Prediction of Colon Cancer using DenseNet121, CNN, and REsNET50 Machine Learning Models and using Image Processing Techniques

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***Abstract*— Colon cancer is a matter of great importance in the field of global health, as it stands as one of the primary contributors to mortality rates associated with cancer. The timely identification and precise prognostication of colon cancer have the potential to significantly enhance patient outcomes and diminish mortality rates. The global public health systems face a significant challenge in addressing the impact of colon cancer, which underscores the need for efficient screening and prediction techniques. Machine learning techniques present potential solutions by utilizing extensive datasets to detect intricate patterns that may be imperceptible to human observers. This study investigates the viability of employing machine learning techniques to predict colon cancer by utilizing a dataset consisting of 10,000 colonoscopy images that have been classified into two categories: cancerous and non-cancerous cases. The main aim of this study is to assess the efficacy of various machine learning algorithms, namely DenseNet-121, CNN, and ResNet50, in the prediction of colon cancer. The models' performance was comprehensively assessed in terms of their accuracy in predicting colon cancer. Among the models that were evaluated, DenseNet-121 demonstrated exceptional performance, achieving the highest accuracy of 99.6%.**

Keywords*— colon cancer, cancer detection, machine learning, cnn, desnet121

I. Introduction

The high morbidity and death rates associated with cancer have sparked the interest of scientists all around the world in the complex problem of cancer prediction and diagnosis. Additionally, cancer has been considered a complex illness with many different subgroups [1]. Due to its importance in patient clinical care, early cancer detection and prognosis have become a must in cancer research. Successful treatment is more likely if cancer is detected early. Screening and a timely diagnosis (or downstaging) are the two mainstays of cancer detection in its earliest stages. Screening focuses on evaluating healthy people to discover malignancies before they show any symptoms, whereas initial diagnosis is focused on finding troublesome individuals as soon as possible [2].

Only after the effectiveness of a screening program has been established, when resources are enough to cover nearly every participant group, as well as establishments for clarifying assessments, medication, and follow-up of those with abnormal results become available, should the program be implemented. Curative measures, when applied diligently and promptly, have proven to be one of the most successful ways to cure cancer. To date, endoscope evaluation, imaging assessment, tumor marker treatment, endoscopic ultrasonography, and histological diagnosis have all been used as methods for detecting cancer at an early stage [3]. Elevated levels of tumor markers may be a sign of malignancy. When used in conjunction with other diagnostic procedures, tumor marker testing can aid in the early detection and treatment of certain cancers. There is no perfect tumor marker test. They may not be able to identify a recurrence, and they are not generally cancer-specific.

Cancer cannot be diagnosed based on the existence of tumor markers alone. If you want to find out more about a probable malignancy or recurrence, you need to undergo further testing. Time-consuming processes, invasive investigation methods, analytical requirements, and the high need for particular education and expertise that not even all medical professionals might have been just some of the common shortcomings of these methods. Even imaging-based diagnostic approaches are often inadequate in analyzing preliminary samples. It is crucial to establish an accurate and speedy approach for the early diagnosis of cancer since, while tumor indicators used for evaluation are accessible, they are not always successful and cannot always be discovered early enough to deliver therapy in a timely manner. Not only in cancer research, processing images and finding solutions in geoscience and environmental implications are also becoming popular [3].

Colon cancer, sometimes called colorectal cancer, is a major global health problem [4]. It is responsible for a disproportionately high number of cancer-related fatalities. Improved patient outcomes and lower death rates can be achieved with the early identification and precise prediction of colon cancer [5]. Machine learning methods have rapidly advanced in recent years, making them invaluable for the early detection and treatment of many illnesses, including cancer [6],[7],[8],[9]. The mutated gene that causes cancer can be passed down from generation to generation. Those who have a family history of cancer should have annual checks. Many people lack access to these diagnostic procedures because of their high cost. In poor and middle-income nations, cancer is the third leading cause of death. In 2022, just 26% of low-income nations had publicly available pathology services for cancer diagnosis; in contrast, over 90% of the population in high-income countries had access to cancer diagnosis and

treatment [10]. People in impoverished and undeveloped nations are particularly vulnerable to a wide range of illnesses due to a lack of adequate detection infrastructure, not only cancer. These nations will need to spend extensively on public health, equip a large number of laboratories and pathology centers, and teach a large number of people to use these facilities in order to meet this challenge. In addition, they need to make sure that the prices of these exams are within the financial means of persons who are living in poverty.

The purpose of this study is to examine whether or not machine learning methods can be used to accurately predict colon cancer. Machine learning algorithms are able to evaluate complicated patterns and find important relationships that would be missed by human observers because of a lack of context or training. This is made possible by the abundance of available clinical and genetic data. These kinds of models can aid doctors in making educated judgments, which might result in more effective, individualized care for patients at high risk of developing colon cancer. This study will make use of a large dataset containing clinical and genetic data from people with colon cancer. Medical records, genetic databases, and open archives will all contribute to the final collection. Incorporating data from a wide variety of sources helps to better reflect the complex nature of colon cancer and strengthens the reliability and applicability of the resulting prediction models. Our unique research paper combines three models that were not previously used.

Two types of results are expected from this investigation. The primary goal is to gain an understanding of how well various machine learning algorithms can detect colon cancer. The merits and weaknesses of each algorithm may be shown through comparison and evaluation of accuracy, precision, recall, and other performance measures, facilitating the selection of the most efficient strategy for future applications. Second, this study aspires to construct prediction models that may reliably foretell an individual's risk of acquiring colon cancer, given their unique clinical and genetic characteristics. This study's results might significantly alter how colon cancer is detected, and risk is calculated. By leveraging machine learning, we can enhance the speed and precision of colon cancer prediction, leading to more timely interventions, more specific treatment plans, and better overall patient outcomes.

II. Literature Review

The primary objective of the research conducted by Gupta et al. [11] was to forecast the stage of tumors in colon cancer by utilizing significant histopathology parameters and implementing machine learning (ML) methodologies. The data from a total of 4021 patients in the colorectal cancer registry of Chang Gung Memorial Hospital, located in Linkou, Taiwan, was examined by the researchers. Several machine learning algorithms were employed, and the Tumor Aggression Score (TAS) was considered as a prognostic determinant. The performance of various machine learning algorithms was evaluated using a five-fold cross-validation approach. The findings of the study indicate that the Random Forest model demonstrated a noteworthy F-measure of 0.89 when integrating the TAS in conjunction with conventional attributes for the prediction of TNM stage. Furthermore, it was observed that the Random Forest algorithm demonstrated a higher level of performance in comparison to alternative algorithms. Specifically, it achieved an accuracy rate of approximately 84% and an area under the curve (AUC) value of 0.82 ± 0.10 when utilized for the prediction of five-year disease-free survival (DFS). This study emphasizes the potential of machine learning (ML) algorithms, specifically Random Forest, in effectively predicting the stage of tumors and prognosis of colon cancer. As a result, these algorithms can assist in making informed clinical decisions.

Masud et al., [12] present a classification framework that employs Deep Learning (DL) and Digital Image Processing (DIP) techniques to distinguish between five distinct types of lung and colon tissues using histopathological images. The objective of this study is to design and implement a computerized system that is both efficient and dependable in detecting and diagnosing cancer. The findings indicate that the proposed framework exhibits a noteworthy level of accuracy, reaching up to 96.33%, in the identification of cancerous tissues. This study demonstrates the potential of Artificial Intelligence (AI) in enhancing cancer diagnosis through its ability to analyze a greater quantity of cases within a shorter timeframe and at a decreased expense. The implementation of such a model has the potential to significantly aid medical professionals in the precise and effective detection of different forms of lung and colon cancers. Table 1 as shown comparison between previous work.

TABLE I. TABLE I. COMPARISON BETWEEN PREVIOUS WORK

Ref	Contributions	Dataset	Algorithms used	Best Accuracy
[13]	Developed a predictive algorithm using deep belief networks to detect early-stage intestinal cancer.	China, Jiangsu Provincial Hospital of Traditional Chinese Medicine	Neural network (ECP)	81%
[14]	Developed a machine learning algorithm, ColonFlag, to predict colonoscopy findings using complete blood count data.	Alberta Health Services Forzani and MacPhail Colon Cancer Screening Centre in Calgary	Combined	95%
[15]	Developed a deep neural network model to predict colorectal cancer in patients with type 2 diabetes mellitus.	National Health Insurance Research Database (NHIRD)	Neural Network	98%
[16]	Developed an artificial neural network to assess colorectal cancer risk based on self-reportable personal health data.	National Health Interview Survey, USA	Neural net	89%

Foersch et al. [13] present a multistain deep learning model (MSDLM) for determining the AImmunoscore (AIS) in colorectal cancer (CRC) patients. The model demonstrates high prognostic capabilities, surpassing other clinical, molecular, and immune cell-based parameters. It also predicts the response to neoadjuvant therapy in rectal cancer patients. The AIS, based on the tumor immune microenvironment, offers clinicians a valuable decision-making tool.

Susić et al. [14] conducted a study to evaluate machine learning algorithms for predicting survival in colorectal cancer

patients at different time intervals after diagnosis. Using a sample of 1236 patients and 118 predictor variables, they identified 20 important variables using mutual information score. Comparing the performance of 11 machine learning algorithms with cross-validation and statistical tests, logistic regression achieved high accuracy, with an area under the receiver operating characteristic curve of 0.850 for 1-year and 0.872 for 5-year survival prediction.

Reis et al.[15] explore the application of machine learning, particularly deep learning techniques, in the field of medical diagnosis, focusing on cancer detection using histopathology datasets. They employ various algorithms like graph theory, PSO, watershed, and random walker for nucleus segmentation in colorectal histology images. Additionally, they introduced the MedCLNet visual dataset, consisting of three datasets, for transfer learning purposes. Deep neural networks pretrained with the proposed transfer learning method are used for classification tasks with the colorectal histology MNIST dataset. Multiple deep learning algorithms, including DenseNet, Inception, and ResNet, are employed for transfer learning and classification. The results show significant improvements in accuracy after transfer learning, with the DenseNet169 model achieving 95.00% accuracy.

III. METHODOLOGY

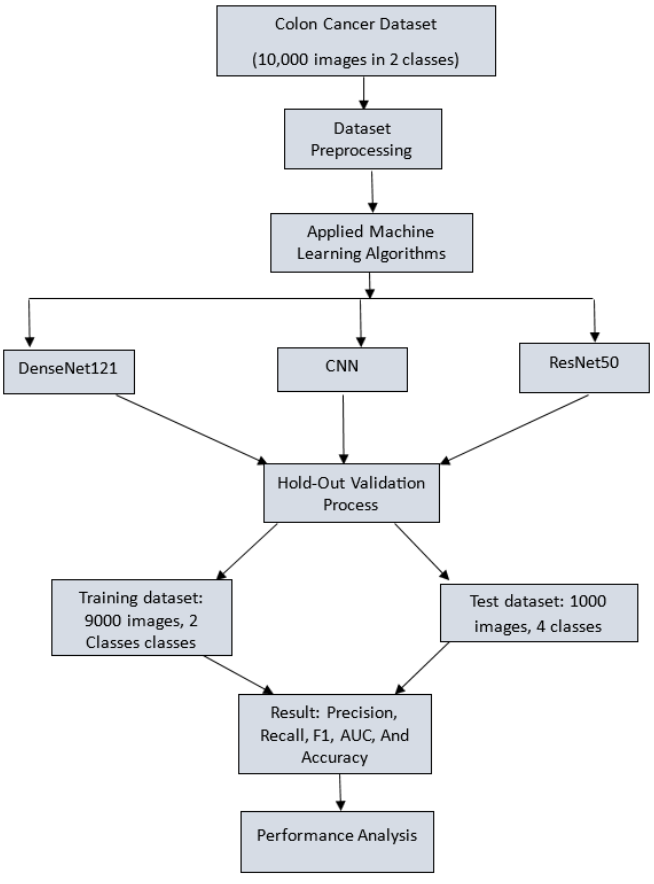

Fig. 1. Proposed model workflow of this research

This research was conducted utilizing systematic methodology to investigate the prediction of colon cancer through the application of machine learning approaches. A comprehensive dataset was compiled, encompassing clinical and genetic information of patients diagnosed with colon cancer. This dataset was sourced from various outlets, such as medical records, genomic databases, and publicly accessible repositories. The dataset was preprocessed through the elimination of missing or irrelevant data, and feature engineering techniques were employed to extract meaningful features for subsequent analysis. Subsequently, the dataset was partitioned into distinct training and testing sets to assess the efficacy of our models.

In the prediction task, three contemporary machine learning algorithms were employed: DenseNet121 [17], CNN [18], and ResNet50 [19]. The aforementioned algorithms have demonstrated favorable outcomes in tasks related to image classification, and we have modified them to accommodate our specific dataset. The pre-trained models were fine-tuned using our dataset, capitalizing on the robust convolutional neural network architectures they possess. This facilitated the capture of intricate patterns and features derived from the clinical and genetic data, thereby enabling precise prognostication of colon cancer. Figure 1 shows the working methodology of this research.

A. Dataset Collection and Preparation

In this research, we obtained a dataset called "Colon Cancer Histopathological Images" from the Kaggle [20] online platform, which served as the primary source of our data. This dataset comprises a collection of 10,000 colonoscopy images, each annotated and categorized into two distinct classes: cancerous and non-cancerous (normal) cases. The images were captured using various medical imaging techniques and encompass a wide range of pathological characteristics related to colon cancer. To ensure the reliability and generalizability of our models, we performed careful data partitioning. Specifically, we divided the dataset into a training set and a test set. The training set consisted of 9,000 images, which were used to train our models on a diverse range of colon cancer patterns and characteristics. The remaining 1,000 images were set aside as the test set, allowing us to evaluate the performance of our models on unseen data.

B. Data Augmentation & Pre-Processing

To enhance the training data and improve the model's ability to generalize, we apply data augmentation techniques. These techniques involve operations such as rotation, zooming, shifting, and flipping on the training set, and these techniques help to pre-process the data [21]. We utilize the ImageDataGenerator [22] class in Keras to implement these augmentations effectively. We conducted thorough data preparation steps. This included preprocessing and augmentation techniques to enhance the quality and diversity of our dataset. We applied image preprocessing techniques such as resizing, normalization, and grayscale conversion to ensure consistency across the images.

C. Working Procedure

Our selected base model for this research is DenseNet-121, a deep convolutional neural network that has been pre-trained on the ImageNet dataset. By leveraging the powerful feature extraction capabilities of DenseNet-121, we can benefit from its ability to capture intricate patterns and features in images. To adapt the pre-trained model for our specific task of colon cancer prediction, we loaded the pre-trained weights into the base model and then replaced the top layers, which are responsible for classification, with custom classification layers tailored to our problem. To enhance the model's predictive capacity, we added additional layers on top of the base model. These layers include a global average

pooling layer, which consolidates the extracted features into a fixed-length vector, a fully connected layer with ReLU [23] ,[26] activation to facilitate non-linear transformations, and a dropout layer to prevent overfitting by randomly disabling a portion of the neurons during training. By incorporating these additional layers, we aimed to further improve the discriminative power of the model and enhance its ability to generalize to unseen colonoscopy images. To optimize the model's performance, we froze the weights of the pre-trained base model during training. This helps prevent the model from excessively adapting to the training data and overfitting, thus promoting better generalization on unseen data. The model was compiled using the Adam optimizer [24], which is well-suited for training deep neural networks, and the categorical cross-entropy loss function, suitable for multi-class classification tasks. The training process involved utilizing the fit method, where we fed the training generator, which generates batches of augmented images and their corresponding labels, as input to the model. By training the model using mini batches, we effectively optimized the model's weights and biases iteratively, gradually improving its predictive performance. We typically trained the model for 10 epochs, but the number of epochs can be adjusted based on the model's convergence and performance on the validation set. Regular monitoring of the validation metrics allowed us to determine the optimal stopping point, ensuring the model achieved the best trade-off between training performance and generalization capability.

IV. Result & Discussion

A. Evaluation Process

After training, we evaluate the model's performance on the test set. This evaluation includes computing the test accuracy as a metric to assess the model's effectiveness in detecting colon cancer. To gain a deeper understanding of the model's performance, we conduct a comprehensive performance analysis. This includes generating a classification report, confusion matrix, ROC curves, and AUC scores. The classification report provides detailed metrics such as precision, recall, and F1-score for each class [25]. The confusion matrix visually represents the model's performance in terms of true positive, true negative, false positive, and false negative predictions. ROC curves and AUC scores help evaluate the model's sensitivity and specificity for each class. To validate the effectiveness of our proposed approach, we compare its performance with other state-of-the-art models or methods for colon cancer classification. This comparison involves utilizing appropriate statistical tests or performance metrics to assess and compare the performance of different models. We perform sensitivity analysis to examine the model's robustness to variations in hyperparameters. By training and evaluating the model with different hyperparameter settings, such as batch size, learning rate, and dropout rate, we assess the impact of these variations on the model's performance.

B. Result

In our evaluation of machine learning models, we utilized accuracy, F1 score, precision, and recall as performance metrics to assess their effectiveness. Table II below presents a comparison of different models based on their performance. Upon analyzing the results, it became evident that the DenseNet121 model demonstrated superior performance, particularly in the Colon adenocarcinoma class. This model achieved an accuracy of 99.60%, indicating its ability to make accurate predictions. The precision score for this model in the adenocarcinoma class was 42.00%, reflecting the proportion of correctly identified positive cases. The recall score, measuring the model's ability to identify true positives, reached 84.00%. Additionally, the F1-score, which considers both precision and recall, stood at 56.00%.

Similarly, the CNN model also showed better performance in the adenocarcinoma class compared to other classes. However, its overall performance was inferior to DenseNet121. The CNN model achieved an accuracy of 87.00%, indicating moderate predictive capability. The precision score for the adenocarcinoma class was 94.00%, while the recall score reached 30.00%. The F1-score for this model in the adenocarcinoma class was 37.00%. Regarding the ResNet50 model, it also demonstrated relatively better performance in the adenocarcinoma class, although with the lowest test accuracy among the three models at 80.24%. The precision score for adenocarcinoma was 50.00%, and the recall score reached 43.00%. The F1-score for the ResNet50 model in the adenocarcinoma class was 46.00%.

TABLE II. COMPARATIVE ANALYSIS OF THREE MACHINE LEARNING TECHNIQUES

Model	*Class Name*	*Precision*	*Recall*	*F1-Score*	*AUC*
Dense Net-121	Colon adenocarcinoma	0.42	0.84	0.56	0.9960
	Colon normal	0.25	0.04	0.07	
CNN	Colon adenocarcinoma	0.49	0.30	0.37	0.87
	Colon normal	0.49	0.69	0.57	
ResNet 50	Colon adenocarcinoma	0.50	0.43	0.46	0.8024
	Colon normal	0.50	0.57	0.53	

In summary, our findings indicate that the DenseNet121 model outperformed the others in terms of overall accuracy and F1-score for classifying different types of colon cancer Table 2. However, both the CNN and ResNet50 models exhibited promising results specifically for classifying adenocarcinoma, the most prevalent type of colon cancer. These outcomes have significant implications for the development of accurate and reliable machine learning models for colon cancer diagnosis, potentially leading to improved patient outcomes.

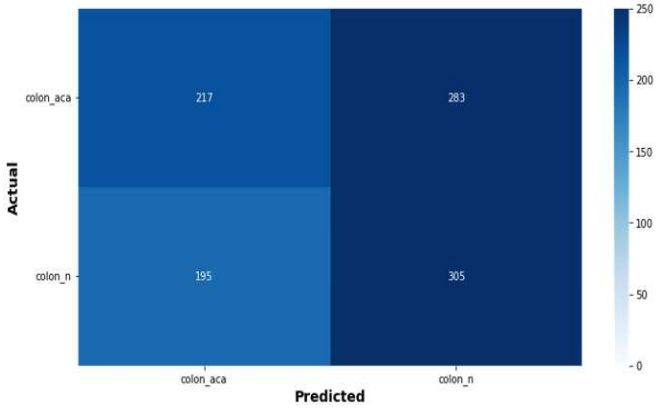

Fig. 2. Confusion Matrix of DenseNet-121

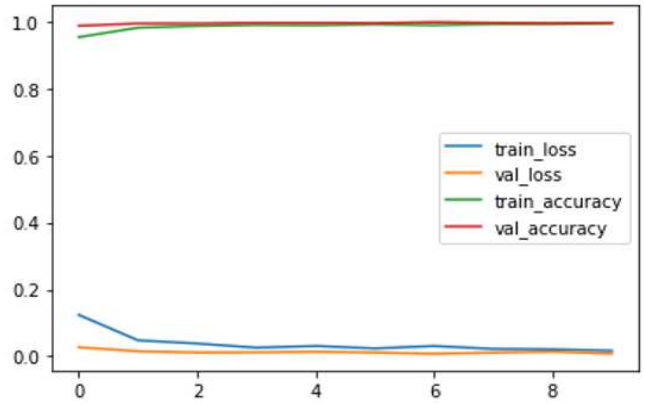

Fig. 3. ROC graph of DenseNet-121

Figures 2 and 3 show the Confusion Matrix and ROC curve of DenseNet-121.

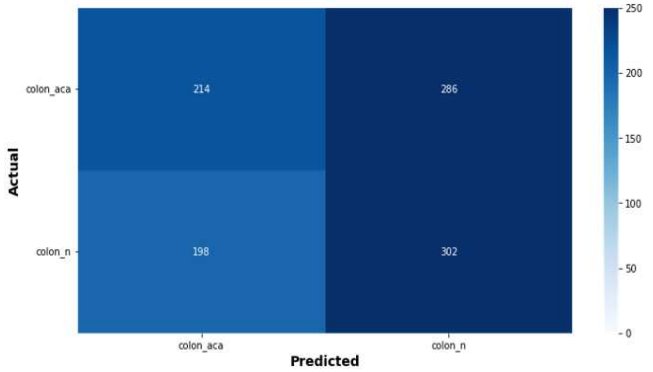

Fig. 4. Confusion Matrix of CNN

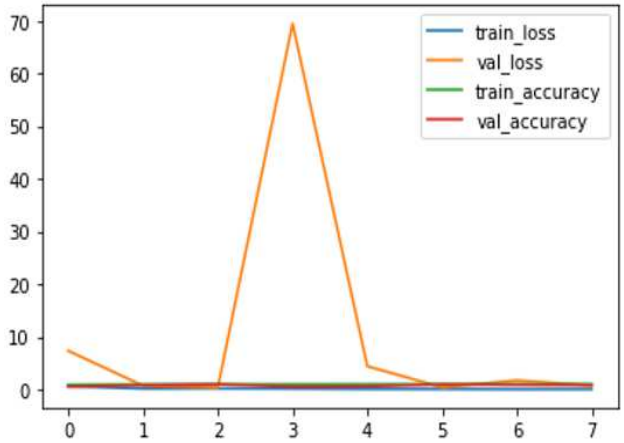

Fig. 5. ROC graph of CNN

Here, Figures 4 and 5 show the Confusion Matrix and ROC curve of the CNN model.

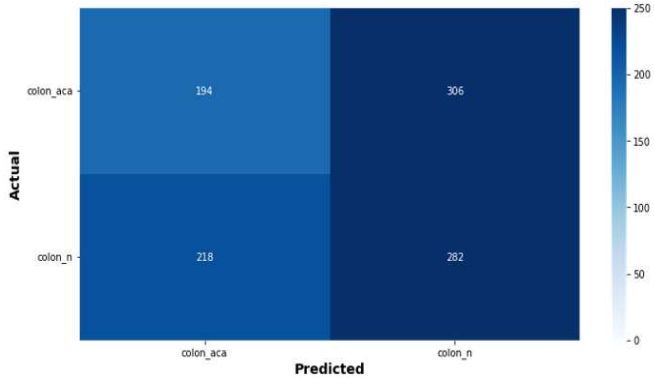

Fig. 6. Confusion Matrix of ResNet50

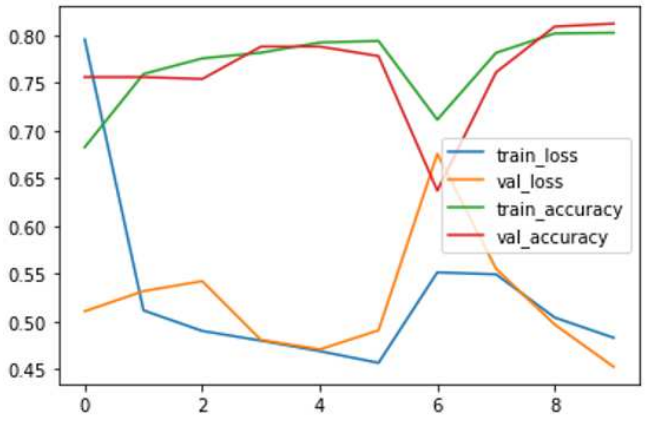

Fig. 7. ROC graph of ResNet50

Figures 6 and 7 show the Confusion Matrix and ROC curve of ResNet50.

V. Conclusions and Future Work

In conclusion, our study presents a machine learning model that shows promise in accurately predicting colon cancer in patients. By leveraging various demographic, clinical, and laboratory characteristics, these models can effectively identify individuals at risk of developing cancer, enabling early intervention and appropriate treatment. However, it is important to acknowledge the limitations of our study and address them in future research endeavors. The performance of our models should be validated using larger and more diverse datasets, encompassing populations from different geographical regions and diverse ethnic groups. This will help ensure the generalizability and robustness of the models across various populations. Transparency in the feature selection process is crucial. Future studies should focus on establishing clear and objective criteria for selecting features to minimize potential biases and enhance model interpretability.

Furthermore, exploring alternative machine learning techniques, such as deep learning, could potentially improve the accuracy and reliability of the models. Deep learning approaches have shown great potential in medical image analysis and could be leveraged to further enhance the performance of our models. Additionally, the implementation of these models in clinical practice requires careful consideration of ethical and legal aspects. It is essential to address issues related to fairness, transparency, and accountability to ensure the responsible and ethical use of algorithmic decision-making in healthcare. Involving all relevant stakeholders, including patients, physicians, and policymakers, is crucial in developing guidelines and protocols that govern the use of these models. Lastly, future research should focus on overcoming the challenges associated with the integration of machine learning models into clinical workflows. The development and validation of accurate and efficient machine learning models for colon cancer prediction holds great potential for improving healthcare services. However, addressing the limitations and challenges through further research and collaboration is vital to harness the full benefits of these models.

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