Evaluation and Optimization of an AI Model for European Canker Detection

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Abstract. *European canker, caused by Neonectria ditissima, is one of the most destructive diseases affecting apple orchards worldwide. Early and accurate diagnosis is essential to reduce economic losses, but traditional methods rely on expert visual inspection, which is often slow and subjective. Advances in Convolutional Neural Networks (CNNs) have shown great potential for plant disease detection by enabling automated image-based diagnosis. This work investigates the application of pre-trained CNN architectures to the identification of European canker symptoms in apple branches. The study demonstrates that CNNs can achieve promising results, although challenges remain due to the complexity of branch-based symptoms compared to leaf diseases.*

1. Introduction

“European canker is one of the most devastating fungal diseases of apple in most temperate regions. The causal agent, *Neonectria ditissima*, infects trees through wounds in the bark forming cankers that girdle the stem and eventually cause tree death.” (Harteveld et al., 2023). In Brazil, particularly in the southern regions, European canker is a growing concern for apple producers. Therefore, early detection of European canker is essential to minimize damage and prevent the spread of the disease. However, visual diagnosis can be challenging and requires expert knowledge, emphasizing the need for more accurate and accessible diagnostic methods.

The Cancontrol platform, developed in 2021, became one of the main resources available for monitoring European canker in apple orchards. Cancontrol allows producers to submit images of their apple trees for analysis by *phytopathologists*. These experts assess the submitted photos and provide diagnostic results on the presence of the disease (Branco Neto et al., 2021). However, this process still relies on human evaluation, which can result in diagnostic delays.

The integration of computer vision models has the potential to enhance disease identification by enabling an initial automated screening, thus reducing the workload of specialists. With advances in artificial intelligence, Convolutional Neural Networks (CNNs) have become promising tools to assist in plant disease identification. CNNs are a class of deep learning models optimized for processing grid-like data structures, such as images, and have demonstrated strong performance in plant disease detection tasks due to their ability to automatically learn hierarchical patterns directly from raw pixel data (Rana et al., 2022). These models have already been successfully applied to the detection of various plant diseases across multiple species, demonstrating their potential for agricultural diagnostics (Mohanty et al., 2016).

This work presents the development and evaluation of a Convolutional Neural Network (CNN)-based model, to be further integrated into the Cancontrol system, designed to accurately identify European canker in apple orchards.

2. Literature Review

The application of deep learning (DL) methods to plant disease detection has yielded consistently promising results. In apple leaf disease classification, Kumar et al. (2023) and Zhang et al. (2021) employed CNNs combined with data augmentation techniques, achieving accuracy levels above 96%. Other works such as Khan et al. (2024) integrated transfer learning and explainable AI (XAI) into CNN architectures with data augmentation, obtaining 97.8% accuracy.

Beyond apples, several studies have combined CNNs with different optimization strategies to improve performance. Min et al. (2023) explored augmentation-based improvements, reaching accuracies from 91.3% to 96.7%. Al-Gaashani et al. (2022) employed MobileNetV2, NasNetMobile, and standard CNNs within an ensemble framework, achieving 99% accuracy. Ahmed et al. (2025) proposed novel ensemble deep neural networks for cucumber disease classification, obtaining 98.91% accuracy.

While convolutional neural networks remain central to most high-performing approaches, emerging trends—such as ensemble learning, lightweight architectures, and model interpretability—reflect a shift toward more adaptable and field-ready solutions. However, despite significant progress in classifying diseases in crops like tomato and apple, no studies have, specifically, addressed the detection of European canker, reinforcing the novelty and relevance of the present research. By leveraging CNNs, data augmentation, and ensemble methods, this research aims to deliver a robust, automated diagnostic solution for a disease that remains underexplored in the current state-of-the-art.

3. Materials and Methods

This is an applied research, with a quantitative approach and an exploratory objective. The technical procedures adopted were literature review and experimental research. The research is being carried out in three main stages.

In the first stage, 669 images of apple trees were collected from multiple sources. These sources include: EPAGRI (Agricultural Research and Rural Extension Company of Santa Catarina), CIDASC (Integrated Agricultural Development Company of the State of Santa Catarina), SENAR (National Rural Learning Service), and the image database of the Cancontrol platform, which includes photos uploaded directly by apple growers.

In the second stage, we evaluated twenty-two different pre-trained models. The models used include: MobileNetV2; MobileNetV3 in both Large and Small versions; ResNet with 18, 50, and 101 layers; VGG with 11, 16, and 19 layers; AlexNet; EfficientNet from B0 to B7; and DenseNet with 121, 161, 169, and 201 layers.

In the third and final stage, data augmentation techniques will be applied to expand the dataset's diversity and size. These techniques include geometric transformations such as rotation, flipping, scaling, and brightness adjustments. Additionally, ensemble learning methods will be employed to combine the outputs of multiple models, enhancing robustness and reducing classification variance.

4. Results

As detailed in Section 3, the results presented in this section were obtained through the training of twenty-two selected CNN models. The images were divided into three distinct sets: 60% for training, 20% for validation, and the remaining 20% for testing. The results aim to identify the most suitable models for European canker detection in order to determine the optimal combination for use in ensemble methods.

The analysis of variance (ANOVA) performed for accuracy, precision, and recall revealed low p-values $\mathrm{PR}(> F)$ in all cases: 2.62×10^{-74} for accuracy, 3.05×10^{-73} for precision, and 6.46×10^{-73} for recall. These values are far below the conventional significance threshold $(p < 0.05)$, providing strong evidence that the observed differences in performance among the twenty-two models are statistically significant.

The Tukey's Honest Significant Difference (HSD) test was applied to compare the mean precision values among all evaluated models. The "Tukey Group" column in Table 1 presents the groupings obtained exclusively based on the precision metric, without considering accuracy or recall for the formation of these groups. Models sharing the same letter do not present statistically significant differences in precision, whereas models assigned to different letters exhibit significant differences at a predefined confidence level. The results show that EfficientNetB2, appearing exclusively in group A, achieved the highest mean precision (0.859540), statistically outperforming all other models.

Table 1. Average accuracy, precision, recall, and Tukey grouping.

Model	Avg. Accuracy	Avg. Precision	Avg. Recall	Tukey Group
EfficientNetB2	0.861994	0.859540	0.861040	A
DenseNet121	0.843302	0.848175	0.839207	B
EfficientNetB0	0.841433	0.840302	0.836821	B
EfficientNetB1	0.837383	0.835223	0.833635	B C
DenseNet201	0.836137	0.834101	0.832530	B C
AlexNet	0.833022	0.833129	0.827907	B C
ResNet18	0.828349	0.831911	0.819071	B C D
DenseNet161	0.830841	0.831509	0.823465	B C D
DenseNet169	0.830841	0.830063	0.825002	B C D
ResNet101	0.823676	0.822190	0.819538	C D E
EfficientNetB7	0.823053	0.821535	0.826509	C D E F
EfficientNetB3	0.819315	0.817526	0.814053	D E F G
ResNet50	0.816511	0.814280	0.816421	E F G H
MobileNetV2	0.814019	0.812641	0.808872	E F G H
EfficientNetB6	0.805919	0.807103	0.811801	E F G H I
MobileNetV3 Small	0.809657	0.806571	0.806379	F G H I
VGG11	0.799377	0.804553	0.786989	G H I
VGG19	0.797819	0.800987	0.787145	H I J
EfficientNetB5	0.793770	0.792257	0.796821	I J
MobileNetV3 Large	0.790343	0.788259	0.783427	J K
EfficientNetB4	0.777259	0.775388	0.769317	K L
VGG16	0.765109	0.767762	0.752395	L

5. Conclusion

This study highlights the potential of deep learning approaches to support the diagnosis of European canker in apple orchards. The experimental results demonstrated that pretrained CNN architectures are able to identify European canker with encouraging levels of accuracy, precision, and recall. The observed differences in performance across the twenty-two tested models, confirmed through statistical analysis, justify the breadth of the comparative evaluation carried out in this work. Notably, EfficientNetB2 emerged as the best-performing architecture, but its performance remains considerably lower than the accuracies reported for CNN-based detection of leaf diseases in other crops. This discrepancy can be partly attributed to the fact that European canker manifests in branches and stems, where symptoms are less visually distinct and harder to capture than in leaves.

These findings underscore both the progress achieved and the challenges that remain. While current results are promising, there is still ample room for improvement. Ongoing work focuses on the application of data augmentation strategies to expand dataset variability, as well as ensemble learning methods to enhance diagnostic robustness. Together, these approaches are expected to improve model performance, bringing the tool closer to practical deployment in real-world apple orchards.

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