

Cassava Disease Classification Challenge

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1 Introduction

Cassava is an important staple crop in many countries, providing food security and income to millions of people. However, cassava plants are susceptible to various diseases that can significantly reduce crop yield and quality. These viral diseases are major sources of poor yields for cassava, the 2nd largest provider of carbohydrates in Africa. Early detection and accurate classification of these diseases are crucial for implementing effective control measures and minimizing crop losses. In this project, we developed a deep learning-based approach to classify 5 fine-grained cassava leaf disease categories using Convolutional Neural Networks (CNNs).

2 Methods

The dataset consists of leaf images of the cassava plant, with 9,436 annotated images and 12,595 unlabeled images of cassava leaves. The goal is to learn a model to classify a given image into these 4 disease categories or a 5th category indicating a healthy leaf. Our data set is divided into training testing and validation sets. For data preprocessing we applied some geometric transformations to move some of the pixels around and then rotate the images a bit, we did horizontal flips, zoom in and out on all the images in the training set. For balance the dataset we use compute class weights function calculates class weights based on the frequency of labels in a dataset. Class weights are commonly used in imbalanced classification problems where some classes have significantly more or fewer samples than others. These weights are used during the training process to give more importance to underrepresented classes and balance the learning. In this work we have experienced some CNN architecture. Using PyTorch deep learning framework, we try first a CNN architecture consisted of three convolutional blocks followed by a fully connected layer. Each block contained a convolutional layer, ReLU activation, and max-pooling. The output of the final convolutional block was flattened and fed into the fully connected layer, which produced the class probabilities and we observe that the result is not good enough. We use batch normalization in our model. Batch normalization

is a technique commonly used in deep learning models to improve the training process and generalization performance. About the learning we train our model in the training set and validate in the validation set. To ensure the generalizability of our model, we applied cross-validation using K-Fold technique. We used the scikit-learn library to perform the cross-validation, splitting the data into multiple folds and the model is trained on a portion of the data called the training set and evaluated on the remaining portion called the validation set. We used the Adam optimizer and Cross Entropy Loss to train our model. We tried to vary the learning rate, we also tried SGD optimizer but we get a big loss. We used RMSprop which is an optimization algorithm commonly used in deep learning to update the weights of neural networks during training. It is an extension of the stochastic gradient descent (SGD) algorithm that adapts the learning rate for each parameter individually based on the recent magnitudes of its gradients.

We used some methods of transfer learning to exploit the pre-trained models. Through the torchvision library, which provides preformed models. We loaded ResNet101, DenseNet 121 and EfficientNet for the feature extraction and adapt it to our classification problem 5 output. With DenseNet we get 82 accuracy, ResNet101 83 and EfficientNet 85 in the validation set.

3 Results and Discussions

The CNN-based approach demonstrated promising results in classifying common diseases of cassava. The model effectively learned distinctive features from the input images, enabling accurate disease classification. The use of cross-validation allowed us to assess the model's performance robustly and mitigate overfitting concerns. The achieved accuracy on the validation set indicated the model's ability to generalize well to unseen data.

In this work we just work on the labeled data, to improve our work in the future, the dataset could be expanded using the unlabeled data to include more samples and additional disease classes to improve the model's ability to generalize to different cassava diseases.