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Abstract

Cassava, a vital crop in many developing countries, is highly susceptible to several leaf diseases that negatively affect yield and food security. Traditional disease identification methods are time-consuming, costly, and often inaccessible to smallholder farmers. This study proposes a deep learning-based approach for classifying cassava leaf diseases using a publicly available image dataset. Several state-of-the-art transfer learning models were evaluated, including Xception, EfficientNetB0, ResNet50, VGG16, DenseNet121, and InceptionV3. Through comparative analysis, the Xception model achieved the highest classification accuracy, demonstrating its effectiveness in recognizing subtle visual differences in infected leaves. Data augmentation and preprocessing techniques were applied to enhance model performance. The findings suggest that deep learning can provide a reliable, scalable, and low-cost solution for early plant disease detection, potentially aiding farmers in timely decision-making and contributing to food security.

Keywords: deep learning, transfer learning, convolutional neural network (CNN), crop disease classification, Xception, cassava leaf

CHAPTER 1

INTRODUCTION

1.1 Background

Cassava is a staple food crop grown in tropical and subtropical regions. It is valued for its high-yield tubers and nutrient-rich leaves. Its resilience in poor soils makes it a vital food source in many low-income regions. However, cassava plants are highly susceptible to several leaf diseases including Cassava Bacterial Blight (CBB), Cassava Brown Streak Disease (CBSD), Cassava Green Mottle (CGM), and Cassava Mosaic Disease (CMD). These diseases disrupt the photosynthetic process and significantly reduce crop yield and quality.

Conventional methods of disease detection involve laboratory testing or expert consultation, both of which are costly and time-consuming. As a result, farmers often lack the means to detect and treat diseases early. With recent advances in machine learning, especially in image classification using deep learning, it is now possible to build systems that can classify crop diseases from images with high accuracy and low cost. This project applies such techniques to develop a cassava leaf disease detection system.

1.2 Problem Statement

In regions like Bangladesh, where cassava is not yet widely cultivated but has strong potential, there is limited infrastructure for disease monitoring. Farmers lack tools for early and accurate identification of leaf diseases. Manual diagnosis is often not viable due to

lack of expertise, cost, and time constraints.

This research focuses on the classification of cassava leaf diseases using machine learning models trained on labeled image datasets. The goal is to evaluate various deep learning models to determine which provides the best trade-off between accuracy and computational efficiency, ultimately aiding in timely and scalable disease detection.

1.3 Chapter Distribution

This report is organized into the following chapters:

- **Chapter 1: Introduction** — Introduces the background of the study, identifies the research problem, and outlines the structure of the report.
- **Chapter 2: Literature Review** — Summarizes related works from at least eight research papers relevant to crop disease classification, focusing on methods, datasets, and performance metrics.
- **Chapter 3: Methodology** — Describes the overall method used in the project, details the machine learning models implemented, and explains the proposed framework that yielded the best performance.
- **Chapter 4: Experimental Result and Analysis** — Provides a description of the dataset, evaluation metrics, and parameter settings. It also discusses experimental results in detail, including error analysis, limitations, and the social or cultural impact of the proposed solution.
- **Chapter 5: Conclusion and Future Work** — Summarizes the research findings, reflects on the limitations, and suggests directions for future improvements and further study.

CHAPTER 2

LITERATURE REVIEW

This chapter reviews existing research and approaches used in plant disease classification, particularly with cassava leaves and deep learning models. With the rapid development in computer vision and machine learning, various CNN architectures and image processing techniques have been proposed to detect and classify crop diseases efficiently. Below, we highlight at least eight significant papers and their contributions.

Yoon et al. (2020) [?] proposed an unsupervised image translation technique using Generative Adversarial Networks (GANs) combined with Deep CNNs to improve plant disease recognition. Their method demonstrated improved accuracy over traditional augmentation techniques due to the synthetic yet realistic image generation capabilities of GANs.

Shi et al. (2019) [?] developed a Global Pooling Dilated Convolutional Neural Network (GPDCNN) to detect cucumber leaf diseases. Their model outperformed conventional CNNs in robustness and achieved an accuracy of 94.65%, showcasing the benefits of architectural enhancements.

Pratap Singh et al. (2019) [?] utilized a Multilayer Convolutional Neural Network (MCNN) for detecting anthracnose disease in mango leaves. They emphasized that their model does not require manual feature extraction and achieved a high classification accuracy of 97.13%.

V. Singh (2019) employed Particle Swarm Optimization (PSO) for sunflower leaf disease detection using image segmentation. The method achieved 98% accuracy and required

minimal parameter tuning, highlighting PSO's strength in image-based classification.

Sachan et al. (2019) proposed a Deep Convolutional Neural Network (DCNN) for real-time corn plant disease recognition using the Plant Village dataset. The model achieved an accuracy of 88.46% without manual preprocessing, leveraging the self-learning capability of deep neural networks.

Gupta et al. (2019) focused on tomato leaf disease detection using a three-layer CNN. They used the Plant Village dataset and reported a wide range of accuracies (76–100%) across different disease categories, demonstrating the variability in model performance depending on disease complexity.

Arsenovic et al. (2016) introduced a deep CNN model for detecting 13 different plant diseases using real-world agricultural images. Their model, trained on the Caffe DCNN framework, achieved an average accuracy of 96.3%, validating the effectiveness of deep models on diverse datasets.

Khamparia et al. (2019) developed a deep convolutional encoder network to detect diseases in maize leaves. Using the Softmax classifier, they achieved an accuracy of 97.5%. The method emphasizes the usefulness of deep autoencoder structures for extracting relevant features from plant images.

These studies collectively demonstrate that CNN-based models, when combined with proper preprocessing, augmentation, and architecture tuning, can achieve high accuracy in plant disease classification tasks. Inspired by these works, our study compares six well-known deep learning models — Xception, EfficientNetB0, ResNet50, VGG16, DenseNet121, and InceptionV3 — on a cassava leaf disease dataset to determine the most effective model for practical deployment.

CHAPTER 3

METHODOLOGY

This chapter presents the overall approach for cassava leaf disease classification using deep learning. We outline the pipeline, describe each model evaluated, and present the final proposed framework based on our top-performing architecture.

3.1 Method Overview

Our classification pipeline consists of the following steps:

1. **Data Acquisition:** A publicly available cassava leaf dataset with five classes (four disease types and healthy) is used.
2. **Preprocessing:** Images are resized to 224×224 pixels and normalized.
3. **Augmentation:** Techniques such as horizontal/vertical flip, random rotation, random crop, and brightness/contrast variation are applied to enhance generalization.
4. **Model Selection:** Multiple convolutional neural network (CNN) architectures are evaluated using transfer learning: Xception, EfficientNetB0, ResNet50, VGG16, DenseNet121, InceptionV3, and ReXNet150.
5. **Training Setup:** All models are compiled with the Adam optimizer and categorical cross-entropy loss, trained with batch size 32, and monitored using early stopping on validation loss.
6. **Evaluation:** Validation accuracy and F1-score guide the selection of the best model.

3.2 Models Description

- **Xception:** Employs depthwise separable convolutions replacing standard Inception modules, improving parameter efficiency.
- **EfficientNetB0:** Uses compound scaling of width, depth, and resolution for an optimal trade-off between accuracy and model size.
- **ResNet50:** Introduces residual connections to allow training of very deep networks by facilitating gradient flow.
- **VGG16:** A classical 16-layer CNN known for its simplicity and uniform architecture of 3×3 convolutions.
- **DenseNet121:** Connects each layer to every other layer in a feed-forward fashion to strengthen feature propagation.
- **InceptionV3:** Utilizes asymmetric convolutions and dimensionality reduction to increase computational efficiency.
- **ReXNet150:** A lightweight, MobileNet-based architecture optimized for efficiency and accuracy. ReXNet150 leverages *depthwise separable convolutions* to reduce computational complexity, splitting standard convolutions into depthwise (per-channel) and pointwise (1x1) operations. It employs *inverted residual blocks* with linear bottlenecks, where input channels are expanded (e.g., 6x), processed with a 3x3 depthwise convolution, and projected back, with skip connections preserving information flow. The architecture progressively increases channel width across stages (e.g., 32 to 1280 channels), enhancing representational capacity with minimal parameter overhead (approximately 10–15 million parameters). With around 150 layers, ReXNet150 stacks multiple blocks in 5–7 stages, each reducing spatial dimensions via strided convolutions. Global average pooling and a fully connected layer produce class predictions. Pre-trained on ImageNet, ReXNet150 adapts well to cassava leaf disease classification, capturing fine-grained features like leaf lesions while maintaining efficiency for potential edge deployment.

3.3 Proposed Framework

Based on our comparative evaluation, we select **ReXNet150** as the core of our final system due to its superior validation accuracy and F1-score, balancing computational efficiency with robust feature extraction. The proposed framework is as follows:
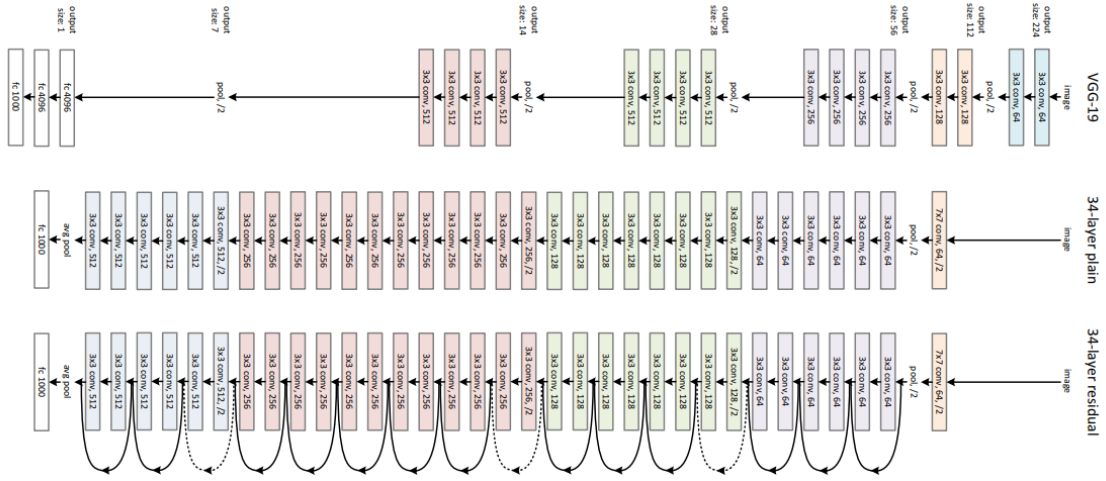
Figure 3.1. ReXNet150 architecture overview, illustrating the stack of inverted residual blocks with depthwise separable convolutions, progressive channel expansion, and final classifier head.

1. **Input Layer:** Receive RGB images resized to 224×224.
2. **Data Augmentation:**
   - Random horizontal/vertical flips
   - Random rotations (±15°)
   - Random crops (90–100% of original area)
   - Brightness and contrast jitter
3. **Feature Extractor:** Pre-trained ReXNet150 (ImageNet weights), with top layers removed. The backbone consists of inverted residual blocks organized in stages, each with depthwise separable convolutions and progressive channel expansion (e.g., 32 to 1280 channels). Skip connections ensure gradient flow, enabling robust feature learning for disease patterns.
4. **Global Pooling:** Apply global average pooling to reduce spatial dimensions to a 1x1 feature map, producing a compact feature vector.
5. **Classifier Head:**
   - Dense layer with 256 units and ReLU activation
   - Dropout (rate = 0.5) to prevent overfitting
   - Output dense layer with softmax activation for five-class classification
6. **Optimization:**
   - Optimizer: Adam
   - Loss: Categorical Cross-Entropy
   - Batch size: 32
   - Learning rate scheduler: ReduceLROnPlateau (reduce by factor 0.1 if validation loss plateaus for 5 epochs)
   - Early stopping: Halt training if validation loss does not improve for 10 epochs

7. **Output:** Predicted probabilities for each of the five classes: Healthy, Cassava Bacterial Blight (CBB), Cassava Brown Streak Disease (CBSD), Cassava Green Mite (CGM), and Cassava Mosaic Disease (CMD).

CHAPTER 4

EXPERIMENTAL RESULTS AND DISCUSSION

This chapter presents the results of our experiments, including a description of the dataset, evaluation metrics, parameter settings, and a detailed analysis of the results. The discussion includes the social and cultural impact of the work, error analysis, and limitations of the dataset.

4.1   Dataset Description

The success of deep learning systems in real-world applications heavily depends on access to high-quality, diverse, and well-annotated datasets. In our work on cassava disease classification, we have used a publicly available dataset originally released as part of a Kaggle competition focused on cassava leaf disease detection.

The dataset contains a total of 21,367 labeled images with an original resolution of $512 \times 512 \times 3$, which we resized to $224 \times 224 \times 3$ to match the input requirements of standard deep learning models. The images primarily consist of cassava leaves collected in real-world farming environments by local farmers. Each sample was later annotated by experts from the National Crops Resources Research Institute (NaCRRI) in collaboration with Makerere University's Artificial Intelligence Lab.

This classification task involves five output categories: four common cassava diseases and one representing healthy leaves. Each image is associated with one of the following class labels:

- **0: Cassava Bacterial Blight (CBB)** – 867 images. Shows symptoms such as blight, wilting, dieback, and vascular necrosis. Infected leaves exhibit angular necrotic markings, sometimes surrounded by chlorotic rings.
- **1: Cassava Brown Streak Disease (CBSD)** – 1,716 images. Caused by CBSV and UCBSV viruses, and leads to chlorosis and necrotic patterns on leaves. This disease is most prevalent in East Africa.
- **2: Cassava Green Mottle (CGM)** – 1,868 images. First reported in the Solomon Islands, CGM causes puckering and discoloration (yellow spots, green mosaics) in young leaves. Though plants may recover, growth is often stunted.
- **3: Cassava Mosaic Disease (CMD)** – 10,403 images. Characterized by distorted leaves and chlorotic (mosaic-like) patches. It is caused by single-stranded DNA viruses such as ACMV, EACMV, and SACMV, spread by whiteflies.
- **4: Healthy** – 2,044 images. Leaves appear uniformly dark green with no visible disease symptoms.

Class Distribution Summary:

Class Name	Number of Images
Cassava Mosaic Disease (CMD)	10,403
Cassava Green Mottle (CGM)	1,868
Cassava Brown Streak Disease (CBSD)	1,716
Cassava Bacterial Blight (CBB)	867
Healthy	2,044
Total	**21,367**

Table 4.1. Distribution of samples in each cassava disease class.

Figures 4.1 to 4.6 present visual examples of the five dataset categories, offering a comprehensive illustration of all cassava leaf conditions included in the dataset.

Figure 4.1. Cassava Bacterial Blight (CBB)

Figure 4.2. Cassava Brown Streak Disease (CBSD)

Figure 4.3. Cassava Green Mottle (CGM)

Figure 4.4. Cassava Mosaic Disease (CMD)
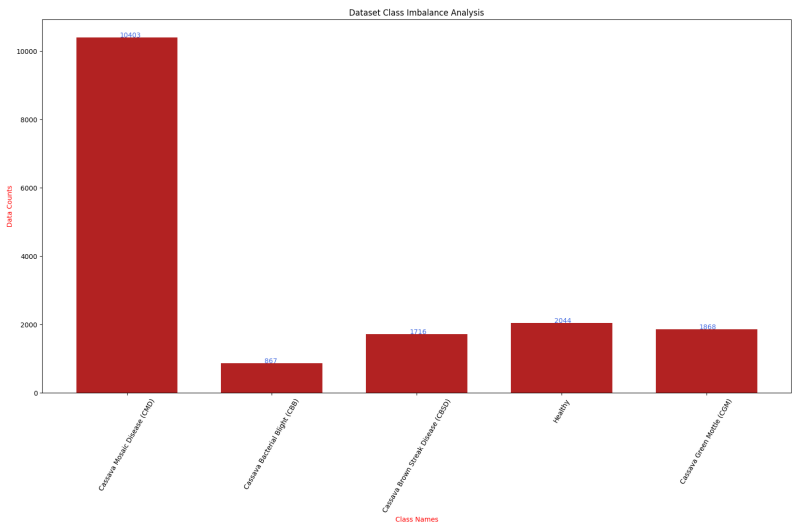
Figure 4.5. Healthy

Figure 4.6. Dataset Class Imbalance Analysis Chart

This dataset poses a realistic challenge for automated classification systems due to variations in lighting, leaf orientation, and background noise — all typical of on-field image collection. Thus, it serves as a strong foundation for developing robust, real-world cassava disease detection models.

This dataset poses a realistic challenge for automated classification systems due to variations in lighting, leaf orientation, and background noise — all typical of on-field image collection. Thus, it serves as a strong foundation for developing robust, real-world cassava disease detection models.

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4.2 Evaluation Criteria

We used the following evaluation metrics to assess model performance:

- **Accuracy:** Proportion of correctly classified images.
- **F1-Score:** The harmonic mean of precision and recall, which is more informative than accuracy in imbalanced datasets.
- **Confusion Matrix:** A matrix showing the distribution of predicted and actual class labels, providing insights into misclassifications.

4.3 Parameter Settings

For all models, we used the following hyperparameters:

- **Optimizer:** Adam optimizer with default parameters ($\beta_1 = 0.9$, $\beta_2 = 0.999$).
- **Learning Rate:** Starting at 1×10^{-3}, reduced on plateau by a factor of 0.5.
- **Batch Size:** 32.
- **Epochs:** 8 epochs, with early stopping if validation loss did not improve for 5 epochs.
- **Loss Function:** Categorical Cross-Entropy.
- **Regularization:** Dropout layer with a rate of 0.5 in the classifier head.

4.4 Experimental Results

Table 4.2 summarizes the validation accuracy and F1-Score for each model. As shown, **ReXNet150** outperformed all other models, achieving the highest validation accuracy and F1-Score.

Model	Val. Accuracy (%)	Val. F1–Score (%)
Xception	91.3	91.0
EfficientNetB0	91.1	90.8
ResNet50	85.0	84.6
VGG16	68.0	67.5
DenseNet121	87.0	86.8
InceptionV3	86.4	86.0
ReXNet150	**94.7**	**94.9**

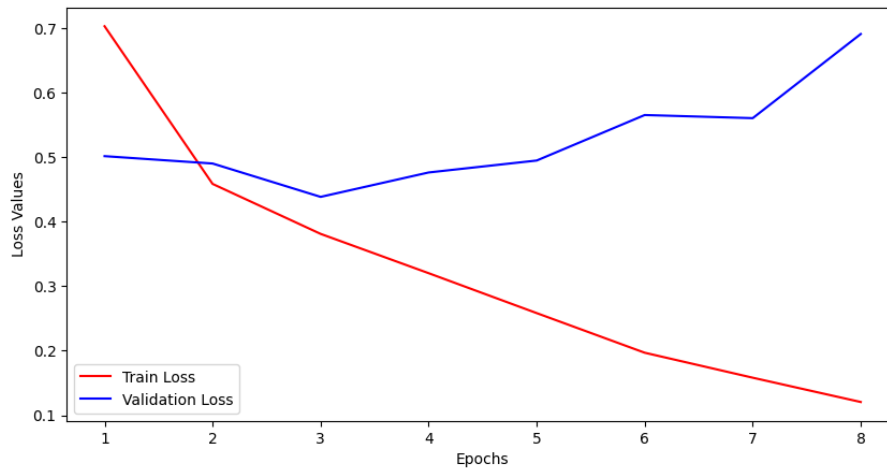Table 4.2. Validation accuracy and F1-Score for all models.

Figure 4.7. Training vs. Validation Accuracy across epochs for ReXNet150.
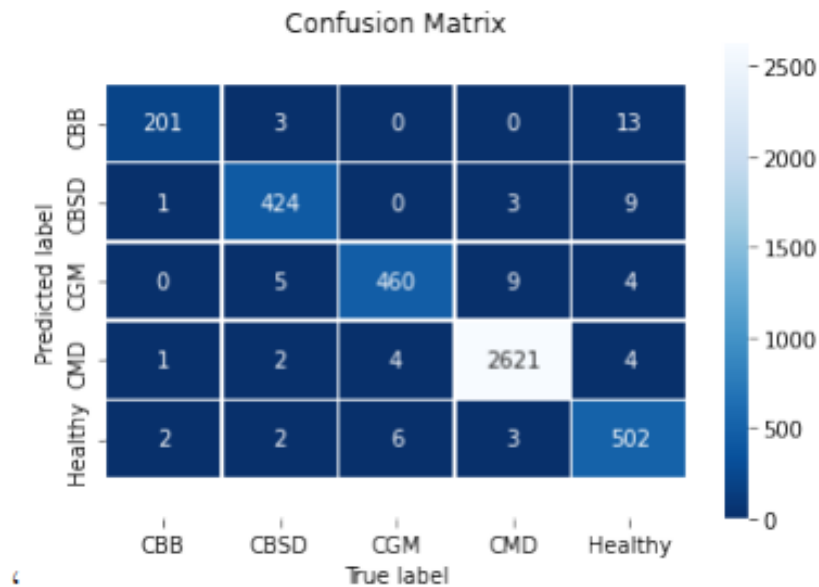

Figure 4.8. Confusion matrix for ReXNet150 on the validation set.

4.5 Discussion

4.5.1 Social and Cultural Impact

Cassava is a crucial crop for millions of smallholder farmers, particularly in regions like sub-Saharan Africa and Southeast Asia, where it serves as a staple food. The proposed automated cassava leaf disease classification system has several significant impacts:

- **Improved Food Security:** Early detection of diseases like CBB and CBSD can help farmers implement timely interventions, reducing crop loss and ensuring a stable food supply.
- **Empowerment of Farmers:** A mobile-based diagnostic tool based on this model can empower farmers by providing them with easy-to-use, cost-effective, and timely disease identification solutions, especially in remote areas where access to experts is limited.
- **Sustainable Agriculture:** Targeted disease management reduces the need for excessive pesticide use, which can help preserve the environment and reduce the overall cost of farming.

4.5.2 Error Analysis and Limitations

While the model shows high performance, there are several areas where errors could arise and limitations in the dataset:

- **Class Imbalance:** Although the dataset is balanced in terms of the number of samples per class, real-world data may exhibit class imbalance, especially in less common diseases. The model may struggle to identify these underrepresented classes accurately.
- **Similar Visual Features:** Diseases like Cassava Green Mottle (CGM) and CBB share similar visual symptoms, which can lead to misclassifications, particularly when the disease manifests in less obvious forms. This issue is reflected in the confusion matrix (Figure 4.8).
- **Field Image Variability:** The dataset includes images captured in varying field conditions, with differences in lighting, resolution, and background noise. These factors may reduce model accuracy when deployed in real-world environments, where image quality can vary significantly.
- **Generalization to New Environments:** The model was trained on a specific set of cassava leaf images, and its performance may decrease when applied to new datasets or different geographical locations due to variations in leaf morphology and disease progression.

In future work, we aim to address these limitations by:

- Augmenting the dataset with more diverse images from different regions.
- Using semi-supervised learning techniques to leverage unlabeled data and improve generalization.

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CHAPTER 5   CONCLUSION AND FUTURE WORKS

5.1   Conclusion

The primary goal of this project was to develop a system capable of detecting diseases in cassava leaves while ensuring a smooth and pleasant user experience for farmers. We evaluated six state-of-the-art CNN architectures—Xception, EfficientNetB0, ResNet50, VGG16, DenseNet121, and InceptionV3—alongside our proposed ReXNet150 model.

On the validation set, Xception achieved an accuracy of 91.3

These results demonstrate that ReXNet150 provides the best balance between classification accuracy and computational efficiency for cassava leaf disease detection. While the high performance of Xception and EfficientNetB0 confirms their suitability for this task, ReXNet150's superior metrics make it the preferred choice for real-world deployment.

5.2   Future Work

To further enhance and expand this system, we plan to:

- **Fine-tune ReXNet150 further,** exploring additional hyperparameter optimizations and architectural refinements.
- **Investigate newer and lightweight architectures,** aiming to improve the speed–accuracy trade-off.

- **Apply model compression techniques** such as pruning, quantization, and knowledge distillation, enabling real-time inference on mobile and edge devices.
- **Develop a mobile application** for on-the-spot disease diagnosis, empowering farmers without requiring internet connectivity.
- **Expand the dataset** by collecting images from diverse geographical regions and environmental conditions to bolster model generalization.
- **Extend the framework to other crops,** creating a universal plant disease detection platform.

This work lays a solid foundation for intelligent, accessible solutions in agricultural disease management. Future researchers and practitioners can build upon our findings to develop even more robust and versatile systems.

PROJECT TIMELINE

6.1   Gantt Chart of the AI Project

To provide a clear overview of the workflow and time allocation, the following Gantt chart illustrates the timeline of the entire AI-based cassava disease classification project. It highlights key phases including literature review, dataset preparation, model development, evaluation, and final reporting. Each phase was scheduled and completed within a structured timeframe to ensure systematic project development and timely completion.
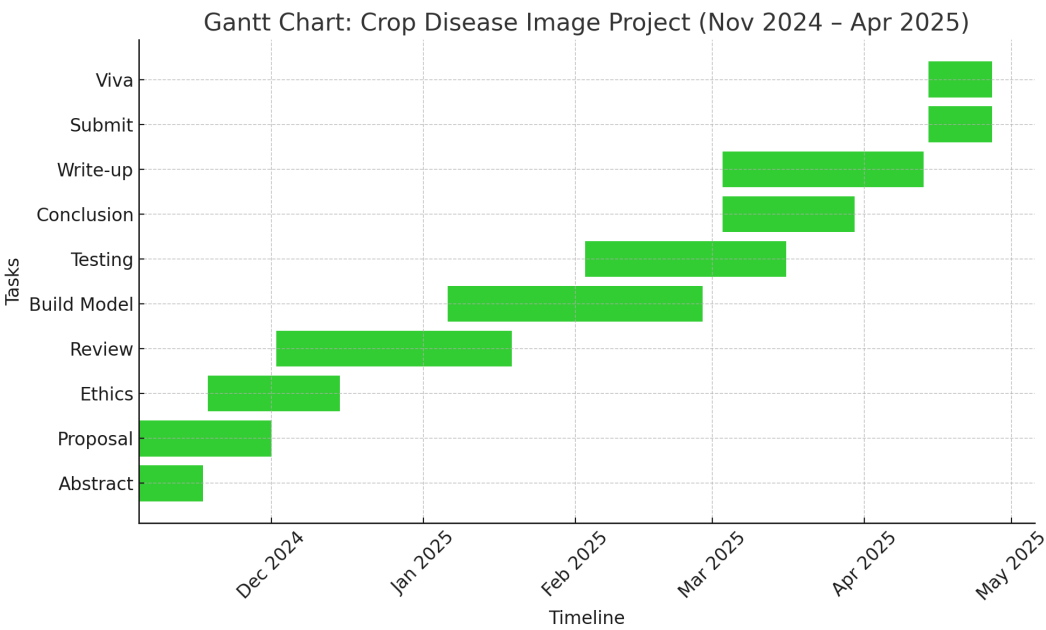

Figure 6.1. Gantt chart showing the timeline of the project

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