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# Introduction (*Heading 1*)

Mango (Mangifera indica), considered as the king of all fruits, belongs to the family Anacardiaceae. It is native to South Asia, particularly India, where it’s been cultivated for over more than 4000 years. Also, it is a very important cultural symbol of the country where it is used in various religious ceremonies. Although, India is the largest producer of the fruit in the world, accounting for around 52.63 percent of total production. The fruit is packed with vitamins like C and A, offering strong antioxidant properties that boost immune function, promote skin health, and support eye health. But a major constraint that follows-up with the crop is that it suffers from low productivity due to the wide range of climatic conditions, environment situations and the diversity of the associated disease and disorder problems. Over 140 pathogens are known to cause damage to the crop. According to agricultural experts, naked eye observation is the traditional method used to recognize plant diseases. This is very expensive and time-consuming as it requires continuous monitoring. This approach leads to the unnecessary use of pesticides, which in turn results in higher production cost. Hence, it is almost impossible to accurately recognize the diseases of plant at an initial stage. There is also a need for an early disease detection system to protect the crop in time. The first step in overcoming the threats from diseases is to accurately identify the problems. Mango is affected by a number of diseases at all stages of its development, right from the seedling in the nursery to the fruits in storage or transit. These diseases manifest themselves as several kinds of rots, die backs, mildews, spots, cankers, sooty moulds, malformations, some diseases of unknown etiology and physiological disorders. Bacterial canker, anthracnose, gall machi, powdery mildew, red rust, black tip, dieback, malformation, sooty mould and phoma blight are of major concern to the growers in India. Also, mango fruit is highly perishable and susceptible to various pathogenic fungi during postharvest. Anthracnose, caused by Colletotrichum gloeosporioides, can cause losses of up to 30 percent the during storage and transportation of mango fruit [2]. Prevention is the only effective means of reducing losses from most mango diseases. In mango, cost of chemical to be used against control of diseases in the tree canopy has major impact because of large quantity of spray material is needed. Various novel approaches such as vain-seg approach for disease detection using leaf vein patterns (for powdery mildew and sooty mould in mango leaves), Multilayer Convolutional Neural Network (MCNN) (for Anthracnose fungal disease classification), Artificial Neural Networks (ANN) (to identify small disease clusters) etc have been formulated to identify various mango diseases at early stages which would help to mitigate the challenges and prevent the losses. Plant extract-based green synthesis of nanoparticles which is an emerging class of nanotechnology which utilize Selenium nanoparticles (SeNPs) synthesized from Melia azaderach leaves to mitigate the diseases associated with mango. Therefore, implementation of models in achieving low-rate of diseases in mango have been a matter of great concern and discussion all over the world. The proposed work aims are making a model involved in disease detection which is performed by using the technique of convolutional neural network (CNN) which is a part of artificial neural network (ANN). Very few research has been performed regarding the recognition of mango leaf diseases .

# LITERATURE REVIEW

The study of recognition of mango leaf diseases using the CNN model [1] focuses on grouping and distinguishing the diseases of mango leaves through the process of CNN and taking infectious prevention measures to improve the quality and harvest yield. DenseNet201, InceptionResNetV2, InceptionV3, ResNet50, ResNet152V2, and Xception models of CNN are used. Image acquisition, image segmentation, and feature extraction are the steps involved in disease detection. Different kinds of leaf diseases such as anthracnose, gall machi, powdery mildew, and red rust are used in the dataset. It contains 1500 images of diseased mango leaves. In this proposed work, six CNN models are utilized for five unique classes of mango disease. After training and testing the image data, a 5×5 confusion matrix was generated. The overall performance metrics revealed that DenseNet201 outperformed with the highest accuracy achieved at 98.00%. The author suggests that in the future there will be a broader range of leaf diseases and the CNN approach aims to achieve accuracy for those targeted diseases.

The article relates to the study[2] of Mango leaf disease recognition and classification using novel segmentation and vein pattern techniques. Automated recognition of mango plant leaf diseases is still a challenge. Manual disease detection is impractical in this digital age due to its exorbitant cost and inconsistent symptom variations. Of all the challenges at hand, the segmentation of diseased parts is a significant hurdle, being the prerequisite for correct recognition and identification. To address this objective, the study introduces a novel segmentation approach to segment the diseased part by considering the leaf’s vein pattern. The leaf vein-seg approach segments the vein pattern of the leaf. Afterward, features are extracted and combined through a fusion process using canonical correlation analysis (CCA). As the concluding step of identification, the study uses a cubic support vector machine (SVM) to validate the outcomes. The proposed model attained the highest accuracy of 95.5%, and two types of mango leaf disease, powdery mildew and sooty mold, were recognized, which proves that the suggested model offers valuable assistance to mango plant growers for prompt recognition and identification of diseases.

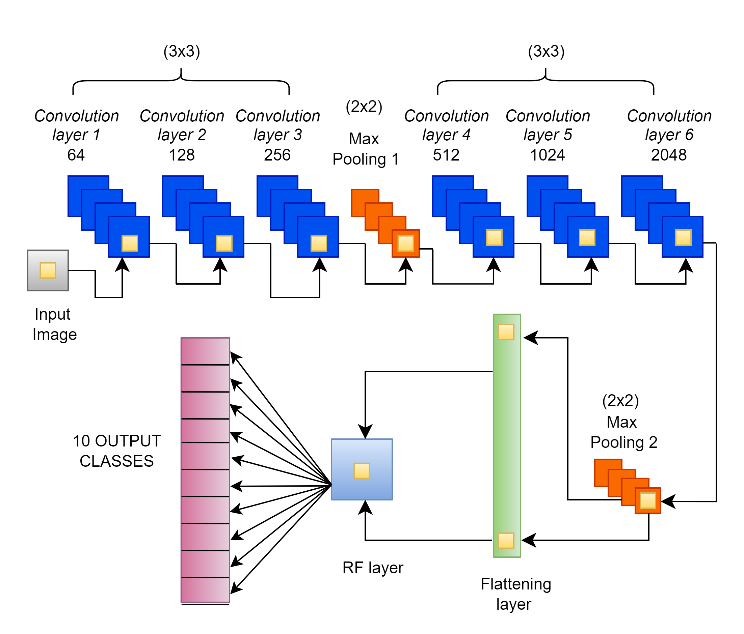
In this research, the authors[3] aim at detecting diseases on plant leaves at an early stage and a multi-class mango leaf disease classification using deep neural networks is introduced. Those small disease blobs, that can be detected only with the help of higher resolution images, by an artificial neural network (ANN) approach. After completing the preliminary step to improve the contrast, all the infested blobs are separated out for entire set of data. Several measurement-based features that describes the chosen blobs are picked. The selected features are used as inputs for ANN. The results obtained are compared using their methods with another approach that involves well-known CNN models (AlexNet, VGG16, ResNet-50) improved using transfer learning. The ANN’s results were better than those of CNNs using a simpler network structure (89.41% vs 78.64%, 79.92%, and 84.88%, respectively). This demonstrates that the approach can be implemented on less-powerful devices like smartphones, providing valuable help to farmers on the field. In future the authors proposed to work with plantations to gather wider range of dataset and aims to create a comprehensive disease monitoring system that can be used on different platforms.

In this study, the author discussed about the postharvest anthracnose[4], caused by the fungus Colletotrichum gloeosporioides, which is considered to be one of the most important postharvest diseases of mangoes all over the world. The use of B. siamensis before storage significantly enhanced disease resistance and led to a reduction in the disease index (DI) of stored mango fruit. Through transcriptome analysis, a total of 234,808 distinct transcripts and 56,704 differentially expressed genes(DEGs) were discovered, aimed at understanding the induction mechanisms of B. siamensis in the mango fruit samples in the context of storage. Enrichment analysis of differentially expressed genes (DEGs) using Gene Ontology (GO) and Kyoto Encyclopedia of Genes and Genomes (KEGG) pathways revealed a significant enrichment of DEGs related to plant-pathogen interaction and the biosynthesis of resistant compounds. The treatment with B. siamensis up-regulated genes like JAZ, BAK1, and PR1, as well as genes linked to plant-pathogen interaction pathways like peroxisome and phenylpropanoid in mango fruit. The outcomes of this study provide a reference for future studies on managing postharvest diseases in fruits and vegetables through antagonistic bacteria, laying a theoretical basis for the practical implementation of an antagonistic agent.

The article relates to the study of plant extract-based green synthesis of nanoparticles is an emerging class of nanotechnology[5] that has revolutionized the entire field of biological sciences. Nanoparticles synthesized through green methods, are known as SeNPs, are used as agents with antifungal properties. Selenium nanoparticles (SeNPs) were synthesized using extract from Melia azedarach leaves as a stabilizing agent, with their properties analysed through UV–visible spectroscopy and energy-dispersive X-ray (EDX) analysis. The green synthesized SeNPs were administrated to Mangifera indica trees affected by mango malformation disease. Among the concentrations tested, 30 μg/mL of SeNPs exhibited the most favourable impact on the physiological factors like chlorophyll content and biochemical aspects such as soluble sugar. The green synthesized SeNPs led to a notable reduction in the biotic stress, achieved by augmenting both enzymatic and non-enzymatic activities. The in vitro assessment of SeNP’s antifungal properties revealed that the concentration of 300 μg/mL exhibited the highest inhibited against Fusarium mangiferae. This marks the initial biocompatible approach to assess the potential of environmentally synthesized SeNPs in enhancing the well-being of mango malformation-infected plants. The findings of current research explained that the mango trees under stress of vegetative malformation exhibited favourable physiological and biochemical responses upon receiving a foliar application of 30 μg/mL SeNPs. It demonstrated evidence establishes that SeNPs can have a significant impact on enhancing plant physiological and biochemical attributes, both in vivo and in vitro conditions.

In this paper, a multilayer convolutional neural network (MCNN) is proposed for the classification of the Mango leaves[6] infected by the Anthracnose fungal disease. This paper is validated on a real-time dataset captured at the Shri Mata Vaishno Devi University, Katra, J&K, India consists of 1070 images of the Mango tree leaves. The dataset contains both healthy and infected leaf images. Computer vision with machine learning methodologies has outperformed in solving a number of plant leaves disease problems including pattern recognition, classification, object extraction etc. The higher performance of the proposed work is confirmed with accuracy of 97.13% when compared with other state-of-the-art approaches for its accuracy. The author suggests some future works as: 1) Enhancing the performance of the CNN by using some other function instead of Softmax making it suitable for numerous classifications of diseases. 2) Implementing strategies to address the inconsistencies faced while working with real-time dataset. 3) Engaging with economically significant plant species and calculating disease severity while also considering other parts of the plants. 4) To develop a disease monitoring system in real-time, integrated with the Web and Internet of Things (IoT).

# Methodology



# Results

In this section, we present the results of our comprehensive investigation into mango leaf diseases. Our research aimed to shed light on the prevalence, identification, and management of various diseases affecting mango leaves, crucial for the sustainable cultivation of this economically significant fruit crop. By conducting thorough data collection, analysis, and experimentation, we have uncovered valuable insights that contribute to the broader comprehension of diseases affecting mango leaves and offer practical solutions for farmers and researchers. In the following subsections, we present our research findings, organized to address the key objectives of this study.

1. confusion matrix

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Actual/Predicted | SL1 | SL2 | SL3 | SL4 | SL5 | SL6 | SL7 | SL8 | SL9 | SL10 |
| SL1 | 476 | 8 | 12 | 15 | 3 | 1 | 2 | 4 | 12 | 34 |
| SL2 | 4 | 378 | 10 | 12 | 15 | 2 | 12 | 9 | 3 | 36 |
| SL3 | 10 | 10 | 567 | 11 | 12 | 11 | 42 | 9 | 3 | 4 |
| SL4 | 21 | 12 | 8 | 500 | 10 | 18 | 32 | 7 | 11 | 12 |
| SL5 | 5 | 16 | 6 | 2 | 401 | 11 | 1 | 5 | 4 | 1 |
| SL6 | 10 | 8 | 7 | 6 | 12 | 412 | 1 | 2 | 4 | 12 |
| SL7 | 2 | 9 | 11 | 17 | 4 | 2 | 465 | 12 | 4 | 1 |
| SL8 | 7 | 10 | 10 | 12 | 2 | 7 | 2 | 398 | 21 | 12 |
| SL9 | 9 | 12 | 2 | 8 | 5 | 6 | 4 | 2 | 498 | 2 |
| SL10 | 13 | 8 | 4 | 6 | 11 | 14 | 2 | 21 | 31 | 400 |

1. Confusion Matrix for Anthracnose Severity Levels

Table 1 illustrates a confusion matrix for encompassing ten distinct severity levels within the context of Anthracnose disease. The dataset used in this confusion matrix comprises a total of 5350 images, each sized at 128x128 pixels. Each severity level here depicts the difference ratio of 10%. Breaking down the severity level distribution within the matrix, the first severity level(0-10%) contains 567 images, the second severity level(10-20%) comprises 481 images, the third severity level(20-30%) encompasses 679 images, the fourth severity level(30-40%) includes 631 images, the fifth severity level(40-50%) contains 452 images, the sixth severity level(50-60%) consists of 474 images, the seventh severity level(60-70%) is represented by 527 images, the eighth severity level(70-80%) also consists of 527 images, the ninth severity level(80-90%) comprises 481 images, and finally, the tenth severity level(90-100%) encompasses 510 images. It's noteworthy that the third severity level(20-30%) exhibits the highest image count, with 679 images, while the fifth severity level(20-30%) demonstrates the lowest, with 452 images.

1. result

|  |  |  |  |
| --- | --- | --- | --- |
|  | True Positive | False Positive | False Negative |
|  | 476 | 81 | 91 |
|  | 378 | 93 | 103 |
|  | 567 | 70 | 112 |
|  | 500 | 89 | 131 |
|  | 401 | 74 | 51 |
|  | 412 | 72 | 62 |
|  | 465 | 98 | 62 |
|  | 398 | 71 | 83 |
|  | 498 | 93 | 50 |
|  | 400 | 114 | 110 |
| Sum | 4495 | 855 | 855 |

1. Classification Results for Anthracnose Severity Levels

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1. meta analysis

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | Precision | Recall | F1-Score | Support | Accuracy |
| SL1 | 85.46 | 83.95 | 84.70 | 567 | 0.97 |
| SL2 | 80.25 | 78.59 | 79.41 | 481 | 0.96 |
| SL3 | 89.01 | 83.51 | 86.17 | 679 | 0.97 |
| SL4 | 84.89 | 79.24 | 81.97 | 631 | 0.96 |
| SL5 | 84.42 | 88.72 | 86.52 | 452 | 0.98 |
| SL6 | 85.12 | 86.92 | 86.01 | 474 | 0.97 |
| SL7 | 82.59 | 88.24 | 85.32 | 527 | 0.97 |
| SL8 | 84.86 | 82.74 | 83.79 | 481 | 0.97 |
| SL9 | 84.26 | 90.88 | 87.45 | 548 | 0.97 |
| SL10 | 77.82 | 78.43 | 78.13 | 510 | 0.96 |
| Macro Average | 83.87 | 84.12 | 83.95 |  |  |
| Weighted Average | 84.07 | 84.02 | 83.99 |  |  |
| Micro Average | 84.02 | 84.02 | 84.02 |  |  |

1. Meta-Analysis of Anthracnose Severity Classification Metrics

This table provides a comprehensive meta-analysis of classification metrics for Anthracnose disease severity levels (SL1 through SL10). Here, the SL1 attains a precision of 85.67 along with recall 83.95, resulting in an F1 Score of 84.70, supported by dataset of 567 images with an accuracy of 0.97. Similarly, SL3 is having the highest precision of 89.01 along with recall of 83.51, attaining an F1 Score of 86.17, with highest support of dataset images and achieving an accuracy of 0.97. The SL9 has shown the highest recall of 90.88 with precision 84.26 attaining the highest F1 Score of 87.45, along with support of 548 images and achieving an accuracy same as SL3 i.e., 0.97. The highest support is observed in the third severity level (SL3) with a support value of 679. The lowest support is observed in the fifth severity level (SL5) with a support value of 452. The overall accuracy of the model is 84.02%, meaning that 84.02% of all instances were classified correctly. In this case, the macro average precision is 83.87%, the macro average recall is 84.12%, and the macro average F1-Score is 83.95%. Also, the weighted average precision is 84.07%, the weighted average recall is 84.02%, and the weighted average F1-Score is 83.99%. In conclusion, the micro average precision, recall, and F1-Score all hover around the 84.02% mark, indicating a consistent level of performance across these metrics.

Acknowledgment *(Heading 5)*

The preferred spelling of the word “acknowledgment” in America is without an “e” after the “g”. Avoid the stilted expression “one of us (R. B. G.) thanks ...”. Instead, try “R. B. G. thanks...”. Put sponsor acknowledgments in the unnumbered footnote on the first page.

##### References

The references section for a comprehensive work on mango leaf diseases is an essential component that provides credibility and acknowledges the sources of information, research, and studies that have contributed to the body of knowledge within the field. In this section, the authors typically list and cite all the relevant publications, academic papers, books, websites, and other sources that were consulted and referenced during the research and writing process.

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