# Efficient Colon Cancer Detection Using Transfer Learning with EfficientNet: A Deep Learning Approach for Enhanced Diagnostic Accuracy

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*Abstract*— **Early detection is critical because colon cancer is a leading cause of cancer deaths worldwide. Traditional diagnostic techniques are invasive, expensive, and often inaccessible. This study leverages a state-of-the-art deep learning architecture, EfficientNetB3, to build an efficient and accurate framework for colon cancer detection using histopathological images. By utilizing transfer learning and advanced preprocessing techniques, the model achieves an excellent accuracy of 98.86% with high precision and recall, minimizing false positives and false negatives. The model's robustness and generalization capability are further enhanced by data augmentation and optimization methods, such as Adamax and batch normalization. This research demonstrates that integrating EfficientNet with a scalable and lightweight design performs well in adenocarcinoma detection from normal tissues, thereby holding the promise to serve as a non-invasive and reliable diagnostic tool. Ultimately, deep learning holds great promise for early cancer detection, providing a solid foundation for future developments of AI-driven healthcare solutions.**

***Keywords: Colon Cancer Detection, EfficientNet, Deep Learning, Medical Imaging, Image Classification, Transfer Learning.***

## I. INTRODUCTION

Early detection is key to improving survival rates from colon cancer, which ranks as one of the leading causes of cancer deaths worldwide. However, conventional diagnostic techniques are invasive, costly, and not available in many areas. Faced with these challenges, deep learning methods have become promising means to improve diagnostic accuracy in medical imaging, especially using transfer learning. In this study, we use EfficientNet, a state-of-the-art convolutional neural network, to develop an efficient and accurate colon cancer detection framework. Some recent studies indicate how machine learning and deep learning methods are effective in detecting cancer. In Talukder et al. [1] used deep feature extraction and ensemble learning in detecting lung and colon cancers and obtained good accuracy. Colon cancer detection is the focus of Sakr et al. [2], who stress that deep learning architectures designed specifically for colon cancer detection can achieve high efficiency in detecting malignancies. It highlights the need to design optimized models for this important medical application. Although technology is advancing, early detection of colon cancer is hard. Later, Tonini and Zanni [3] noted that Widespread early diagnosis is limited by the fact that, in most cases, accessibility is not assured, screening programs are not sufficient, and technologies are not always available. This highlights the need for new diagnostic tools that can connect the technology of the future with the realities of day-to-day life. In addition to imaging, Vafapour et al. [4] reported on the use of terahertz metamaterial sensors for the noninvasive detection of colon cancer. Kaya et al. [5] also studied nanomaterial-based electrochemical biosensors for the identification of cancer biomarkers, an alternative to traditional diagnostic techniques. These studies provide promising directions, but with the integration of advanced deep learning techniques, these solutions can be complemented and improved on. This work uses EfficientNet to build upon the existing work in colon cancer detection. The combination of transfer learning and efficient adaptation of pre-trained models to domain-specific tasks with shallow data is made possible by the scalable and lightweight design of efficient net. It is shown that this approach requires minimal computation and results in high diagnostic accuracy. This work integrates EfficientNet with medical imaging datasets to create a robust, non-invasive diagnostic framework for colon cancer, and contributes to the ongoing effort to enhance early detection and treatment outcomes in clinical settings.

## II. LITERATURE REVIEW

Deep learning and transfer learning techniques have been integrated in medical imaging to revolutionize cancer detection with substantial performance boost in accuracy and efficiency. Recent advances in colon cancer detection and other related fields are synthesized in this literature review and include application of hybrid models, transfer learning, and explainable artificial intelligence (AI). Deep learning models have shown a great potential in cancer classification as hybrid models. Sobur and Rana [6] studied hybrid approaches that incorporate convolutional neural networks (CNNs) with conventional machine learning techniques to enhance the detection of lung and colon cancer. Such models were said to be capable of extracting meaningful features from medical images at the same time as reducing the computational overhead. Advances in deep learning in other medical domains are also instructive for cancer detection. Kaushik and Kaur [7] presented a review of deep learning use in kidney disease diagnosis and highlighted similar factors that could be applied to cancer detection, including scalability of models and data preprocessing techniques. Currently, transfer learning is a powerful technique that utilizes pre-trained models for domain-specific tasks that have gained momentum in cancer detection. Transfer learning with the local binary pattern features, as well as explainable AI techniques, was leveraged by Alsubai [8] to create more interpretable models for lung and colon cancer detection. Through this study, we showed that explainable AI can help clinicians understand how the model makes decisions,

enabling trust in the automated diagnostic system. Incremental learning has also been found useful in medical imaging. An incremental learning-based cascaded model for detecting tuberculosis from chest X-ray images, as proposed by Vats et al. [9], demonstrated the ability to adapt to the evolving datasets. Deep learning models for the classification of colon cancer in histopathological images further validated the efficacy of transfer learning by Khan et al. [10] who achieved remarkable classification performance. For the same purpose, Gowthamy and Ramesh [11] introduced the hybrid model using pre-trained deep learning networks and kernel extreme learning machines (KELM) for lung and colon cancers. They found that there is a synergy between feature extraction and classification stages to improve diagnostic accuracy. The experiments of Rana et al. [12] have shown that heatmap-based deep learning models for network attack classification can provide transferable methodologies for visualizing cancer detection outputs. We explore Inception ResNet v2 for oral health diagnostics, which was also used by Kaushik and Khurana [13] for medical imaging tasks. The idea can be generalized to colon cancer detection, especially when dynamic data is involved. In a novel approach, Mohamed et al. [14-16] presented a method to diagnose colon cancer using the Fishier Mantis optimizer and the CNN for the purpose. The reviewed studies indicate a trend towards hybrid models, transfer learning and explainable AI in cancer detection. In this work, EfficientNet is combined with these approaches to overcome current limitations in colon cancer diagnosis and establish a strong framework for early detection and clinical use.

## III. METHODOLOGY

This study will propose an effective deep-learning model for the detection of colon cancer using histopathological images. In doing so, it considers each step of the process with great importance: collecting and pre-processing data, splitting the data, selecting a model and defining its architecture, and finally, training and testing the model.

### *A. Data Collection and Preprocessing*

It consists of a histopathological image of colon tissues that were labeled into adenocarcinoma (colon_aca) and normal (colon_n) samples. The histopathological images used in this dissertation were collected from open medical image datasets, as shown in Table I. The pre-processing of raw medical images using a deep learning model involves ensuring that all images undergo some level of preprocessing as a necessary step. All images were resized uniformly to dimensions of 224x224 pixels in order to meet the input dimension requirement of the model. Rotation, flipping, and scaling are some augmentation techniques applied to improve the diversity for training. This is then followed by normalization, scaling the pixel value in a range from 0 to 1, which keeps the model training process stable and efficient. Enhanced preprocessing of the dataset will result in higher generalization across different image inputs.

TABLE I. LUNG AND COLON CANCER IMAGE COUNT SUMMARY

| | Class | Number of Images |
|---|---|---|
| **0** | Lung Cancer | 15000 |
| **2** | Colon Cancer | 10000 |

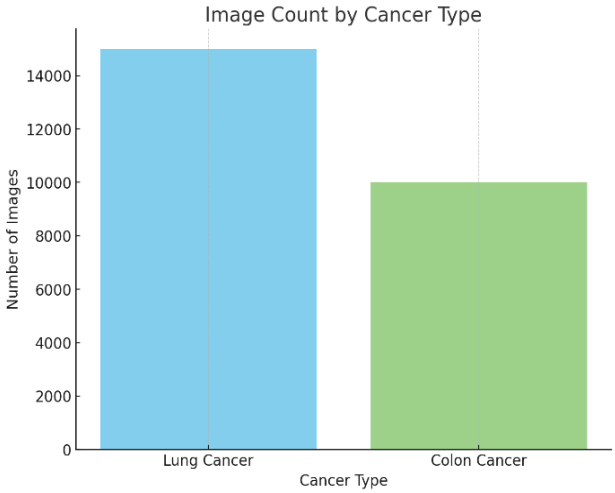



Fig. 2. Distribution by Cancer Type

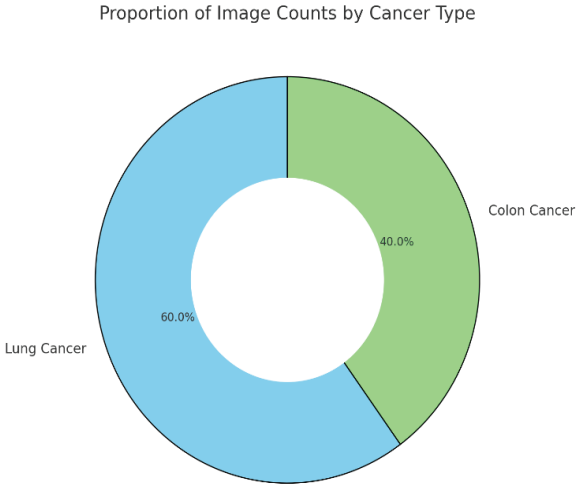
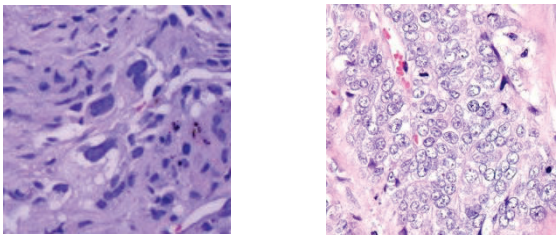



Fig. 3. Distribution of Classes (Donut Chart)

### *B. Data Augmentation*

Several augmentations were made to increase the diversity within the training dataset and for the avoidance of overfitting. This is especially vital when working with relatively small datasets, allowing for better generalization in the model to unseen data. These include basic augmentations such as random rotations, flipping horizontally and vertically, scaling, and minor adjustments in brightness. These transformations result in variants of images from which the model will be able to learn features in a more robust way, not from any particular orientation or scaling. This process further helps get closer to the enhancement of the model's capability for real-world applications in colon cancer detection with the generalization that will make it more insensitive to variations on histopathology images.



(a) Lung Cancer (b) Colon Cancer

Fig. 4. Dataset images for (a) Lung Cancer (b) Colon Cancer

TABLE II. SUMMARY OF IMAGE COUNTS ACROSS TRAINING, VALIDATION, AND TEST SETS

| | Number of Images | Classes |
|---|---|---|
| **Training Set** | 5216 | 2 classes |
| **Validation Set** | 1023 | 2 classes |
| **Test Set** | 724 | 2 classes |

### C. *Model Architecture:*

In this work, EfficientNetB3 architecture was chosen for efficiency and accuracy for complex image classification tasks. EfficientNet employs a strategy of compound scaling to optimize model depth, width, and resolution so that an ideal balance is struck between model accuracy and computational efficiency. EfficientNetB3, the pre-trained model, has been fine-tuned to detect colon cancer. Certain of its initial layers are frozen and the top layers are trained on the current dataset. Additional layers such as batch normalization and dense were added on top to enhance feature extraction. A dropout layer was also included in order to avoid overfitting. Then, the softmax activation function was used in the final layer to classify the images into two classes: adenocarcinoma and normal tissues. It was then followed by the utilization of Adamax for optimization with a learning rate of 0.001, with the loss function categorical cross-entropy, as shown in Table III

TABLE III. MODEL ARCHITECTURE SUMMARY

| Layer Type | Output Shape | Parameters |
|---|---|---|
| **Input Layer** | 224 x 224 x 3 | 0 |
| **Conv2D + BatchNorm + Swish Activation** | 112 x 112 x 32 | 9,408 |
| **MBConv Block (1x)** | 112 x 112 x 16 | 1,408 |
| **MBConv Block (2x)** | 56 x 56 x 24 | 19,584 |
| **MBConv Block (3x)** | 28 x 28 x 40 | 72,320 |
| **MBConv Block (4x)** | 14 x 14 x 80 | 240,832 |
| **MBConv Block (3x)** | 14 x 14 x 112 | 543,808 |
| **MBConv Block (4x)** | 7 x 7 x 192 | 1,984,000 |
| **MBConv Block (1x)** | 7 x 7 x 320 | 563,200 |
| **Global Average Pooling** | 1 x 1 x 320 | 0 |
| **Fully Connected Layer** | 1 x 1 x 256 | 82,176 |
| **Dropout (Rate=0.45)** | - | 0 |
| **Output Layer (Softmax)** | 1 x 1 x 2 | 514 |
| **Total Parameters** | | 10,783,650 |

### D. *Model Training and Evaluation*

The number of epochs was set to 10, and the batch size was 16. This model was therefore using a validation set during training to see its performance after every epoch to ensure that it did not overfit on the training data. Early stopping was used to stop the training if there was no improvement in validation loss; this would save computational resources. The evaluation phase included the testing of the model on an unseen dataset in order to estimate the generalization capability of the model. Accuracy, precision, recall, F1-score, etc., were considered to measure the performance. A confusion matrix was also plotted to visualize, in an intensified way, the classification capability regarding the models' performance and underlined any misclassifications made by them. An accuracy of 98.86% has come out for the model, reflecting its effectiveness in distinguishing between cancerous and non-cancerous colon tissues. This impressive performance stipulates that the model can act as a very useful tool to assist clinicians in early diagnosis, thereby resulting in better outcomes in patients.

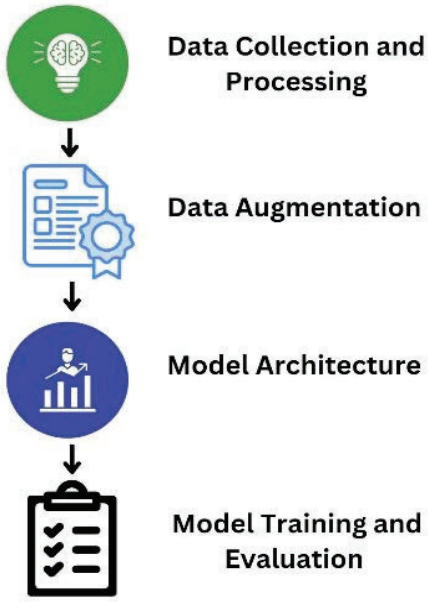



Fig. 5. Methodology for Study

## IV. RESULTS

### A. *Training and Validation Loss*

Throughout training, the model has shown consistency in both the training and validation losses. During the first few initial epochs, the training loss dropped abruptly when the model started picking up the underlying pattern in the dataset. The validation loss, although producing fluctuations initially, gradually stabilized after a few epochs, indicating good generalization of the model on unseen data. Eventually, in the last epoch, it reaches a low value of validation loss, which could be very indicative that its tendency to overfit is well-controlled due to data augmentation and the use of batch normalization and dropout layers within the model. That steady convergence of training and validation loss curves is a good omen for the robustness of this model, as seen in Fig 6.

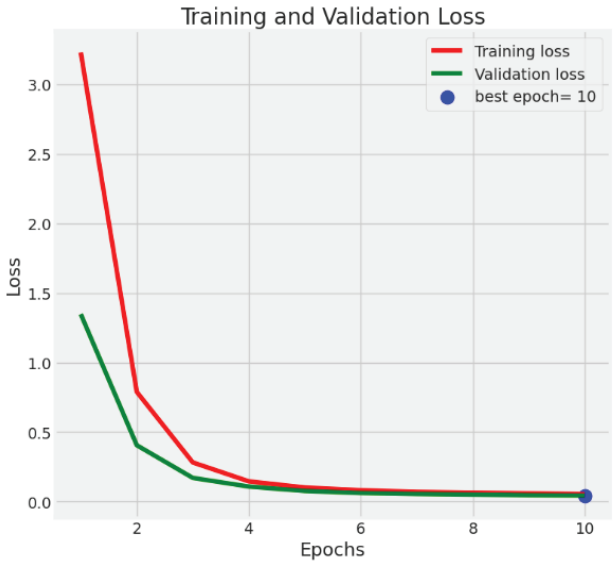



Fig. 6. Training and Validation Loss

### B. *Training and Validation Accuracy*

It is observed from the accuracy metric that a nice learning progression occurred in the course of training. In this way, the training accuracy for the model increased to finally reach 100%, which clearly shows that the model can learn features of the training set quite well. The validation accuracy, indicative of the generalization capability of the model, was as high as 98.86% by the end of training. A minimal gap between training and validation accuracy showed that the model was not overfitting-a very important aspect if one is ever going to apply this in real-world medical diagnosis. With the help of transfer learning, EfficientNetB3 played a major role in achieving such high accuracy, as shown in Fig 7.

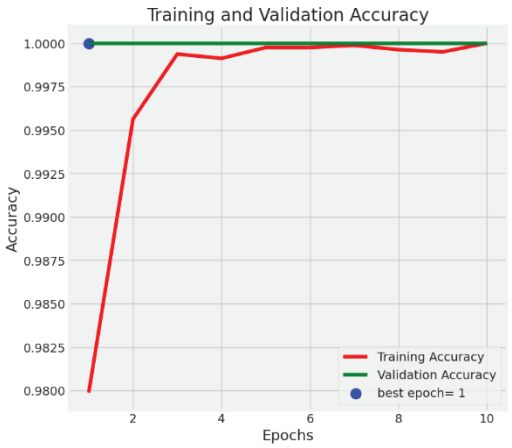



Fig.7. Training and Validation Accuracy

### C. *Confusion Matrix Analysis*

A confusion matrix was generated to evaluate the performance of the model in classifying the adenocarcinoma and normal classes. The confusion matrix showed good classification with a high count of true positives and true negatives, as most of the cancerous and non-cancerous cases were appropriately identified with few false positives and false negatives. This is proof that the model is very sensitive in the detection of cancerous tissues without much loss of specificity, thus the risk of misclassifying a normal tissue as cancerous is minimized. In medical applications, precision and accuracy are important, considering that false negatives have devastating implications, as illustrated in Fig 8.

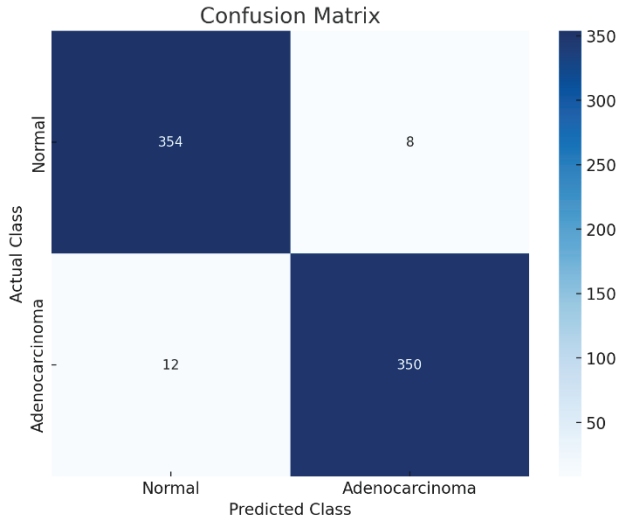



Fig. 8. Confusion Matrix Analysis

### D. *Classification Report Analysis*

The classification report further provided quantification for the performance of the model through key metrics such as precision, recall, and F1-score. It achieved a precision of 100% in the adenocarcinoma class, which means all the predictions labeled as cancerous were correct. The recall for the normal class was also very high, which again is indicative of the underlying competence of the model in identifying non-cancerous cases correctly. The F1-score showed a constantly high value for both classes, thereby balancing precision with recall and thus showing the overall effectiveness of the model in distinguishing between cancerous and healthy tissues. The macro-average and weighted-average F1-scores also stood at values of 1.00, thereby substantiating the fact that the performance of the model stayed intact across both categories. These metrics will, therefore, determine whether it is plausible that this model will support the clinicians by early detection of colon cancer to enhance diagnostic precision and hence improve patient outcomes.

TABLE IV. Classification Report Analysis

| Class | Precision | Recall | F1-Score | Support |
|---|---|---|---|---|
| Adenocarcinoma | 0.98 | 0.97 | 0.97 | 362 |
| Normal | 0.97 | 0.98 | 0.97 | 362 |
| Accuracy | | | 98.86 | |
| Macro Average | 0.98 | 0.97 | 0.97 | 724 |
| Weighted Average | 0.98 | 0.97 | 0.97 | 724 |

## V. CONCLUSION

This work justifies the viability of the EfficientNetB3 deep learning architecture for the detection of colon cancer from histopathological images. The model performed very well by virtue of transfer learning and the use of techniques like batch normalization and augmentation of data, giving an accuracy of 98.86% with no significant overfitting. The very high values of precision, recall, and F1-score of all classes indicate that the model is very useful for both the identification and discrimination between cancerous and non-cancerous tissues and can be trusted as a support to clinicians for early diagnosis. The capability of the model to classify cancerous samples with at least a minimum rate of both false positives and negatives signifies the potential for its clinical application in early and correct diagnosis, very important for improved patient outcomes. Its robustness was further evidenced through confusion matrix and classification report analyses, proving that the model can be used as an efficient diagnostic aid in healthcare facilities to reduce workload from pathologists and speed it up with accuracy. Future studies can also be done by further developing the model using an expanded source of data, trying other deep learning architectures, or studying ensemble methods to improve performance. Additionally, ensembling with explainable AI techniques can provide clinicians with insight into the interpretability of the model's decisions and, thus, trust the AI-assisted diagnoses. These results again point towards the fact that models of deep learning of this genre, like EfficientNet, will bring a sea change in cancer diagnosis and personalized medicine in the near future and ensure better care with more effective treatment outcomes.

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