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Mangrove Tree Species Classification Based on Leaf, Stem, and Seed Characteristics Using Convolutional Neural Networks with K-Folds Cross Validation Optimalization

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Abstract*. Mangrove classification plays a pivotal role in environmental monitoring and conservation efforts. In this study, our meticulously curated dataset comprised diverse mangrove tree images standardized to 250 x 250 pixels, capturing the nuances of various species. Employing advanced deep learning techniques, our models demonstrated exceptional accuracy, reaching 99.23% without K-Folds and a slightly enhanced 99.78% with K-Folds. These models exhibited outstanding consistency, showcasing recall, precision, and F1-Score metrics all surpassing 99%. Through rigorous testing in 10 experiments, both K-Folds and non-K-Folds methods consistently achieved 100% accuracy, evidenced by the presence of True Positives in every classification scenario. This remarkable performance underscores the robustness of our algorithms in precisely classifying mangrove species, offering a valuable tool for ecological research and conservation initiatives. The practical implications of our findings are profound, providing an invaluable resource for environmentalists, conservationists, and policymakers engaged in mangrove preservation. Accurate species classification is pivotal in understanding biodiversity, aiding in targeted conservation efforts, and ultimately promoting the sustainable management of these vital coastal ecosystems.*

Keywords: Mangrove, Image Classification, CNN, K-Folds

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1. Introduction

The classification of mangrove tree species based on image analysis, a field known as digital plant taxonomy, has become integral to ecological research, contributing significantly to biodiversity conservation and sustainable environmental management [1]. This process involves extracting meaningful information from images, enabling the identification of plant species through computational methods. Traditional methods of species identification, reliant on manual observation and expertise, are often time-consuming and prone to errors [2]. In response to these challenges, the integration of

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advanced technologies has become imperative in the field of botanical taxonomy. With the advent of computer vision and machine learning, the landscape of species classification has undergone a transformative evolution, enabling the development of highly efficient and accurate automated identification systems [3].

Contemporary technologies used for species classification primarily encompass image processing algorithms and machine learning models. These technologies leverage features such as leaf shape, texture, and color to differentiate between plant species. However, the limitations of these methods are apparent when dealing with intricate botanical characteristics, necessitating the exploration of more sophisticated approaches. One such groundbreaking technology is Convolutional Neural Networks (CNN), a class of deep learning algorithms specifically designed for image recognition tasks [4]. CNNs have demonstrated unparalleled proficiency in pattern recognition, allowing them to discern complex patterns within images and make highly accurate classifications [4], [5]. This methodology holds immense promise in revolutionizing the classification of mangrove tree species, addressing the limitations of traditional techniques and significantly enhancing the precision and efficiency of species identification efforts [6].

In this research, the primary research objective is to investigate how these distinct features can be effectively utilized to differentiate between various mangrove species. Additionally, the study endeavors to optimize the performance of the CNN model using K-Folds cross-validation, ensuring robustness and minimizing overfitting.. By harnessing the capabilities of deep learning, this study aims to create a robust and reliable system capable of accurately identifying mangrove species based on their distinct leaf, stem, and seed characteristics. The utilization of CNN not only represents a significant advancement in botanical research but also opens new avenues for ecological studies, conservation initiatives, and sustainable environmental practices. Through this research, we strive to contribute to the ongoing efforts in preserving the invaluable biodiversity of mangrove ecosystems, emphasizing the critical role of cutting-edge technology in shaping the future of ecological studies and environmental conservation. This study will include a detailed analysis of specific cases, showcasing the effectiveness of CNN in resolving intricate botanical classification challenges and providing valuable insights into the applicability of this technology in real-world ecological contexts. The results derived from the fulfillment of these research objectives will be comprehensively detailed and discussed in the "Results and Discussion" section of the research paper.

2. Methods

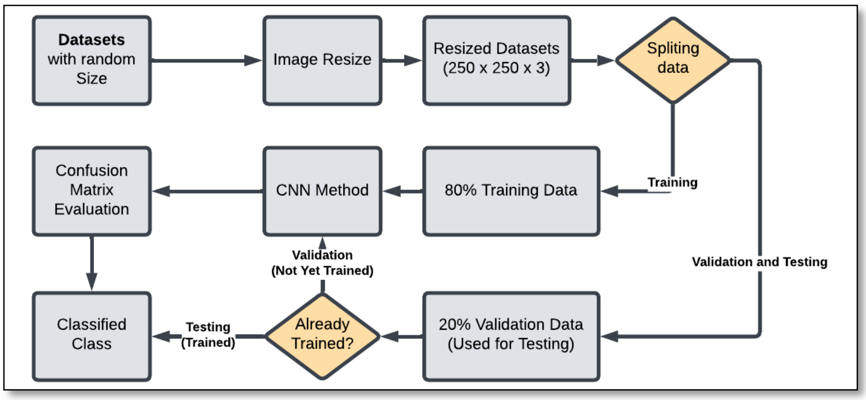


Figure 1. Research Methodology

Figure 1 represent proposed workflow, the study begins by acquiring diverse datasets containing images of mangrove tree species with varying sizes. To ensure uniformity and consistency in the analysis, the images undergo a resizing process, standardizing them to a resolution of 250 x 250 pixels and maintaining the RGB color channels. This step ensures that all images are of the same dimensions, allowing for seamless processing within the neural network. The dataset is then split into two subsets: 80% of the data is allocated for training the Convolutional Neural Network (CNN) model, enabling it to learn and recognize patterns from the images, while the remaining 20% serves as validation data for testing the trained model's accuracy and performance. During the training phase, the CNN method is employed to process the training dataset, allowing the model to analyze and extract intricate features from the resized images. This training process involves iteratively adjusting the network's parameters to minimize errors and enhance accuracy. The model's performance is continuously evaluated using the 20% validation data, which acts as a benchmark for its classification capabilities. The confusion matrix, a powerful tool for evaluating classification models, is utilized to assess the CNN's accuracy, providing a detailed breakdown of the model's predictions against the actual classes. Following the training and validation phases, the model is tested using the 20% validation data to assess its real-world performance.

2.1. Datasets

In this study, our dataset comprised a comprehensive collection of mangrove tree images, capturing the diverse array of sizes and complexities inherent to different species. To ensure consistency and facilitate effective analysis, the images underwent meticulous resizing, all standardized to a uniform dimension of 250 x 250 pixels. This careful standardization process was paramount as it preserved the essential visual intricacies of mangrove stems, leaves, and seeds, allowing for precise computational analysis. The dataset, thoughtfully curated into eight distinct classes, represented a variety of mangrove species, including Avicennia marina (146 samples), Avicennia officinalis (149 samples), Avicennia rumphiana (116 samples), Rhizophora mucronata (120 samples), and Sonneratia alba (120 samples). Based on sample image, can be seen in **Figure 2**. For the purpose of this study, 80% of the total dataset, meticulously organized into these distinct classes, was allocated for the training phase. The remaining 20% of the dataset was dedicated to testing and validation, serving as a robust benchmark for evaluating the trained CNN accuracy and performance. By segregating the dataset in this manner, we ensured a rigorous evaluation process, enabling us to validate the model's proficiency in classifying mangrove species accurately and reliably.

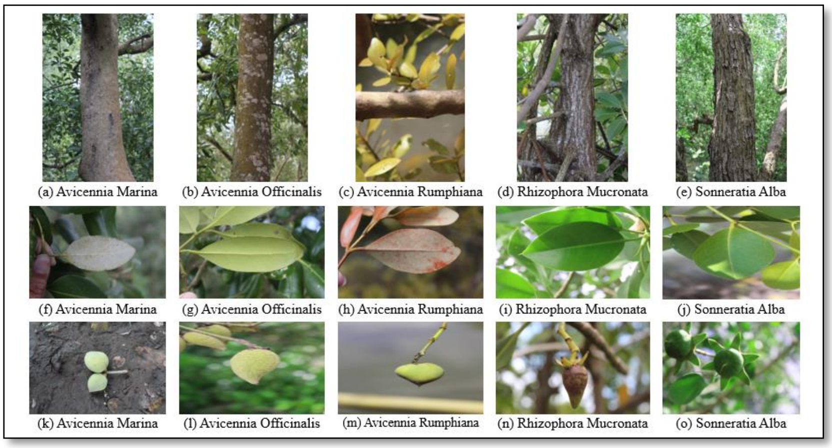

(a) Avicennia Marina (b) Avicennia Officinalis (c) Avicennia Rumphiana (d) Rhizophora Mucronata (e) Sonneratia Alba
(f) Avicennia Marina (g) Avicennia Officinalis (h) Avicennia Rumphiana (i) Rhizophora Mucronata (j) Sonneratia Alba
(k) Avicennia Marina (l) Avicennia Officinalis (m) Avicennia Rumphiana (n) Rhizophora Mucronata (o) Sonneratia Alba

Figure 2. (a) – (e) represents Stems, (f) – (j) represents Leaf, (k) – (o) represents seed.

2.2. Convolutional Neural Netwrks (CNN) Classification

CNN stand as a pioneering force in the realm of artificial intelligence, revolutionizing the field of image recognition and classification [7]. Rooted in deep learning, CNN are intricately designed neural networks inspired by the visual processing capabilities of the human brain. What distinguishes CNN from traditional neural networks is their ability to automatically learn and extract intricate features from images through convolutional layers [4]. By employing filters that slide across the input image, CNN can identify patterns such as edges, textures, and complex shapes, enabling them to comprehend visual data in a manner akin to human perception. This powerful methodology has found profound applications in diverse domains, ranging from facial recognition systems and autonomous vehicles to medical image analysis and natural language processing. The adaptability and accuracy of CNN have propelled them to the forefront of cutting-edge technology, cementing their status as a cornerstone in the evolution of machine learning and computer vision [4], [6].

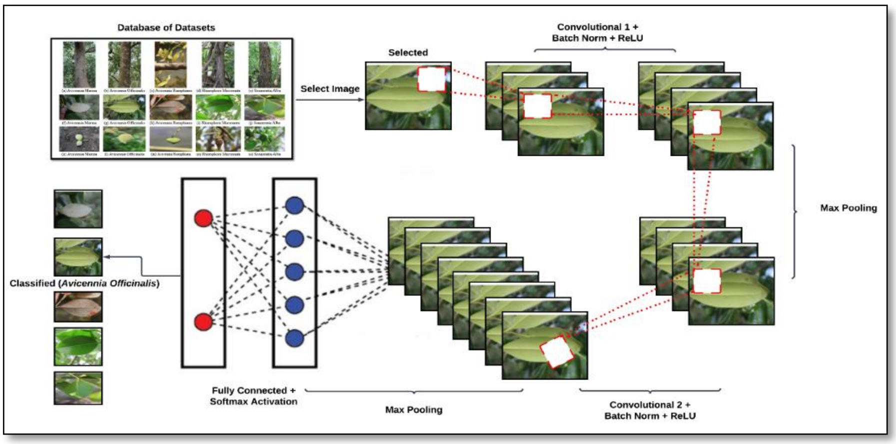


Figure 3. CNN Classification Layers Based on Proposed Method.

2.3. *Confusion Matrix Evaluation*

Confusion matrix is a fundamental tool in the realm of classification tasks, offering a clear and comprehensive snapshot of a model's performance across multiple classes [8]. The confusion matrix [9] serves as a foundational step in the evaluation process, enabling data scientists and machine learning practitioners to gauge the efficacy of classification models and make informed decisions to enhance their predictive capabilities. Following the Confusion Matrix Equation, can be seen below, where, True Positive (TP) values lie along the diagonal, indicating correct predictions, while off-diagonal elements represent misclassifications. False Positive (FP) signifies instances wrongly classified as positive, and False Negative (FN) represents instances incorrectly labeled as negative. True Negative (TN) values denote correct rejections.

$$Accuracy = \frac{TP + TN}{TP + TN + FP + FN} \tag{1}$$

$$Precision = \frac{TP}{TP + FP} \tag{2}$$

$$Recall = \frac{TP}{TP + FN} \tag{3}$$

$$F1 - Score = \frac{2 \times Precision \times Recall}{Precision \times Recall} \tag{4}$$

2.4. *K-Folds Cross Validation Optimalization*

K-Fold Cross-Validation stands as a critical strategy for refining the performance of CNN [10]. With the challenge of classifying five distinct mangrove species, employing K-Fold Cross-Validation becomes indispensable. This technique involves dividing the dataset into k subsets and iteratively training the CNN on $K - 1$ folds while validating on the remaining fold. By systematically cycling through the data, each subset is used for both training and validation, ensuring a comprehensive assessment of the model's ability to discern intricate features specific to each mangrove class [11]. The iterative nature of K-Fold Cross-Validation minimizes the risk of overfitting and provides a more accurate estimation of the CNN's performance across diverse instances of mangrove species [12]. This rigorous validation methodology not only optimizes the network's architecture and hyperparameters but also fosters a model that exhibits robustness and reliability in classifying the intricate variations within the mangrove ecosystem. Through K-Fold Cross-Validation, CNN-based mangrove classification achieves a level of precision essential for ecological studies and biodiversity conservation efforts [13]. For example, when employing K-Fold Cross-Validation with $K = 5$, the dataset is divided into five subsets, enabling the Convolutional Neural Network to be trained and validated iteratively on distinct portions of the data, ensuring a robust evaluation of its performance. **Figure 4** represents new flow with previous study with addition of K-Folds Cross Validation Optimization parameters. K-Folds cross-validation technique was employed with a value of K set at 5. This means that the dataset, which consisted of approximately 3200 iterations in the pre-processing phase of the Convolutional Neural Network (CNN), was divided into five subsets or folds. The training and validation process was then repeated five times, each time utilizing a different subset as the validation data and the remaining four subsets for training. This approach effectively resulted in 5 iterations, with each iteration serving as both the validation and training set once. The purpose of this meticulous division was to ensure comprehensive model assessment and avoid biases that might arise from a singular split of the data. The choice to employ K-Folds cross-validation over other techniques stems from its ability to address the crucial concern of overfitting in machine learning models. Overfitting occurs when a model learns the training data too well, capturing noise and irrelevant patterns instead of generalizing to new, unseen data. K-Folds cross-validation mitigates this risk by rigorously evaluating the model's performance across multiple subsets of the data [14].

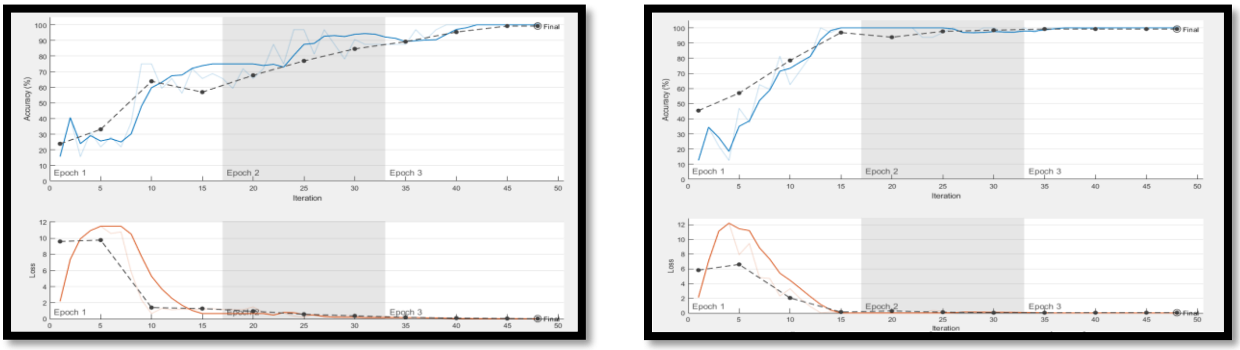
Figure 4. Addition of K-Folds Cross Validation Optimization parameters

3. Results and Discussion

Based on the proposed method, the results and discussion are intricately intertwined with the two algorithmic approaches described below. The first algorithm, employing an 80-20 training-validation split, utilized a neural network architecture with convolutional layers, batch normalization, ReLU activation, and max-pooling, culminating in a multi-class classification model. The second approach focused on the analysis of specific performance metrics such as accuracy, precision, and recall through confusion matrix evaluation. Notably, the intricate interplay between these algorithms illuminates the nuanced intricacies of the proposed methodology, showcasing its robustness in handling complex classification tasks. Based on the pseudocode algorithm provided in **Table 1**, an evaluation graph has been generated, reflecting the precision and performance of the designed model. This graph, as depicted in the image below, illustrates the progress of both loss and accuracy throughout the training process. The graph becomes a valuable window, allowing an in-depth understanding and assessment of the model's convergence. The Graph can be seen below. In **Figures 5**, the generated graphs led to the production of the following confusion matrix. This matrix encapsulates the classification outcomes, providing a clear and detailed overview of the model's performance in categorizing various mangrove species. The values within the confusion matrix serve as a quantitative reflection of the model's accuracy and effectiveness, essential for a comprehensive evaluation of its classification capabilities. The results of confusion matrix evaluation, can be seen in **Table 2**.

Table 1. Pseudocode Algorithm Based on Proposed Method

```
CNN With and Without K-Folds
Initialize the training data split ratio: $numTrainFiles = 0.80$
Split the dataset into training and validation sets using splitEachLabel function (Without K-Folds):
$[imdsTrain, imdsValidation] = splitEachLabel(imds, numTrainFiles, 'randomize')$
Split the dataset into training and validation sets using splitEachLabel function (With K-Folds):
$[imdsTrain, imdsValidation] = splitEachLabel(imds, numTrainFiles, 'Kfold', 5)$
Input layer: imageInputLayer with size [250 250 3]
Convolutional layers:
    • 2D Convolutional layer with 8 $filters, 3x3\ kernel\ size, and\ 'Padding'$ set to 1
    • Batch normalization layer
    • ReLU activation layer
    • 2D Max-pooling layer with $2x2\ pool\ size\ and\ 'Stride'$ set to 2
    • Repeat the above convolutional block with 16 $and$ 32 $filters$ respectively
    • Fully connected layer with 5 $output$ nodes
    • Softmax layer for classification
    • Classification layer
Define training options:
    • Use stochastic gradient descent with momentum $(sgdm) optimizer$
    • Set GPU as the execution environment
    • Maximum number of epochs: 3
    • Mini-batch size: 32
    • Validation data: $imdsValidation$
    • Validation frequency: $every$ 5 $iterations$
    • Disable verbose mode during training
Confusion Matrix Evaluation
```



(a) Training and Loss Progress without K-Folds (b) Training and Loss Progress with K-Folds

Figure 5. Training and Loss Progres with and without K-Folds

Table 2. Confusion Matrix Evaluation

Evaluation	**Without K-Folds**	**With K-Folds**
Accuracy	99,23%	99,78%
Recall	99,13%	99,17%
Precision	100%	100%
F1-Score	99,56%	99,58%

Table 3. Classification Testing with and without K-Folds

Input Image	Classification Testing Without K-Folds			Classification Testing With K-Folds		
	Actual Class	**Predicted Class**	**Result**	**Actual Class**	**Predicted Class**	**Result**
Avicennia Marina1.jpg	Avicennia Marina	Avicennia Marina	TP	Avicennia Marina	Avicennia Marina	TP
Avicennia Marina32.jpg	Avicennia Marina	Avicennia Marina	TP	Avicennia Marina	Avicennia Marina	TP
Avicennia Officinalis2.jpg	Avicennia Officinalis	Avicennia Officinalis	TP	Avicennia Officinalis	Avicennia Officinalis	TP
Avicennia Officinalis48.jpg	Avicennia Officinalis	Avicennia Officinalis	TP	Avicennia Officinalis	Avicennia Officinalis	TP
Avicennia Rumphiana3.jpg	Avicennia Rumphiana	Avicennia Rumphiana	TP	Avicennia Rumphiana	Avicennia Rumphiana	TP
Avicennia Rumphiana66.jpg	Avicennia Rumphiana	Avicennia Rumphiana	TP	Avicennia Rumphiana	Avicennia Rumphiana	TP
Rhizophora Mucronata4.jpg	Rhizophora Mucronata	Rhizophora Mucronata	TP	Rhizophora Mucronata	Rhizophora Mucronata	TP
Rhizophora Mucronata6.jpg	Rhizophora Mucronata	Rhizophora Mucronata	TP	Rhizophora Mucronata	Rhizophora Mucronata	TP
Sonneratia Alba7.jpg	Sonneratia Alba	Sonneratia Alba	TP	Sonneratia Alba	Sonneratia Alba	TP
Sonneratia Alba21.jpg	Sonneratia Alba	Sonneratia Alba	TP	Sonneratia Alba	Sonneratia Alba	TP

For future research, an intriguing avenue to explore would be integrating image segmentation techniques to identify specific regions within whole mangrove ecosystems. This segmentation approach could distinguish between different mangrove species, such as Mangrove A or Mangrove B, within a single image. By employing advanced image analysis methods, researchers can delve deeper into the intricate structures and ecological patterns of various mangrove species, enhancing our understanding of their distinct characteristics and contributions to the ecosystem.

4. Conclusion

In conclusion, the evaluation results depicted in **Table 2** demonstrate exceptional performance for both models, with an accuracy of 99.23% for the approach without K-Folds and a slightly improved accuracy of 99.78% for the K-Folds methodology. Notably, both models exhibited remarkable consistency across key metrics, showcasing high recall, precision, and F1-Score, all exceeding 99%. Analyzing the detailed classification outcomes in **Table 3**, it is evident that in all 10 experiments (testing), both the K-Folds and non-K-Folds approaches consistently achieved 100% success rates. This is evidenced by the presence of True Positives (TP) exclusively in the "Result" column for each classification scenario, signifying accurate predictions for every mangrove species tested. This outstanding achievement underscores the robustness of the models, regardless of the utilization of K-Folds. Therefore, the application of both methods yielded flawless results, reaffirming the effectiveness of the developed algorithms in precisely classifying mangrove species within the dataset. Furthermore, the robustness of the developed algorithms ensures their efficacy in real-time field applications, enabling scientists, researchers, and conservationists to make informed decisions for the preservation and restoration of mangrove ecosystems worldwide. The successful application of these models underscores their potential to revolutionize how we understand and protect delicate ecological environments, making a tangible impact on the preservation of biodiversity and the overall health of our planet.

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