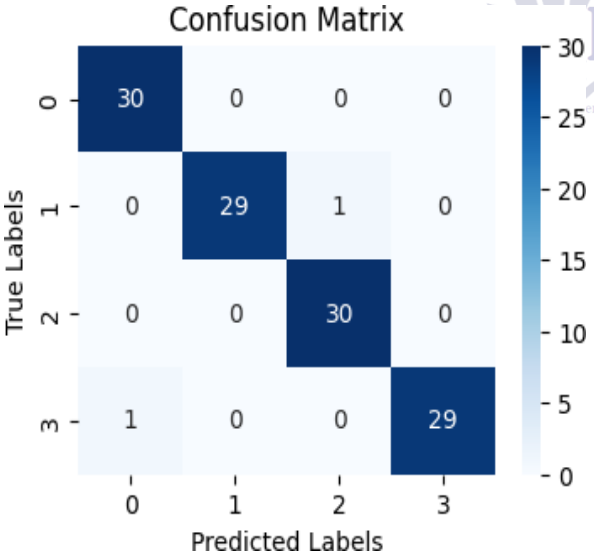


Figure 8: Confusion matrix illustrating a classification accuracy of 98.33%, with only two misclassifications out of 120 predictions across four classes.

The evaluation of the InceptionV3-based model for rice leaf disease classification was carried out using several important metrics: Confusion Matrix, Accuracy, Precision, Recall, F1-Score, Cohen's Kappa, and Hamming Loss. These metrics offer an in-depth look at the model's performance, with each focusing on different aspects of the classification task. The evaluation results help to understand how well the model performs across the four classes of rice leaf diseases (LeafBlast, Hispa, BrownSpot, and Healthy). The Confusion Matrix for the classification task illustrated in Figure 8

This matrix in figure 8 shows the true positives, false positives, false negatives, and true negatives for each class. For instance, the first row corresponds to LeafBlast (class 0), where 30 samples were correctly classified, and there were no misclassifications. Similarly, the second row corresponds to Hispa (class 1), where one sample was misclassified as LeafBlast (false negative), but the rest (29) were correctly identified. The diagonal elements represent the correct classifications (True

Positives), while the off-diagonal elements represent misclassifications. Accuracy measures the overall effectiveness of the model, calculated as the ratio of correct predictions to the total number of samples.

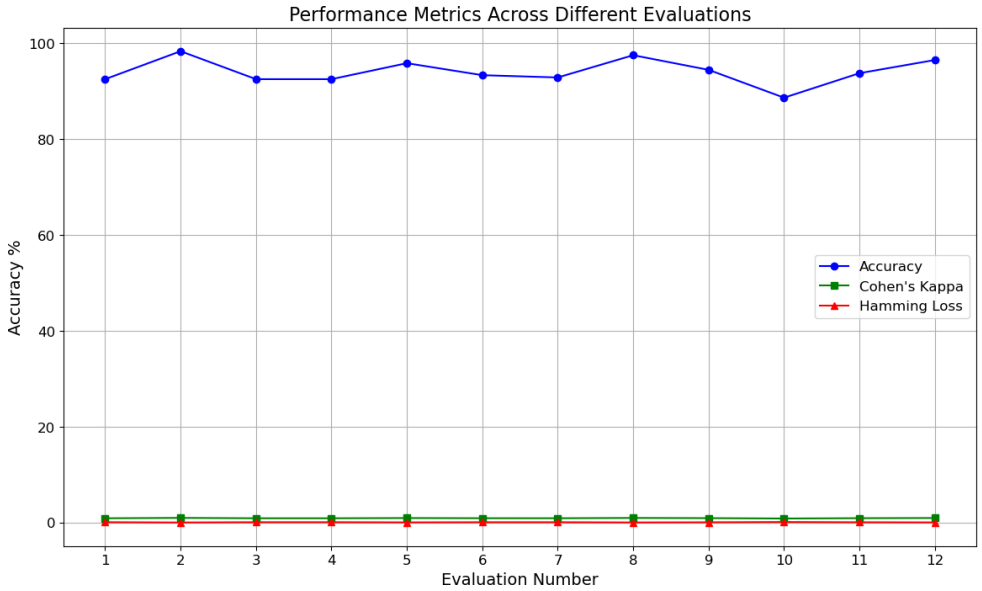


Figure 9: Performance Metrics across Different Evaluations.

Table 6: Classification report summarizing precision, recall, F1-score, and support for each class. The model achieved an overall accuracy of 98.33%, a Cohen's Kappa score of 0.9778 indicating strong agreement, and a low Hamming Loss of 0.0167, reflecting minimal multi-class error.

Class Label	Precision	Recall	F1-Score	Support
0	0.97	1.00	0.98	30
1	1.00	0.97	0.98	30
2	0.97	1.00	0.98	30
3	1.00	0.97	0.98	30
Accuracy	-	-	0.98 (98.33%)	120
Macro Avg	0.98	0.98	0.98	120
Weighted Avg	0.98	0.98	0.98	120
Cohen's Kappa	0.9778			
Hamming Loss	0.0167			

In this case, the table 6 accuracy is 98.33%, indicating that the model correctly classified 98.33% of the samples. The model architecture includes a series of convolutional layers followed by fully connected layers. These layers learn hierarchical representations of the input image, starting from simple features like edges and textures to more complex patterns like shapes and object parts. The dense layers at the end of the network map the learned features to the output classes, where each class represents a specific type of rice leaf disease or a healthy leaf. This setup is ideal for the classification of leaf diseases, as it allows the model to distinguish between fine-grained patterns in images.

The high Cohen's Kappa and accuracy values suggest that the InceptionV3 model with dense layers is performing exceptionally well at identifying rice leaf diseases. The use of pre-trained weights from ImageNet and the model's depth are crucial factors contributing to this high performance. Moreover, the model's ability to

handle multi-class classification and its impressive Hamming Loss and F1-Scores highlight its robustness and generalizability, ensuring that it performs well on previously unseen images.

The 4-way 15-shot learning variation, which was implemented for the evaluation, achieved the highest accuracy of 98.33% illustrated in Figure 9 . This variation was particularly effective, with the model being trained on four classes, 15 support samples, and 30 query samples. The combination of these parameters allowed the model to generalize well, resulting in the optimal performance across all evaluations. The graph visually highlights this accuracy trend, reinforcing the effectiveness of this specific setup.

4.2 Comparative Performance of Baseline Models

To validate the effectiveness of the proposed **ProtoIncNet**, several baseline architectures including VGG16, ResNet50, DenseNet121 and EfficientNetB0, were trained and evaluated using the same dataset of rice leaf disease. All models were subjected to consistent pre-processing, including resizing images to 224×224 pixels and normalization implemented using MinMax Scaling to the range [0,1]. Each model was trained using the Adam optimizer for 10 epochs with a batch size of 32, ensuring fairness through identical training settings across all architectures.

The comparative performance is summarized in Table 3 which highlights that ProtoIncNet outperformed traditional architectures, especially in handling class imbalance and rare disease categories.

4.3 Comparative Performance of Baseline Models

The comparative results, summarized in Table 7, reveal significant performance disparities. The standard **InceptionV3** baseline achieved an accuracy of only 71.83%, struggling significantly with the Hispa class (F1-score: 0.52). While the **Hybrid Fusion** approach improved accuracy to 82.56% using an SVM classifier, it still failed to match the precision of our proposed method.

Deep learning baselines often struggle with class imbalance, a challenge effectively addressed by ProtoIncNet. By utilizing few-shot meta-learning, ProtoIncNet outperformed the best baseline (Hybrid Fusion + SVM) by a margin of over 15%, achieving 98.33% accuracy. This underscores that while feature fusion enhances standard CNNs, the prototypical approach is superior for distinguishing subtle disease patterns in limited-data scenarios.

5 Comparative Analysis Summary

Consolidated comparison of all models, highlighting InceptionV3 as the best.

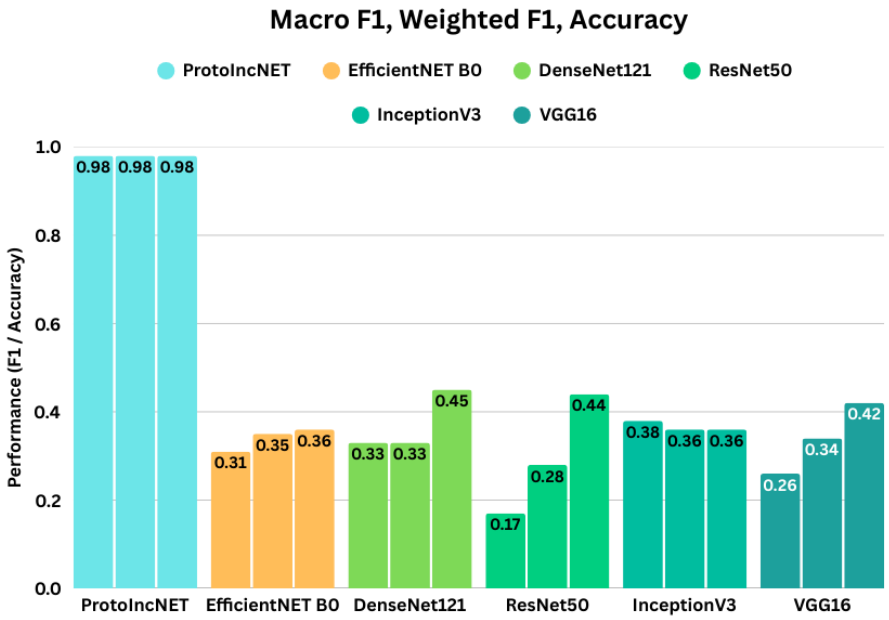


Figure 10: Performance Comparison Across different baseline

This graph (see Figure 10) clearly demonstrates the comparative performance of different deep learning models, highlighting ProtoIncNet as the most effective and balanced model, while others show significant weaknesses in specific classes of disease.

6 Discussion of Findings

This section highlights the practical implications, strengths, and limitations of the proposed approach. As presented in Table 7, the proposed **ProtoIncNet** consistently outperforms all experimental baselines, achieving an exceptional accuracy of 98.33% and an F1-score of 0.98 across all disease categories.

In comparison, the **Hybrid Fusion** experiments (combining EfficientNetB3 and DenseNet201) peaked at 82.56% accuracy when using an SVM classifier. While the Hybrid Fusion approach significantly improved upon the standard InceptionV3 baseline (71.83%), it still exhibited weak- nesses in handling class imbalance. Specifically, the baseline models struggled to distinguish the Hispa class from Healthy leaves, yielding F1-scores between 0.52 and 0.64 for that category. In contrast, ProtoIncNet effectively mitigated these issues through its few-shot meta-learning architecture. By generating robust class prototypes from limited support samples, it achieved a perfect balance (0.98 F1-score) even on the minority Hispa class. This validates that while feature fusion and advanced classifiers (like SVMs) can enhance traditional CNN performance, the prototypical network approach provides a superior solution for agricultural disease classification where distinguishing subtle disease patterns is critical.

Table 7: Comprehensive Performance Comparison: Proposed ProtoIncNet vs. Baseline Experiments

Method	Classifier	Accuracy	BS (F1)	Healthy (F1)	Hispa (F1)	LB (F1)	Remarks
ProtoIncNet	**Prototypical Net**	**98.33%**	**0.98**	**0.98**	**0.98**	**0.98**	**Proposed Method.** Best performer, perfectly balanced.
Hybrid Fusion	SVM (RBF)	82.56%	0.86	0.86	0.64	0.84	Best Baseline. Excellent non-linear separation.
Hybrid Fusion	Dropout MLP	82.56%	0.86	0.87	0.63	0.85	Strong Baseline. Robust generalization.
Hybrid Fusion	Shallow MLP	80.92%	0.84	0.86	0.60	0.83	Good, but slight bottleneck in hidden layers.
Hybrid Fusion	Linear Softmax	78.24%	0.81	0.84	0.60	0.78	Linear boundary insufficient for complex features.
Hybrid Fusion	Logistic Reg.	76.60%	0.82	0.83	0.56	0.77	Struggled with class imbalance.
InceptionV3	Standard MLP	71.83%	0.77	0.77	0.52	0.73	Weakest Baseline. Single-model features lacked detail.

Note: ProtoIncNet (Proposed) uses Few-Shot Meta Learning. Hybrid Fusion combines EfficientNetB3 + DenseNet201.
BS=BrownSpot, LB=LeafBlast.

6.1 Class-Level Performance Discussion

The proposed ProtoIncNet model exhibited robust performance across all disease categories, including minority classes like Hispa and LeafBlast, where other models consistently struggled. For instance, ResNet50 and VGG16 failed to detect the Hispa class entirely, resulting in zero F1-scores. These models showed strong performance for majority classes like Healthy but lacked generalization in class-imbalanced settings. On the other hand, ProtoIncNet's meta-learning structure allowed it to learn more discriminative class prototypes even with limited support examples, resulting in near-perfect classification. The macro and weighted F1-scores of 0.98 further confirm its balanced performance across all classes, regardless of sample distribution. Overall, the comparative evaluation highlights the superiority of the proposed ProtoIncNet

framework. Unlike traditional CNNs, which exhibited class bias and inconsistent performance, ProtoIncNet maintained high classification accuracy and reliability in both balanced and few-shot settings. Its ability to generalize from limited data makes it an ideal candidate for real-world agricultural disease

diagnosis tasks, especially when annotated datasets are scarce.

6.2 Comparative Analysis with Existing Studies

Table 8 outlines the progression of rice leaf disease classification methods from 2019 to 2025, emphasizing the evolution of model accuracy and dataset usage. Initial approaches like CNN (2019) and Random Forest (2021) achieved moderate results with accuracies of 89.34% and 91.74%, respectively. Later developments incorporating VGG16 (2020), SVM (2022), and XceptionNet with DMD (2023) demonstrated improved performance, reaching up to 94.33%. More recent models, including MobileNetV2 (2024) and Vision Transformer (2025), further enhanced accuracy to 95.12% and 96.78%.

In comparison, the proposed ProtoIncNet framework, which integrates InceptionV3 for feature extraction and Prototypical Networks for classification, achieved the highest accuracy of 98.3% on the Rice Crop Dataset. This model demonstrates improved classification effectiveness and shows potential resilience to varied imaging conditions such as lighting, background, and leaf orientation, based on the dataset characteristics

Table 8: Comparison of Rice Leaf Disease Classification Studies (2019–2025)

Year	Technique / Model Used	Dataset	Accuracy
2019	Convolutional Neural Network	Kaggle based rice leaf dataset	89.34%
2020	VGG16 (Transfer Learning)	Custom-collected RGB images	94.12%
2021	Random Forest	Public dataset with BrownSpot, LeafBlast	91.74%
2022	Support Vector Machine (SVM)	Rice leaf dataset with 4 classes	90.27%
2023	XceptionNet + Dynamic Mode Decom- position	Rice Leaf Disease Dataset (Bacterial Blight, Leaf Blast, Brown Spot)	94.33%
2024	MobileNetV2	Field images from South Asia	95.12%
2025	Vision Transformer (ViT)	Rice Disease Dataset with augmentation	96.78%
Proposed Approach	ProtoIncNet (InceptionV3 for feature extraction + Prototypical Networks for classification)	Rice Crop Dataset	98.3%

7 Conclusion and future work

In this study, we successfully implemented a machine learning model using InceptionV3 for rice plant disease classification, focusing on four key disease categories: LeafBlast, Hispa, BrownSpot, and Healthy leaves. The model demonstrated high accuracy (98.33%) in classifying rice leaf diseases, supported by excellent precision, recall, and F1 scores. Additionally, the inclusion of multiple well-known deep learning architectures for comparison has validated the strength and consistency of the proposed model across different conditions. The approach leveraged 4-way 15-shot learning, ensuring efficient use of limited training data. By using techniques such as the Prototypical Networks and fine-tuning the InceptionV3 model, the system showed significant promise for real-world deployment in agricultural monitoring systems, offering reliable and automated plant disease detection.

7.1 Future work

We will enhance model performance by experimenting with hyperparameter tuning and data augmentation techniques. Additionally, we

will integrate the model into real-time systems for field deployment, such as mobile apps or edge devices, to enable immediate disease detection. Future improvements will also involve expanding the dataset to include more plant diseases and utilizing techniques like explainable AI for better model interpretability. Lastly, we will explore multi-crop disease classification to broaden the model's application in agriculture.

Ethical approval

This article does not contain any studies with human participants or animals performed by any of the authors.

Informed consent

Informed consent was obtained from all individual participants included in the study.

CrediT authorship contribution statement

Muhammad Adeel Zafar: supervision, conceptualization, methodology, software, investigation, validation, writing - original draft. **Muhammad Noman Zafar:** writing – review & editing, data curation, visualization, methodology. **Abdul Mannan Zafar:** writing - original draft, visualization, investigation. **Iftikhar Sarwar:** critical review, project administration, visualization, investigation.

Declaration of competing 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.

Data availability

Data will be made available on request.

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